

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 21:07:17 : Search time 470 Seconds
(without alignments)
9039.902 Million cell updates/sec

Title: US-09-724-584-2

Perfect score: 9626

Sequence: 1 gattccggagcgcgtagg.....ttaaaaaaacgagattc 9626

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620.4	6.4	8257	4 US-09-595-684B-30	Sequence 30, Appl
2	620.4	6.4	8503	4 US-09-620-112D-130	Sequence 130, App
3	147.4	1.5	3837	4 US-09-724-517-1	Sequence 1, Appl
4	147.4	1.5	3837	4 US-09-641-807A-1	Sequence 1, Appl
5	147.4	1.5	3837	4 US-09-723-096-1	Sequence 1, Appl
6	140	1.5	1023	4 US-09-724-517-3	Sequence 3, Appl
7	140	1.5	1023	4 US-09-641-807A-3	Sequence 3, Appl
8	140	1.5	1023	4 US-09-723-096-3	Sequence 3, Appl
9	135.2	1.4	1421	4 US-09-592-054-5	Sequence 5, Appl
10	135.2	1.4	1421	4 US-09-592-054-3	Sequence 5, Appl
11	133.6	1.4	4348	4 US-09-595-684B-22	Sequence 22, Appl
12	127.2	1.2	4127	4 US-09-592-054-7	Sequence 7, Appl
13	116	1.2	4308	4 US-09-592-054-1	Sequence 1, Appl
14	98	1.0	1011	4 US-09-641-806-3	Sequence 3, Appl
15	98	1.0	1011	4 US-09-723-129-3	Sequence 3, Appl
16	98	1.0	1011	4 US-09-722-862-3	Sequence 3, Appl
17	98	1.0	1026	4 US-09-641-806-1	Sequence 1, Appl
18	98	1.0	1026	4 US-09-723-129-1	Sequence 1, Appl
19	98	1.0	1026	4 US-09-722-862-1	Sequence 1, Appl
20	95.8	1.0	1542	4 US-09-724-519-5	Sequence 5, Appl
21	95.8	1.0	1542	4 US-09-592-037-5	Sequence 5, Appl
22	95.8	1.0	1728	4 US-09-724-519-7	Sequence 7, Appl
23	95.8	1.0	1728	4 US-09-592-037-7	Sequence 7, Appl
24	95.8	1.0	3741	3 US-09-541-782-9	Sequence 9, Appl
25	95.8	1.0	3741	3 US-09-723-820-9	Sequence 9, Appl
26	95.8	1.0	3741	4 US-09-627-122-20	Sequence 20, Appl
27	95.8	1.0	3741	4 US-09-220-132-23	Sequence 23, Appl

28	95.8	1.0	4858	4 US-09-595-684B-28	Sequence 28, Appl
29	90	0.9	29793	4 US-09-302-812-38	Sequence 38, Appl
30	90	0.9	29793	4 US-09-511-477-38	Sequence 38, Appl
31	90	0.9	29793	4 US-09-511-507-38	Sequence 38, Appl
32	88	0.9	5093	2 US-08-468-036-23	Sequence 23, Appl
33	88	0.9	5093	2 US-08-468-036-23	Sequence 23, Appl
34	86.2	0.9	1107	4 US-09-724-519-9	Sequence 9, Appl
35	86.2	0.9	1107	4 US-09-592-037-9	Sequence 9, Appl
36	85.2	0.9	7218	1 US-08-332-463-14	Sequence 14, Appl
37	82.8	0.9	1077	4 US-09-722-139-3	Sequence 3, Appl
38	82.8	0.9	1077	4 US-09-721-832-3	Sequence 3, Appl
39	82.8	0.9	1077	4 US-09-721-689-3	Sequence 3, Appl
40	82.8	0.9	4176	4 US-09-722-139-1	Sequence 1, Appl
41	82.8	0.9	4176	4 US-09-721-832-1	Sequence 1, Appl
42	82.8	0.9	4176	4 US-09-721-689-1	Sequence 1, Appl
43	82	0.9	1230	4 US-09-572-191-5	Sequence 5, Appl
44	82	0.9	1230	4 US-09-723-262-5	Sequence 5, Appl
45	82	0.9	1230	4 US-09-723-219-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-595-684B-30

Sequence 30, Application US/09595684B

Patent No. 6544766

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

APPLICANT: Ohashi, Cara

APPLICANT: Sakowicz, Roman

APPLICANT: Valsberg, Eugeni

APPLICANT: Wood, Kenneth

APPLICANT: Yu, Ming

TITLE OF INVENTION: Human kinases and methods of producing

FILE REFERENCE: cytop036

CURRENT APPLICATION NUMBER: US/09/595,684B

PRIOR FILING DATE: 2002-06-24

PRIOR APPLICATION NUMBER: 09/295,612

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30

LENGTH: 8257

TYPE: DNA

ORGANISM: Human

US-09-595-684B-30

Query Match

Best Local Similarity 65.5%; Pred. No. 2,2e+143;

Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;

69	GCGCCAAAGGACTTAAGTACAGAGACAGGAGCGGTGCGTACCGATTCTTCAC	128
17	GCGGCTTGAGAGCCCTGMAATGCCGCCGAGAGGCTCTGCGCATTTTGTTGGACAG	76
129	TAATCGGTCTCAAAATGTCGAGAGATGCACTTAAGTGTGTGAGGCTTGCGCCG	188
77	TTGAGCTGATAGAGGCGAGAGAGAGCGCTGCGCTGCGTGTGCGAGTCCGCGCG	136
189	TTTATACAGAGACAA-----GGGATCAACCCCACTCGAATGGAAAGCTGGAAACA	242
137	TGAACAGCAGAGAGATGACCTTGAGAACTGCCCAAGTTTACTGAAACCTGACATA	196
243	ACACATTTCCCAAGTTGATGGACAAAGCTTTCAATTTCGATCTGTATTTATTTCTC	302
197	ATGTCATTATCAAGTTGATGAGAAATCTTCAATTGATCTGTCTTTCAATGCTA	256
303	ACCAATCAACAACTCAATTTTACCAAGAAATAGACAGTACATACATGATGCTTTGC	362
257	ATGAACCTACCAAAATGTGTATGAGAAATAGACACCAATCATCATGATTCGCATAC	316

QY	363	AGGCAATATA	TG	CA	CAATTTT	GC	AT	GC	GA	CA	GC	CA	AT	CT	TG	AG	CA	CA	GC	TA	CA	CA	422				
Db	317	AAGCTACAT	TG	TA	CTT	AT	TT	GG	CT	AT	TG	CA	CA	GC	TA	CA	CA	GC	TA	CA	CA	376					
QY	423	TGATGGAA	CA	CCAA	TT	CA	TT	GG	GA	TAA	TAC	CC	CA	AG	CA	TAC	AG	AA	GT	TTTT	AAAA	482					
Db	377	TGATGGTT	CA	GA	AG	TA	CA	TT	GG	AG	TAA	TAC	CC	CA	AG	CA	TAC	AG	AA	GT	TTTT	436					
QY	483	TTATTAGG	AA	TAC	CG	AA	CAG	GA	CT	TT	CT	T	A	G	AT	TT	CT	T	A	T	G	GA	542				
Db	437	AAATTAGA	AG	TT	CT	CT	GA	TG	GG	AA	TT	CT	CT	A	G	AT	TT	CT	T	A	T	G	GA	496			
QY	543	ATGAAA	CT	GT	GA	AA	GA	CT	TA	CT	GT	GA	TG	AC	GA	GA	AA	GA	AA	GA	AA	GA	602				
Db	497	ATGAAA	CC	AT	T	CA	GA	TT	TA	CT	CT	GT	GG	CA	CT	CA	AAAA	T	G	AA	CC	TT	TA	556			
QY	603	AGGATTTT	TA	T	A	T	A	GA	AA	C	GT	AT	GT	TT	GC	T	GA	C	T	T	A	GA	662				
Db	557	AAGATGT	CA	AT	AG	AA	T	GT	TA	GT	GT	CT	GA	T	CT	CA	GA	GA	AA	GT	TA	T	TA	616			
QY	663	AA	CAT	TA	T	A	T	A	C	AG	T	CA	AAAA	AG	GT	GA	AAAA	AA	CA	GA	CA	TT	T	GA	722		
Db	617	AA	T	GG	CT	TT	GA	AA	T	T	GA	TT	CA	AA	GG	GA	AAAA	AA	GG	CA	GC	TT	T	GA	676		
QY	723	TGA	AT	GA	T	CA	T	AG	T	AG	T	CT	TA	CA	T	A	CA	T	A	T	T	A	GA	782			
Db	677	TGA	AT	CA	T	AA	CA	AA	GA	CA	GT	CT	TA	CA	CA	CA	CT	TT	T	A	GA	T	T	GA	736		
QY	783	GAA	AT	AT	CC	CA	CA	AA	TT	CA	GA	AA	CT	GT	GA	TG	AG	AG	CT	GA	CT	GA	CT	GA	842		
Db	737	AAG	GT	CA	CT	CT	TA	T	-----	T	G	AA	AG	AT	CT	TT	A	AG	AT	CC	TT	T	GA	787			
QY	843	TG	T	AG	AT	CT	T	CT	GG	CA	T	GA	AA	GA	CA	AG	CA	AA	CT	GA	AG	CT	GA	CT	902		
Db	788	TG	T	AG	AT	CT	T	CA	GG	CA	T	GA	AA	GA	CA	AG	CT	GA	AG	CT	GA	AG	CT	GA	847		
QY	903	AG	AA	AG	GC	T	CA	AT	CA	A	CC	GA	CT	T	T	A	T	CT	T	GA	CA	AG	T	T	A	962	
Db	848	AG	AA	AG	GC	T	CA	AT	CA	A	CC	GA	CT	T	T	A	T	CT	T	GA	CA	AG	T	T	A	907	
QY	963	G	C	A	G	G	C	C	A	G	C	T	G	G	A	T	T	T	A	A	A	C	T	A	C	A	1022
Db	908	G	T	A	T	GA	T	GA	CA	A	T	T	G	T	T	C	A	T	A	A	T	A	T	A	T	A	967
QY	1023	AAA	AT	T	C	A	T	T	G	G	A	AA	T	G	C	T	A	A	A	A	A	A	A	A	A	A	1082
Db	968	AAA	AT	T	C	A	T	T	G	G	A	AA	T	G	C	T	A	A	A	A	A	A	A	A	A	A	1027
QY	1083	T	T	GA	T	GA	G	A	C	T	T	A	C	A	T	T	C	A	T	T	G	C	A	A	T	T	1142
Db	1028	T	T	GA	T	GA	A	C	T	T	A	C	A	T	T	C	A	T	T	G	C	A	A	T	T	T	1087
QY	1143	C	C	A	T	T	A																				

Db 1382 TGAAGAA-----CTCAACTATGAGATCTCAATTTAATATATCCAAACAAATATAA 1429
 Qy 1500 GCAAGAAAGCCAAAGTTCTGCACATGCCCTTCAITTCAGAAATGATGACTCTGTTTGA 1559
 Db 1430 CAAACAAAACACATAAAGCTTTCTATTAATTTATTAACAGAAATGATGATCTGTCTGT 1489
 Qy 1560 CAGAGTTTCTGATTTTGATGAGGCCCT 1587
 Db 1490 CAGAGTCTGATGTTTTCAGTAAACCTCT 1517

RESULT 2

```

US-09-620-312D-130
Sequence 130. Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghaast
APPLICANT: Dmanac, Radcoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: Polypeptides
FILE REFERENCE: 784C1P28
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc FL-gene Version 1.0
SEQ ID NO 130
LENGTH: 8503
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (91)..(8082)
US-09-620-312D-130

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	Query Match	Score	620.4	DB 4	Length	8503
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QY	69	GGCCGCAAAAGGACCTAAAGTCACAGACAGAGGACGGTGGTACCGATTTCTCCAC	128			
Db	17	GGCGCGCTGAGCCCTGAAAGTGC CGGCGCGAGAGGCTGGCCATTTTGGTGGACG	76			
QY	123	TAAATGGGTCTCAAAATGTCGAGGGAGATCACTTAAATGTGTGTGAGAGTTCCGCCG	188			
Db	77	TTCAACCTCGATAGGATGGCGGAGAAAGAACCTGTGCCGTGCGCAAGCGCGCG	136			
QY	189	TTATACAGAGAAACA-----GGGGATCAACCCAACTGCATATGAGAGCTGGAACA	242			
Db	137	TGAACAGAGAGGAAGAACTCACTTGGAAAACTCCCAATTTACTGGAAAATGACAAATA	196			
QY	243	ACACCACTTTCCCAAGTTGATGGACAAAGTCTTTCAATTTGCATGCTGATTTAAATTC	302			
Db	197	ATGTCATTTATCAAGTTGATGGAAGTAAATCTTCAATTTTATCGTGTCTTCAATGTA	256			

QY 303 AGCAATCAACAAGTCAAAATTACCAAGAAATAGCAGTACCTATCATGATCAGCTTGC 362
 DB 257 ATGAACTACCAAAATGTGTATGAAAGAAATAGCAGACCAATATGATTCGCCATC 316
 QY 363 AGGATATATAATGGCACAATATTTGCATACGACAGACATCTTCAGGCAAGCGTACAA 422
 DB 317 AAGCTACAAATGGTACTATATTTGCCATATGAGACGATCGCTTCAGGAAAAACATATCA 376
 QY 423 TGTGGGACACCAAAATTCATTGGGCATTAATCCCAAGCCATACAGAAATTTTAAA 482
 DB 377 TGTGGGTTCCAGAAATCATTTGGGAGTTATCCCAAGGCAATTCAGAAATTTTCCAA 436
 QY 483 TTATGAGGATACCGAAGAGAGTTCCTCAAGATTTCTTATATGAGATTACA 542
 DB 437 AAATTAAGAAATTCCTGATAGGAAATTCCTTACCTGATCTTACATGAAATATACA 496
 QY 543 ATGAACTGTGAAGACCTACTGTGTATGACAGAAAGAAAGCCCTTGGAAATTCGCG 602
 DB 497 ATGAACTACCAAAATGTGTATGAAAGAAATAGCAGACCAATATGATTCGCCATC 556
 QY 603 AGGATTTTAAATAGAAACGTGTATGTTGCTGACCTGACGAAACCTTGTATGTTCTG 662
 DB 557 AAGATGCAATAGGAATGTATGTTGCTGATCTCAAGAAAGTTGTATATACATCAG 616
 QY 663 AATATGTAATACGATGATCAAAAAGGTTAAAAAAGGACATTAATGAGACTTAAA 722
 DB 617 AAATGCTTTGAAATGATTAACAAAGGAGAAAGACAGGACCTTATGAGAAACAAAA 676
 QY 723 TGAATGATCATAGTATGCTTACATCATATATTTAATGATTTGTTGAAGCCGAGACA 782
 DB 677 TGAATCAAGAAAGACGTCGTTCTCATACATCTTTAGGATGATTTTGAAGACAGAGA 736
 QY 783 GAAATGATCCCAAAATTCAGAGAACTGTATGAGAGCTGTATGATCTCACTGTAAT 842
 DB 737 AGGATGAACCTTCTAAT-----TGTGAAGATCTGTTAAGTATCCCATTTGAAT 787
 QY 843 TGTGATATCTTCTGCTGGAGTGAAGAGCAAGCCAACTGAGCTGAAGGTGTGACTTA 902
 DB 788 TGGTTATCTTGGACGAGTGAAGAAAGACCTCTCAAAAGCGCTGACGGGTGCGGTCA 847
 QY 903 AGGAGGCTGCAATCATCAACGCGAGCTTGTATTCCTGAGCAGGTATTAAGAGCTTA 962
 DB 848 AGGAGGCTGTAATATTAATCGAAGCTTATTTTGGACAGATGATCAAGAACTTA 907
 QY 963 GCGACGCGCAGGCTGTGATTTTATTAATCAAGACAGCAAACTCCACAGAAATTC 1022
 DB 908 GTGATGAGCAAGTTGGTGTTCATTAATATGAGATAGCAAGTTAACAGAAATCTTC 967
 QY 1023 AAAATTCATTGGAGAGAAATGCTAAACGGTTATTAATTTGCAACAATTAAGCCAGTTCT 1082
 DB 968 AGAATTCCTTGGAGAGAAATCCAAAGACAGTATTAATCTGACAAATTAATCCAGTATCT 1027
 QY 1083 TTGATAGACTCTAAGTACACTTCAGTTTGCAGTACTGCGCAAACTGATAGAAATCTC 1142
 DB 1028 TTGATGAATCTTACTGCTCCAGTTTGCAGTACTGCTAAATATATGAAGAAATCTC 1087
 QY 1143 CCCATTTAATGAGTCTCTGATGATGAAGCGTTGCTAAAGGTAAGGAAAGAAATCT 1202
 DB 1088 CTTATGTTAATGAGTATCAACTGATGAAGCTCTCCGAAAGGTAATGAAGAAATTA 1147
 QY 1203 TGGATTTAAGAAACAATTAGAGAAATTTAGAGTATGCTGTGAAACAAAGCTCAAGCA 1262
 DB 1148 TGGATCTTAAGAAACAATTAGAG-----GAGGTTCTTATAGAGACGCGGCTCAGGCA 1201
 QY 1263 TGGCTAAGAGAGCAATACAGTGTGCTAGTGAATCAACAACAATTAAGAGAGAG 1322
 DB 1202 TGGAAAAAGCAATGGCCCACTTTTGAAGAAAAAAGATTTGCTTCAAAAGTACAGA 1261
 QY 1323 AAGATGAATATGAGCTTGACAAATATTTGTTG---CTTCATCCCAAGAAATCTCAAC 1379
 DB 1262 ATGAGAAAAATTGAAACTTAACAGATGCTGTGAGACTTCTTCTCCCTACAGTTGCAAC 1321

QY 1380 AGGACCAAAAGGTCAAAACGAAACGAAAGTTACTGTGGGCCGACGAAAAATCCAAATA 1439
 DB 1322 AGGAATTTAAAGCTTAAAGAAAGAAAGTTACTGTGGGCCGACGAAAAATTAACAAA 1381
 QY 1440 GTTTACATGCTTCTGTGTTTCTGACTTTGATATGCTATTCAGATTAATCTGGCAATTTTA 1499
 DB 1382 TGAAGAA-----CTCAAACTATGCAATCAATTAATATACCAAAATATATA 1429
 QY 1500 GCAAGAAAGCAAGTTCTGCAATGCTTCATTTCCAGAAATGATGATCTGTTGTA 1559
 DB 1430 CAACAAAAACATTAAGCTTTCTATTAATTTATTAACGAGAAATTAAGAAATCTGCTGT 1489
 QY 1560 CAGAGTTTCTGATTTTGAATGAGCCCT 1587
 DB 1490 CAGAGTCTGATGTTTTCAGTACACTCT 1517

RESULT 3
 US-09-724-517-1
 ; Sequence 1, Application US/09724517
 ; Patent No. 6379941
 ; GENERAL INFORMATION:
 ; APPLICANT: Berard, Christophe
 ; APPLICANT: Freedman, Richard
 ; TITLE OF INVENTION: No. 6379941el motor proteins and methods for
 ; TITLE OF INVENTION: their use
 ; FILE REFERENCE: 1031
 ; CURRENT APPLICATION NUMBER: US/09/724, 517
 ; CURRENT FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: US/09/641, 807
 ; PRIOR FILING DATE: 2000-08-17
 ; NUMBER OF SEQ. ID NOS.: 4
 ; SOFTWARE: PatsSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3837
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1226) ... (1337)
 ; OTHER INFORMATION: n = a, c, c, or g
 US-09-724-517-1

Query Match 1.5%; Score 147.4; DB 4; Length 3837;
 Best Local Similarity 51.3%; Pctd. No. 2, 2e-26;
 Matches 467; Conservative 0; Mismatches 411; Indels 33; Gaps 4;

QY 275 TTCAATTTGATGCTGTATTTAATTCACGAATCAACAGTCAAAATTTTCAAGAAATA 334
 DB 136 TTCACTTTGATTTTGTGTTTGGCAAAATTCACATCAAGATGAAGTTTATTAACACATGT 195
 QY 335 GCAGTACTATCATACATGATGCTTTCAGAGGATATATATGCAAAATTTTGCATACGA 394
 DB 196 ATTAAGCCCTAGTGTGTACATCATTAAGGCTATTAATGCAACGTGTTTGTCTATGGA 255
 QY 395 CAGACATCTTCAGCAAGACGTACACAAATGATGGAACACCAAAATTCATT----- 444
 DB 256 CAAACTGATCTGTGGAAGACATACCAATTTGAGGGGCGCATTTCTTCAGTTGTGAG 315
 QY 445 -----GGGCAATAATACCCCAAGCATACAGAGATTTTAAATTAATTCAGAGATA 496
 DB 316 GGCAAAAGGATATCAATTCCTGAGCTATTCAGAAATTTTCAAGCAATCTGTGACAT 375
 QY 497 CCGAAGAGAGTTCTTCTTAAGAGTTCTTATATGAGATTTTACATGAACTGTGAA 556
 DB 376 CTTAGATTTGATCTTAAATGTAAGATATCTTATATGAAGTGAAGAGAGCTTAAGA 435
 QY 557 GACCTACTGTGTATGACAGAAAGAAAGCCCTTGAATTCGAGAGATTTTAAATAGA 616
 DB 436 GATCTTCTGAATTTGAGACATCATGAAGAGATCTTCATACCGAAGATGAAGAAAGGA 495
 QY 617 AAGCTGATGTTGCTGACCTGACGATGAAGAACTTGTATATGTTCTTGAACATGTAATACAG 676

Db 496 AACACAGTGTATGTTGGGCGCAAGAAATGCCATGTGGAGATGAGTGAATGATGAT 555
Qy 677 TGGATCAAAAAGGTGAAAAAAGAGCATTAATGAGAGCTAAATGATGATGAT 736
Db 556 CTTTGGAGATGGGGAATGAGCGAGCATATGAGTACCAATGAAATGAGCACTCC 615
Qy 737 AGTGTTCACATCAATATTTAGAAATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
Db 616 AGCAGATCAGATCAATTTTACATCAGATTTGCAATGATTAATAAATATGAGAGCA 675
Qy 791 CCCAACAATTCAGAGAACTGTGATGAGCTGTGATGATCTCACTTTGAAATTTGATGAT 850
Db 676 GCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
Qy 851 CTGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
Db 736 TTGGCAGGATCAAAAAGATGACCAAAACGGGGAATATGATGAAACGGTTCAAAAGATCC 795
Qy 911 TGCACATCAACCGAGCTGTTTATCTTGAACAGGTTATTAAGAACTTTAGCGAG-- 968
Db 796 ATTCAAATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 855
Qy 969 -GCCAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1027
Db 856 CCGAGGAAGATTCACATATTCATATGAGGATGCTAAATTTACCGGCTTCTGAAAGAT 915
Qy 1028 TCATTGGGAGAAATGCTAAACGGTTATTAATTTGCAATTTAGCGCAGTTTCT--T 1081
Db 916 TCTCTGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 975
Qy 1082 TTTGATGAGATCTTAAGTACATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1141
Db 976 TTTGATGAGTCTTAATTTCTTCAATATGCGCAACGAGCAAGCAATTAGAAACAA 1035
Qy 1142 CCCCATGTTAA 1152
Db 1036 CCCACTGTAAA 1046

RESULT 4
US-09-641-807A-1
; Sequence 1, Application US/09641807A
; Patent No. 6440731
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6440731el motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/641,807A
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3837
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1226) ... (1336)
; OTHER INFORMATION: n = a, t, c, or g
US-09-641-807A-1

Query Match 1.5%; Score 147.4; DB 4; Length 3837;
Best Local Similarity 51.3%; Pired. No. 2,2e-26;
Matches 467; Conservative 0; Mismatches 411; Indels 33; Gaps 4;

Qy 275 TTTCAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 334
Db 136 TTTCAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 195
Qy 335 GCAGTACTATCATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 394

Db 196 ATAAAGCCCCAGTGTGTTGCTACTCATTTGAGGCGTATTAATGCACTGTTTTCCTATGGA 255
Qy 395 CAGACATCTTCAGGCAAGCGTACCAATGATGGGAACCAATTCATT----- 444
Db 256 CAAACTGATCTGGGAGACATACCATTTGAGGGGCGCATATTTGCTTCAAGTTGGAG 315
Qy 445 -----GGGCAATATACCCCAAGCCATACAGAAATTTTAAATTTATGAGAGATA 496
Db 316 GGCCAAAAGGATATCATTTCTGAGTATTTCAAGAAATTTTCAAAAGCATCTGAAACAT 375
Qy 497 CCGAACAGAGATTTCTTTAAGATTTTATTAATGAGATTTTACATATAAATCTGAAA 556
Db 376 CTTAGCATTTGATTTATTTAATGATTTTATTAAGATTTTATTAAGATTTTATTAAG 435
Qy 557 GACCTATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 616
Db 436 GATCTTTTAAATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 495
Qy 617 AACGTGTATGTTGCTGACCTGACCTGAGAACTTTGATGATGATGATGATGATGAT 676
Db 496 AACACAGTATTTGTTGGGCGCAAGGAATGCCATGTGGAGATGAGTGAATGATGAT 555
Qy 677 TGGATCAAAAAGGTGAAAAAAGACATTTATGAGAGATTAATAATGATGATGAT 736
Db 556 CTTTGGAGATGGGGAATGACCGACATACAGGATACCAATCAATGATGATGATGAT 615
Qy 737 AGTGTTCATATCAATATTTAGATGATGATGATGATGATGATGATGATGATGATGAT 790
Db 616 ACAGATGATCAATGATTTTCAATGATGATGATGATGATGATGATGATGATGATGAT 675
Qy 791 CCCAACAATTCAGAGAACTGTGATGATGATGATGATGATGATGATGATGATGATGAT 850
Db 676 GCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 735
Qy 851 CTGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
Db 736 TTGGCAGGATCAGAAAGATGACCAAAACGGGGAATATCTGTGAAACGGTTCAAAAGATCC 795
Qy 911 TGCACATCAACCGAGCTGTTTATCTTGAACAGGTTATTAAGAACTTTAGCGAG-- 968
Db 796 ATTCAAATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 855
Qy 969 -GCCAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1027
Db 856 CCGAGGAAGATTCACATATTTCCATATGAGGATGCTAAATTTACCGGCTTCTGAAAGAT 915
Qy 1028 TCATTGGGAGAAATGCTAAACGGTTATTAATTTGCAATTTAGCGCAGTTTCT--T 1081
Db 916 TCTCTGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 975
Qy 1082 TTTGATGAGATCTTAAGTACATTTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1141
Db 976 TTTGATGAGTCTTAAATTTCTTCAATATGCGCAACGAGCAAGCAATTAGAAACAA 1035
Qy 1142 CCCCATGTTAA 1152
Db 1036 CCCACTGTAAA 1046

RESULT 5
US-09-723-096-1
; Sequence 1, Application US/09723096
; Patent No. 6448026
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6448026el motor proteins and methods for
; FILE REFERENCE: 1031
; CURRENT APPLICATION NUMBER: US/09/723,096
; CURRENT FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US/09/641,807
; PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 3837
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1228)...(1337)
 OTHER INFORMATION: n = a, t, c, or g
 US-09-723-096-1

Query Match 1.5%; Score 147.4; DB 4; Length 3837;
 Best Local Similarity 51.3%; Pred. No. 2.2e-26;
 Matches 467; Conservative 0; Mismatches 411; Indels 33; Gaps 4;

275 TTCATTTGCGATGCTGATTTAATTCACGAATCAACAAGTCAAAATTTACCAAGAATA 334
 136 TTCACCTTTGATTTGTTTGGCAAAAATTCACCTCAAGATGAAGTTTAAACACATGT 195
 335 GCAGTACCTATCATACGATCAGCTTGCAGGATATATGACACATATTTGCATACGGA 394
 196 ATAAACCCCTAGTGTGACCATGAGGCTATATGCAACTGTTTTGCCATGGA 255
 395 CAGACATCTTCAGGCAAGATGACAAATGATGGAACACCAATTCAT-----444
 256 CAAACTGATCTGGAGACATACCATTTGAGGGGCCATTTGCTTACGTTGTGAG 315
 445 -----GGGCATTAATCCCAAGCCATACAGAAATTTTAAATTTATTCAGAGATA 496
 316 GGCCTAAAGGATTCATCTCGAGCTATCAAGAAATATTTCAAGCATCTGGAACAT 375
 497 CCGAACAAGAGATTTCTTCTTAAGATTTCTTATATGAGATTTTCAATGAACCTGGA 556
 376 CTTAGATTTGATCTTATATGTAAGATCTTATATGAGATGTAAGAGACCTAAGA 435
 557 GACCTACTGTGATATACAGAAAGAACCCCTTGGAAATGCGAGATTTTAAATAGA 616
 436 GATCTTCTAGAAATGGAGACATCCATGAAGATCTTCACATCCGAGAAAGTGAAGAA 495
 617 AACGTATATGTTCTGACCTGACGTAAGAACTTGTATGTTCTGTAACATGTAATACAG 676
 496 AACACAGTATTTTGGGGCCAAAGAAATGCCATGTGAGAGTGCAGTGAAGTATGACT 555
 677 TGGATCAAAAAGGTTGAAAAAAGACATATATGAGAGACTAAATGATGATCACTACT 736
 556 CTTTGGAGATGGGAAATGACGACAGACATACAGATCACTCAATGATGAGACTCC 615
 737 AGTCCTTACATCATATTTTAAGATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
 616 AGCAGATCAATCAATTTTTCATCAATCAGATTTGTCAGATTTCAATTAAGATGAGGA 675
 791 CCCCAAAATTCAGAGAACTGTATGAGCTGTATGATCTCACTTGAATTTGTATAGAT 850
 676 GCTGAAGATGATCAATGATTTCCCTCGGCAATTTGTCTCAAGTTTCCATTTGTGAT 735
 851 CTTGCTGCGAGTAAAGAGACCAAACTGAGCTGAGAGTGTGAGACTTAAGAGAGGC 910
 736 TTGGCAGGATCAAGAAAGATTAACAAAAGGGAATCTGTGAACGGTTCAAAAGATCC 795
 911 TGCACATCAACCGCAGCTTTTATCTTGGACAGTTTATTAAGAGCTTACGAGC--968
 796 ATTCAATCAATGATGATTTGCTGCTTAAAGAAATGTAATGAAGCCTCTTGGGAGCCCA 855
 969 -GCCAGCTGCTGATTTTAACTTACAGAGACAGCAAACTCACGAATTTCTCAAAAT 1027
 856 CCGAGAAAGATTCATATTTCCATATAGGATGCTAAATTTACCCGGCTTCTGAAAGAT 915
 1028 TCATTTGGAGAAATCTAAACGTTATATTTGACCAATTAAGCCGCAAGTTT-----T 1081
 916 TCTCTGGAGGAGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 975
 1082 TTTGATGAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1141

Db 976 TTTGATGAGCTCTTAATTTCTCAATATATGCCAAGAGCAGCAACTTGAAGACAA 1035
 QY 1142 CCCCATGTTAA 1152
 Db 1036 CCCCATGTTAA 1046

RESULT 6
 US-09-724-517-3
 ; Sequence 3, Application US/09724517
 ; Patent No. 6379941
 ; GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Freedman, Richard
 ; TITLE OF INVENTION: No. 6379941el motor proteins and methods for
 ; FILE REFERENCE: 1031
 ; FILE REFERENCE: their use
 ; CURRENT APPLICATION NUMBER: US/09/724,517
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: US/09/641,807
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1023
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-724-517-3

Query Match 1.5%; Score 140; DB 4; Length 1023;
 Best Local Similarity 51.0%; Pred. No. 7.3e-25;
 Matches 456; Conservative 0; Mismatches 405; Indels 33; Gaps 4;

275 TTCATTTGCGATGCTGATTTAATTCACGAATCAACAAGTCAAAATTTACCAAGAATA 334
 130 TTCACCTTTGATTTGTTTGGCAAAAATTCACCTCAAGATGAAGTTTAAACACATGT 189
 335 GCAGTACCTATCATACGATCAGCTTGCAGGATATATGCAACATATTTGCATACGGA 394
 190 ATAAACCCCTAGTGTGACCATGAGGCTATATGCAACTGTTTTGCCATGGA 249
 395 CAGACATCTTCAGGCAAGATGACAAATGATGGAACCAAAATTCAT-----444
 250 CAAACTGATCTGGAGAACATACACATGAGAGGGGCCATATTTGCTGATGAG 309
 445 -----GGGCATTAATCCCAAGCCATACAGAAATTTTAAATTTATTCAGAGATA 496
 310 GGCCTAAAGGATTCATTTCTGAGCTATTCAGAAATTTTCAAGCATCTGGAACAT 369
 497 CCGAACAAGAGATTTCTTAAAGATTTCTTATATGAGATTTTAAATTTTCAATGAAC 556
 370 CTTAGATTTGATCTTATATGTAAGATCTTATATGAGATGTAAGAGAACTGTAAGA 429
 557 GACCTACTGTGATATACAGAAAGAACCCCTTGGAAATTCGAGATTTTAAATAGA 616
 430 GATCTTCTAGAAATGGAGATTCATGAAGATCTTCAATCCGAAATGAAAGAAAGGA 489
 617 AACGTATATGTTCTGACCTGACGTAAGAACTTGTATGTTCTGTAACATGTAATACAG 676
 490 AACACAGTATTTTGGGGCCAAAGAAATGCTATGAGAGTGCAGAGTGAAGTATGAT 549
 677 TGGATCAAAAAGGTTGAAAAAAGACATTTATGAGAGACTTAAATGAATGATCATAGT 736
 550 CTTTGGAGATGGGAAATGACGACAGACATACAGATCACTCAATGATGAGCACTCC 609
 737 AGTCCTTACATCAATATTTTAAGATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
 610 AGCAGATCAATGCAATTTTTCATCAATGACATTTTGTCAATTAATTAATATGAGGA 669
 791 CCCCAAAATTCAGAGAACTGTATGAGCTGTATGATGATGATGATGATGATGATGATGAT 850
 670 GCTGAAGATGATCAATGATTTCCCTCGGCAATTTGTCTCAAGTTTCCACTTTGTGAT 729

QY 851 CTGTGGCAGTGAAGAGCAAGCAAGCTGAGGTGTGAGACTTAAAGAGGC 910
DB 730 TTGGCAGGATCAGAAAAGATTAACCAAGGGAATCTGTGAACGGTTCAAAAGATCC 789
QY 911 TGCACATCAACCGCAGCTTGTATCTTGGACAGGTATTAAGAGCTTAGCAGC-- 968
DB 790 ATTCAATCAATAGTGAATTTGGCTTGAAGAAATGTAATAAGGCTCTTGGGACCCA 849
QY 969 -GCCAGCTGTGTGATTTTAACTACAGACAGCAAACTACCAAGATTTCTCCAAAT 1027
DB 850 CGCAGAGAAAGTTCAATATTCATATAGGATGCTAAATTAACCGGCTTCTGAAGAT 909
QY 1028 TCATTGGAGAAATGCTAAACGGTATTAATTTGACAAATTAGCGCAGTTTC-----T 1081
DB 910 TCTCTGGAGGAGCAGTGTAGACTGTCTGATGATCAATGTGTGACCCCTCTCTCGAAT 969
QY 1082 TTTGATGAGCTCTAAGTACCTTGAATTTGGCAGTACTGCCAAACATGTGAGA 1135
DB 970 TTTGATGAGTCTCTAAATTTCTCTCAATATGCGCAACAGACGGAACATTAGA 1023

RESULT 7
US-09-641-807A-3

Sequence 3, Application US/09641807A
Patent No. 6440731
GENERAL INFORMATION:
APPLICANT: Berard, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6440731el motor proteins and methods for
FILE REFERENCE: 1031
CURRENT APPLICATION NUMBER: US/09/641.807A
CURRENT FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1023
TYPE: DNA
ORGANISM: Human
US-09-641-807A-3

Query Match 1.5%; Score 140; DB 4; Length 1023;
Best Local Similarity 51.0%; Pred. No. 7.3e-25;
Matches 456; Conservative 0; Mismatches 405; Indels 33; Gaps 4;
QY 275 TTCAATTCGATCGTGTATTTAATTCACGAATCAACAGCAATTTTACCAAGAAAT 334
DB 130 TTCACTTTGATTTTGTGTTTGGCAAAATTCATCAAGATGAATTTAATACATGT 189
QY 335 GCGATACATATCAATGATCAGCTTTGACAGGATATATGSCAATATTTGATACGA 394
DB 190 ATTAAGCCCCCTAGTGTGTACATCATTTAGGGCTATTAAGCAATGTTTTCCTATGSA 249
QY 395 CAGACATCTTCAGGCAAGCGTACATATGATGGAAACCAATTCATT----- 444
DB 250 CAACTGATCTGGGAAGCATACACATTGAGGGGGCCATATGCTTCAGTTGTGAG 309
QY 445 -----GGGATAATATACCCCAAGCCATACAGAAATTTTAAATTAATTTAGAGATA 496
DB 310 GGCAGAAAGGATATCTTCCTGAGCTATTCAGAAATTTTCAAGCATCTCTGACAT 369
QY 497 CCGAAGAGAGATTTTCTTAAGATTTCTTAATGAGATTTTACATGAAGAACTGTGAA 556
DB 370 CTAAGATTTGATTTAATGTAAGATCTTATATGAAAGTGTACAGGAAGAACTAGA 429
QY 557 GACCTACTGTGATGACAGAGAAAGAAAGCCCTTGAAATTTGCGAGAGATTTTAATGA 616
DB 430 GATCTTTGATTTGAGATTCATTCATGAAGATCTTCAATCCGAGAAAGAAAGAA 489
QY 617 AAGGTATATGTTGCTGACCTGACCTGAAGAACTTTAATGTTTCTGAACATGTAATACG 676
DB 490 AACACAGATGATTTGTGGGCGCAAGAAATGCCATGTGAGATGTCAGTGAAGTATGAGT 549

QY 677 TGGATCAAAAAGGGTGAAGAAAAACAGACATTTATGAGAGACTTAAATGATCATACT 736
DB 550 CTTTGTGAGATGGGAAATGAGCAGACATACAGGATACATCTCAATGATAGACATCC 609
QY 737 AGTCGTTACATACATTAATTTAGATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
DB 610 AGCAGATACATGCAATTTTTCATATCAGCATTTTTCATATTAATAATATGAGAGCA 669
QY 791 CCCAAATTCAGAGAACTGTATGAGAGCTGTATCTGATCTCTGATTTTGTAGAT 850
DB 670 GCTGAAGATGATCATGTATTTCCCTGGCATATTTCTCAAGTTCTCATTTGTGAT 729
QY 851 CTGTGGCAGTGAAGAGCAAGCCAACTGAGCTGAAGGTGAGACTTAAGAGGC 910
DB 730 TTGGCAGATCAGAAAAGATTAACCAAGGGAATACGTGTGAACGGTTCAAGAAATCC 789
QY 911 TGCACATCAACCGCAGCTTGTATCTTGGACAGGTATTAAGAGCTTAGCAGC-- 968
DB 790 ATTCAATCAATAGTGAATTTGCTGTGAGAAATGTAATAGCGCTTTGGGACCCA 849
QY 969 -GCCAGCTGTGTGATTTTAACTACAGACAGCAACCTCACAGAAATTTCTCCAAAT 1027
DB 850 CGCAGAGAAAGTTCAATATTCATATAGGATGCTAAATTAACCGGCTTCTGAAGAT 909
QY 1028 TCATTGGAGAAATGCTAAACGGTATTAATTTGCACAATTAAGCCAGTTTC-----T 1081
DB 910 TCTCTGGAGGAGCAGTGTAGACTGTCTGATGATCAATGTGTGACCCCTCTCTCGAAT 969
QY 1082 TTTGATGAGCTCTAAGTACCTTGAATTTGGCAGTACTGCCAAACATGTGAGA 1135
DB 970 TTTGATGAGTCTCTAAATTTCTCTCAATATGCGCAACAGACGGAACATTAGA 1023

RESULT 8
US-09-723-096-3

Sequence 3, Application US/09723096
Patent No. 6448026
GENERAL INFORMATION:
APPLICANT: Berard, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6448026el motor proteins and methods for
FILE REFERENCE: 1031
CURRENT APPLICATION NUMBER: US/09/723.096
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US/09/641.807
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1023
TYPE: DNA
ORGANISM: Human
US-09-723-096-3

Query Match 1.5%; Score 140; DB 4; Length 1023;
Best Local Similarity 51.0%; Pred. No. 7.3e-25;
Matches 456; Conservative 0; Mismatches 405; Indels 33; Gaps 4;
QY 275 TTCAATTCGATCGTGTATTTAATTCAGAAATCAACAGCAATTTTACCAAGAAAT 334
DB 130 TTCACTTTGATTTTGTGTTTGGCAAAATTCATCAAGATGAATTTAATACATGT 189
QY 335 GCGATACATATCAATGATCAGCTTTGACAGGATATATGSCAATATTTGATACGA 394
DB 190 ATTAAGCCCCCTAGTGTGTACATCATTTAGGGCTATTAAGCAATGTTTTCCTATGSA 249
QY 395 CAGACATCTTCAGGCAAGCGTACATATGATGGAAACCAATTCATT----- 444
DB 250 CAACTGATCTGGGAAGCATACACATTGAGGGGGCCATATGCTTCAGTTGTGAG 309
QY 445 -----GGGATAATATCCCAAGCCATACAGAAATTTTAAATTAATTTAGAGATA 496

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Db      310 GGGCAAAAGGATTCATCTCCGAGCATTCAGAAATATTTCAAGACATCTCTGAACAT 369
QY      497 CCGAAGAGAGATTTCTTCTTAAGATTTCTTAATGAGATTTCAATGAAGCTGAGAA 556
Db      370 CTTAGCATTTATTAATGTAAGATCTTAATATAGAGTACAAAGAAAGCACTAAGA 429
QY      557 GACTACTGTGTATGACAGAAAGAAAGCCCTTGAAATTTGCCGAGATTTTAATAGA 616
Db      430 GATCTCTTAGAATTTGAGACATCTAGAAAGATCTTCACATCCGAGAAAGTGAAGAA 489
QY      617 AACGTATGTTGTCTGACCTGACGAGAACTTGATGTTCTGCTGAACATGTAATACAG 676
Db      490 AACACAGTATTTTGGGGCCAAAGAAATGCCATGTGAGAGTGCAGGTGAAGTATGAGT 549
QY      677 TGGATCAAAAAGGTTGAAAAAAGACATTTATGAGAGACTAAATATGAATGATCATAGT 736
Db      550 CTTTGGAGATGGGGAATGACGACAGCATACAGGTACCACTCAATGAATGAGCACTCC 609
QY      737 AGTCGTTCACTACATATTTTAAGATGATTTGAAAGCCGAGACAGAAAT-----GAT 790
Db      610 AGCAGATCAATCAATCTTTTACATCAGCATTTGTCMAAGTTCAATAAAATATGAGGCA 669
QY      791 CCCACAAATCAGAGAACTGTGATGAGCTGTGATGATCTGATCTGATCTGAATTTGATAGT 850
Db      670 GCTGAAGATGATCATGTGATTTCCCTCGGACATTTGTCTCAAGTTCCACTTTGTGAT 729
QY      851 CTTGCTGAGAGTAAAGAGCAAGCCAACTGAGCTGAAAGTGTGAGACTTAAGAAAGGC 910
Db      730 TTGGCAGGATCAGAAAGATGACCAAAACGGGGAATCTGTGAAAGGTTCAAAAGATCC 789
QY      911 TGCACATCAACCGCAGCTTTTATCTTGTGACAGTTTAAAGAGCTTAAGAGCTTAAGCAG-- 968
Db      790 ATTCAATCAATGATGATGATGCTGCTTTAGAAATGTAATAGCCGCTTTGGGAGCCA 849
QY      969 -GCCAGCTGGTGGATTTAATACTACAGACAGCAAACTCACAGAAATTTCCAAAT 1027
Db      850 CCGAGAAAGATTCATATTTCCATATAGGAGTCTTAATTAACCGGCTTTCTGAAAGAT 909
QY      1028 TCATTGGAGGAATGCTAAACGGTTAATTTGCAATTTAGCCGCAAGTTTC-----T 1081
Db      910 TCTCTGGAGGAGCTGTGAAGCTGTATGATGATGATGATGATGATGATGATGATGATGAT 969
QY      1082 TTTGATGAGACTTAAGTACATTCAGTTGCTGCAAGTACGCCAAACATGTGAGA 1135
Db      970 TTGATGAGCTCTTAATCTCTCAATATGATGCCAAGCAGCAGCAACATTTAGA 1023

RESULT 9
US-09-592-054-5
; Sequence 5, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592.054
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-5

Query Match      1.4%; Score 135.2; DB 4; Length 1421;
Best Local Similarity 50.6%; Pred. No. 1,3e-23;
Matches 468; Conservative 0; Mismatches 408; Indels 48; Gaps 4;
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QY      257 GTTGATGGGACAAAGCTTTCAATTTGATTCGATTCGTTAATTTAATCTCAGCAATCAACAAGT 316
Db      123 GTTGTGACAGATTAATCTTACCTACCTACGATTTTGTATTTTGATCCCTCTACTGAACAGAA 182
QY      317 CAATTTACCAAGAAATAGCAGTACCTATCATACGATTCAGCTTTGAGGAGATTAATGAGC 376
Db      183 GAAGTCTTCAATACAGCAGTAGCGCACATATAAAGGTATTTAAAGGATTAATAGCA 242
QY      377 ACAATATTTGCAATGAGACAGACATCTTACGCGCAAGCTACCAATGATGGCAACCA 436
Db      243 ACCGTCTGCGCTTATGAGGACAGATGAGCTCTGAAAAAACCTATTCAATGAGAGGTGATAT 302
QY      437 AATTCAATG-----GGCATATACCCCAACCCATACAGAAAGT 475
Db      303 ACTGACAGACAGAGAAATGACCAACAGATTTGGGTTATTTCTTAGGTAATACATGCTCTC 352
QY      476 TTTAAATTAATTCAGAGATACCGAAACAGAGACTTTCTTAAGATTTCTTAATATGAG 535
Db      363 TTCAAGAAATTTGATTAAGAAAGTGAATTTGAATTTACTGTGAAGTGTCTTAATAGAG 422
QY      536 ATTTACATGAACCTGTAAAGACTACTGTGTGATGACAGAAAGAAAGAAAGCCCTTGAA 555
Db      423 ATTTACATGAAGAAATTTGGATCTTATGCCCCATCTGTGAGAAAGCTCAAAATTAAT 482
QY      596 ATTGGGAGGATTTTAATAGAAACGTTATGTTGCTGACCTGACGTAAGAACTGTATG 655
Db      483 ATACGAGAGATCTTAAGAGAGCATTAAGATTTGAGACTACCTAGAGAACTGTTTGG 542
QY      656 GTTCTGAAACATGTAATACAGTGTGATCAAAAGAGGTGAAGAAAGACACTTAATGAGAG 715
Db      543 GTTGCTTGTGATCTGTTTCTGTTTGTGAAACAGGAGCAACAACCTGTGAGACTGTGGCTCC 602
QY      716 ACTAAATGATGATCATAGTACTGCTTCAATCAATATTTGAATGATTTGAAAGC 775
Db      603 ACCGCTATGAACTCCAGTCTGCTCCGATCTCATGCCATCTTTAAT--CTCCTTAGAGC 660
QY      776 CAGACAGAAATGATCCCAAAATTCAGAGAACTGTGAGAGCTGTCAATGATCTCAC 835
Db      661 AAGAAAGAAAGTGAACAAGATGACG-----CTTTGCTCCAG 701
QY      836 TTGAATTTGATAGATCTTCTGAGCAGTGAAGAGCAAGCAAACTGAGCTGAAGGTGTG 895
Db      702 CTGATCTTGTAGACTCTGCTGATCAGAAAGCAGAAAGAAACAAAGCTGAAGGGAT 761
QY      896 AGACTTAAGAAAGCTGCAACATCAACCGAGCTGTTTATCTTGTGACAGTTATTAAG 955
Db      762 CGCTAAAGAGGCTATTATATTAACGAGGCTCTTAATGCTTGGGAAATGTAATCAGT 821
QY      956 AAGCTTAGGAGCGGCGAGCTGTGATTTTAACTACAGACAGCAAACTCACCAAG 1015
Db      822 GCTCTTGAGAGTGAAGAAAGGTGCTTTGTCCTTACAGAAATTTCAAGTTGACTGCA 861
QY      1016 ATTCTCAAAATTCATTTGGAGGAATGCTAAACGGTTAATTTGCAATTTAGCCCA 1075
Db      882 CTGCTCAAGATTTCTAGAGGTAATAGCAATCTTATGATTAACCTGTGTGAGTCTT 941
QY      1076 GTT-----TCTTTGATGAGACTTAAGTACATTCAGTTGCGAGTACTGCCAAACAT 1129
Db      942 GCTGACTCAATATAGAGAAACATTAATACCTCTTGCTATGTGACAGAGCAAGAAAA 1001
QY      1130 GTGAGAAATATCTCCCATGTTAAT 1153
Db      1002 ATCAAGAACAAACCTATTTGTTAAT 1025
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RESULT 10
US-09-592-054-3
; Sequence 3, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
```

APPLICANT: Sakowicz, Roman
 APPLICANT: Wood, Kenneth
 TITLE OF INVENTION: No. 6440684el motor proteins and methods for
 FILE REFERENCE: 1016
 CURRENT FILING DATE: US/09/592,054
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 3
 LENGTH: 1569
 TYPE: DNA
 ORGANISM: Human
 US-09-592-054-3

Query Match 1.4%; Score 135.2; DB 4; Length 1569;
 Best Local Similarity 50.6%; Pred. No. 1.4e-23;
 Matches 468; Conservative 0; Mismatches 408; Indels 48; Gaps 4;

257 GTTGATGGACAAAGCTTTCAATTGATCGTGTATTAATTCTACGAATCAACAGT 316
 187 GTTGTACAGATTAATCTTCACTACATTTTGTATTTGATCCCTTACTGAACAGAA 246
 317 CAAATTACCAAGAAATACAGTACCTATCATACATCAGCTTGACAGGATATATGCG 376
 247 GAAGTCTTAATACAGCAGTACGCGCCTCATTAAGGATGATTAAGATATATATGCA 306
 377 ACAATATTGTCATACGACAGACATCTTCAGCAGACGTCACAAATGATGGAAACCA 436
 307 ACGGTCTGGCTATGAGGACGACTGGCTGTGAAAACTTAAATGGAGGTCATAT 366
 437 AATTCATG-----GGCATATATCCCAAGCCATACAGAAAGT 475
 367 ACTGACAGCAAGAGATGAACCAACAGTTGGGGTTATTCTTAGGATATACATGCTTC 426
 476 TTTAAATATTATTCAGAGATACCGAAGAGAGATTTCTTAAAGATTCTTATATGAG 535
 427 TTCAAGAAATTGATTAAGAGAGTGAATTTACTGTAAGGTCTTACTTAGAG 486
 536 ATTATCATGAACTGTGAAGAACCTTCTGTGATGACAGAAAGAAAGCCCTTGAA 595
 487 ATTACATGAAAGAAATTTGGATCTTATGCCATCTGTGAGAAAGTCAATTAAT 546
 596 ATTGCGAGATTTTATAGAAAGGTATGTGCTGACTGACGTAAGACTTGTATG 655
 547 ATACGAGAGATCTTAAGAAAGCATTAAGATTTGGGACTCTAGAAAGTCTTTTG 606
 656 GTTCTGAACATGTAATACAGTGCATCAAAAGGTGAAAGAAAGACATTAATGAGAG 715
 607 GTTGCTTGGATCTGTTCTCTGTTGGAAAGGGAACAACCTTAGACTGTGCTTC 666
 716 ACTAAATGAATGATATAGTACTGTTACATCAATATTAGATGATTTGAAAGC 775
 667 ACGGCTATGAATCTCCAGTGTGCTCCGATCTCAAGCCATCTTAAAT--CTCCTTAGAGC 724
 776 CGAGACAGAAATGATCCCAAAATTCAGAGAACTGTGATGAGCTGTATCTAC 835
 725 AAAAGAAAGAAAGTGAACAAGATAGAG-----CTTTCGCTCCAG 765
 836 TTGAATTTGGTATTTCTGTCAGTGAAGAGACCAAACTGAGCTGAAGGTG 895
 766 CTGCACTTGTAGACCTCGCTGATCAGAAAGACAGAAAGAAAGCCAGCTGAAGGGAT 825
 896 AGACTTAAGAGAGCTGCAACATCAACGCAAGCTTGTATCTTGGACAGGATATTAAG 955
 826 CCTTAAAGAGAGATTAATTAATTAACGAGGCTCTTATGCTTGGAAATGATATAGT 885
 956 AAGCTTAGGACGCGCAGCTGTGATTTAACTACAGACAGCAAACTACAGCA 1015
 886 GCTCTTGGAGATGACAAAAGGGTGGCTTTGGCCCTACAGAGATTCAGAGTTGACTGCA 945
 1016 ATTCCAAATTTGATTTGGAGAAATCTAAAGCGTTATATTGTCACAAATTAACCCA 1075

Db 946 CTGCTCAAGATCTCTAGAGGAAATAGCCATCTTATATGATACCTGTGTACTCT 1005
 Oy 1076 GTT-----TCTTTGATGAGATCTTAAGTACACTTCAGTTGGCCAGTACTGCCAAACAT 1129
 Db 1006 GCTACTCCATCTAGAGGAAACATTAAATACCTTCGCTATGCTGACAGACCAAGAAA 1065
 Oy 1130 GTGAGAAATATCCCATGTTAAT 1153
 Db 1066 ATCAGAAACAACTATTTGTTAAT 1089

RESULT 11

US-09-595-684B-22
 Sequence 22, Application US/09595684B
 Patent No. 6544766
 GENERAL INFORMATION:
 APPLICANT: Beraud, Christophe
 APPLICANT: Ohashi, Gara
 APPLICANT: Sakowicz, Roman
 APPLICANT: Vaisberg, Eugeni
 APPLICANT: Wood, Kenneth
 APPLICANT: Yu, Ming
 TITLE OF INVENTION: Human kinesins and methods of producing
 and purifying human kinesins
 FILE REFERENCE: cytop036
 CURRENT FILING DATE: 2002-06-24
 PRIOR APPLICATION NUMBER: 09/295,612
 PRIOR FILING DATE: 2000-04-20
 NUMBER OF SEQ ID NOS: 105
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 22
 LENGTH: 4348
 TYPE: DNA
 ORGANISM: Human
 US-09-595-684B-22

Query Match 1.4%; Score 133.6; DB 4; Length 4348;
 Best Local Similarity 50.5%; Pred. No. 6.1e-23;
 Matches 467; Conservative 0; Mismatches 409; Indels 48; Gaps 4;

257 GTTGATGGACAAAGCTTTCAATTGATCGTGTATTAATTCTACGAATCAACAGT 316
 187 GTTGTACAGATTAATCTTCACTACATTTTGTATTTGATCCCTTACTGAACAGAA 246
 317 CAAATTACCAAGAAATACAGTACCTATCATACATCAGTTCAGGAGATATATGCG 376
 247 GAAGTCTTAATACAGCAGTACGCGCCTCATTAAGGATGATTAAGATATATATGCA 306
 377 ACAATATTGTCATACGACAGACATCTTCAGCAGACGTCACAAATGATGGAAACCA 436
 307 ACGGTCTGGCTATGAGGACGACTGGCTGTGAAAACTTAAATGAGGTCATAT 366
 437 AATTCATG-----GGCATATATCCCAAGCCATACAGAAAGT 475
 367 ACTGACAGCAAGAGATGAACCAACAGTTGGGGTTATTTCTAGGATATCAACTGCTC 426
 476 TTTAAATATTATTCAGAGATACCGAAGAGATTTCTTAAAGATTCTTATATGAG 535
 427 TTCAAGAAATGATTAAGAAAGGTGACTTGAATTTACTGAAAGGTCTTACTTAGAG 486
 536 ATTACAAATGAATCTGTGAAGACTACTGTGTATGACAGAAAGAAAGACCCTTGAA 595
 487 ATTACATGAAGAAATTTGGATCTTGTATGTCCATCTCTGAGAAAGCTCAATTAAT 546
 596 ATTGCGAGATTTTATAGAAAGGTATGTGCTGACCTGACGTAAGAACTGTATG 655
 547 ATACGAGAGATCTTAAGAGAGCATTAAGATTTGGGACTCTACTGAAAGACTGTTTG 606
 656 GTTCTGAACATGTAATACAGTGCATCAAAAGGTGAAAGAAAGACATTAATGAGAG 715
 607 GTTGCTTGGATCTGTTCTCTGTTGGAAAGGGAACAACCTTAGAGACTGTGCTTC 666

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QY 716 ACTAAATGATGATCATAGTACGTTCAATCATATTTAGATGATTTGAAGC 775
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Db 667 ACCGCTATGAACCTCCAGTGTGCCGATCTCATGCCATCTTTACAT--CTCCTAGAGC 724
QY 776 CGAGACGAAATGATCCCAAAATTCAGAGAACTGTAGAGCTGTATCTAC 835
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Db 725 AAGGAAAGAAAGTACAGAAATGACAG-----CTTCGCTCAAG 765
QY 836 TTGAATTTGATAGTCTTCTGCGACGAGAAAGCAAGCAAGCAAGTGAAGCTG 895
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Db 766 CTGATCTTGTATGACCTCGCTGATCAAGAAAGCAAGAAACCAAGGCTGAAGGGAT 835
QY 896 AGACTTAAGGAGGCTCAATCAATCAAGCGAGTTGTTATCTTGACAGATTATTAAG 955
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Db 826 CGTCTAAAGAGGATATTAATTAACCGAGGCTCTTATGCTTGGAAATGTAATAGT 885
QY 956 AAGCTTAGCGACGCGCAGCTGTGATTTATTAATACAGAGACAGCAAACTCACAGA 1015
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Db 886 GCTCTTGAGATGACAAAGAGGAGGCTTGGCGCTACAGAGATTCAGATTGACTCGA 945
QY 1016 ATTCTCCAAATTCATTGGAGAGAAATGCTAAAACGTTTATTTGACAAATTAAGCCA 1075
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Db 946 CTGCTTCAAGATTCCTAGAGAGTAATAGCCATATCTTATGATAGCTGTGAGTCTT 1005
QY 1076 GTT-----TCTTTGATGAGACTCTAAGTACACTTGCAGTTGCGAGTACTGCAAAACAT 1129
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Db 1006 GCTGACTCCAAATTAAGAGAAACATTAATACCTTTCCTATGCTGACAGAGCAAGAAA 1065
QY 1130 GTGAGAAATACCTCCCATGTTAAT 1153
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Db 1066 ATCAGAGCAAAACCTATGTTAAT 1089
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RESULT 12

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US-09-592-054-7
; Sequence 7, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592.054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FaetsEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-7

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Query Match 1.3%; Score 127.2; DB 4; Length 4127;
Best Local Similarity 50.1%; Pred. No. 2,3e-21;
Matches 463; Conservative 0; Mismatches 413; Indels 48; Gaps 4;

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QY 257 GTTGATGGGACAAAGTCTTCAATTTGATCGTGTATTTAATCTCAGCAATCAACAGT 316
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Db 229 GTTGTACTGATTAATCTTACCTACGATTTGTGTTTACCCTGTACTAGACAGAA 288
QY 317 CAAATTTACCAAGAAATAGCAGTATCATCATGATCAGCTTTGACGGAGTAAATGCG 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 289 GAAGTCTTCAATTAAGAGTAGGCGGCTCATAAAGGCAATTTAAAGATTAATAGCA 348
QY 377 ACAATTTTGCATAGGACAGACATCTTCAGCAAGACGTACCAATGATGGAAACCA 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 349 ACCGTCTGCGCTATGGGAGCTGCTGAGAAAACCTATTCATGGAAGGTGATAC 408
QY 437 AATT-----CATTTGGCATATATACCCAGACATACGAGAAAGT 475
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Db 409 ACTGCGAGACGAGAGATGACCAACAGTTGCAATTAATCTAGGTAATACAACTGCTC 468
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QY 476 TTTAAATTTATAGAGATACCGAAGAGAGTTCTTTAGATTTCTTATGAG 535
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Db 469 TTTAAAGAAATTTGATCAAAAGAGTCTTGAATTTACTGAAATGCTTTAAGAG 528
QY 536 ATTTACAAATGAACTGTGAAGACCTACTGTGTATGACAGAAAGAAAGCCCTTGAA 595
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Db 529 ATTTACAAATGAAATTTTGTGATCTTTATGCCCATCTCTGAGAAAGCTCAAAAT 588
QY 596 ATTGCGAGATTTTAATGAACGTTATGTTTCTGACCTGATGAAGAACTTGTAATG 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 ATACGGAGAGATCTTAAGAAAGCATAAAGATTTGTGGACTCACTGAAAGACTGTTTA 648
QY 656 GTTCTGMACTATATACAGTGAATCAAAAAGGTTGAAAAAAGACACTTATGAGAG 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 GTTGCTTGGATCTGTCTTCTGTTGGAGCAGGGAACAACTGTGAGACTGTGCTCC 708
QY 716 ACTAAATGATGATCATAGTACGTTCAATCATATTTAGATGATTTGAAGC 775
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Db 709 ACAGCTATGAATCTCCAGATGCTCCGATCTCATGCCATCTTTACAT--CTCCTTAGAGC 766
QY 776 CGAGACGAAATGATCCCAAAATTCAGAGAACTGTAGAGCTGTATCTAC 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 767 AAGGAAAGAAAGTACAAAGAAATGACAG-----CTTCGCTCAAG 807
QY 836 TTGAATTTGATAGTCTTCTGCGACGAGTAAGAGCAAGCAAGCAAGTGAAGCTG 895
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Db 808 CTGATCTTGTATACCTCGCTGATCAGAAAGCAGAAAGAAACCAAGCTGAAGGGAT 867
QY 896 AAGCTTAAGGAGGCTGCAACATCAACCGCAGCTGTTTATCTTGGACAGTTATTAAG 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 868 CGTCTAAAGAGGATTTAATTAATTAACAGGCTCTCTATGCTTGGAAATGTAATAGT 927
QY 956 AAGCTTAGCGACGCGCAGCTGTGATTTATTAATACATAGAGACAGCAAACTCACAGA 1015
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Db 928 GCTCTTGAGATGACAAAGAGGAGTCTTGTGCTTACAGAGATTCAAAGTTAACTCGA 987
QY 1016 ATTCTCCAAATTCATTGGAGAGAAATGCTAAAACGTTTATTTGACAAATTAAGCCA 1075
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Db 988 CTGCTCAAGATTCCTAGAGAGTAACAGCCACACTTATGATACCTGTGTGAGTCTCT 1047
QY 1076 GTT-----TCTTTGATGAGACTCTAAGTACACTTGCAGTTGCGAGTACTGCAAAACAT 1129
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Db 1048 GCTGACTCCAAATTAAGAGAAACATTAATAGTACCTTTCCTATGCTGACAGAGCAAGAAA 1107
QY 1130 GTGAGAAATACCTCCCATGTTAAT 1153
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1108 ATCAGAGCAAAACCTATGTTAAT 1131
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RESULT 13

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US-09-592-054-1
; Sequence 1, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592.054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FaetsEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-1

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Query Match 1.2%; Score 116; DB 4; Length 4308;
 Best Local Similarity 49.4%; Pred. No. 1.4e-18;
 Matches 456; Conservative 0; Mismatches 420; Indels 49; Gaps 4;

QY 257 GTTGATGGGCAAAAGCTTTCAATTTGATGATGATTTAATTTTACAGATCAACAAGT 316
 DB 187 GTTGATGAGATTAATCTTCACTACGATTTTGTATTTGATCCCTACTCAACAGAA 246
 QY 317 CAAATTTACCAAAATAGACGATCATACATACAGCTTTGAGAGATATATATG 376
 DB 247 GAAGCTTCAATACAGACATAGCCACTCATTAATAAGGATTAATAAGATATATGCA 306
 QY 377 ACAATATTTGATACAGACAGATCTTACAGCAAGGTAACAATGATGAGAAACCA 436
 DB 307 AGGCTCTGGCTATAGGAGAGAGCTGTGAAAAACCTATTTCAATGGAGAGTCAAT 366
 QY 437 AATTCATTG-----GGCAATATACCCCAAGCCATACAGAAATT 475
 DB 367 ACTGAGAGCAAGAAATGAAACCAAGTTGGGTTATTTCTAGGGTAAATCAACTGCTC 426
 QY 476 TTTAAATTTATTCAGAGATACCGAAGAGAGTTCTTTAAGGTTCTTATATGAG 535
 DB 427 TTCAAGAATTTGATTAATAAGATGATCTTTGATTTACTTGAAAGTCTTACTTATGAG 486
 QY 536 ATTTACATGAACCTGTGAAAGCTTCTGTGTATGACAGAGAAAGAAAGCCCTTGAA 595
 DB 487 ATTTACAAATGAAGAAATTTGGATCTTATGTCCATCTGTGAAAGATCAATTGAG 546
 QY 596 ATTGCGAGAGATTTTATATGAAGCGTATGTTGCTGATCTGATGAAAGCTTTGATG 655
 DB 547 ATTTACATGAAGAAATTTGGATCTTATGTCTGATCTGATGAAAGCTTTGATG 606
 QY 656 GTTCCGAACTGTAATACAGTGTATCAAAAAGGATGAAAAAACAAGATTTAGAGAG 715
 DB 607 GTTCCCTTGATCTGTTCTGTTTGAAGAGGCAACAACCTAGAGATCTGAGCTC 666
 QY 716 ACTAATTTGATGATCAATAGTCTGATCAATCAATTTTGAATGATTTGTAAGC 775
 DB 667 ACGGCTTGAAGCTCCAGTGTCCGATCTCATGCCATCTTAACAAT--CTCCTTAGAG 724
 QY 776 CGAGACAGAAATGATCCCAAAATTCAGAGAACTGTATGAGCTGTCAATGATCTCAG 835
 DB 725 AAGGAAGAAAGTGAACAAGATAGCAG-----CTTTGCTCAAG 765
 QY 836 TTGAATTTGATGATCTTCTGCTGAGTGAAGAGCAAGCCAACTGAGCTGAGAGTGTG 895
 DB 766 CTGATCTTGTAGCTGCTGCTGATCAGAAAGACAGAAAGAAACCAAGGCTGAAGGGAT 825
 QY 896 AGACTTAAAGAGGCTGCAACATCAACCGAGCTGTTTATCTTGAACAGTTTATAG 955
 DB 826 CGCTTAAAGAGGATTAATTAATTAACGAGGCTCTCTATGCTTGGAAATGTATCACT 885
 QY 956 AAGCTTACGAGCGGAGCTGTGATTTAATACTACAGAGACGCAATCTCAACGAG 1015
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 QY 1016 ATTCTCCAAATTTCAATTTGGAGAAATGCTAAACCGTTATATTTGCAATTAAGCCA 1075
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 QY 1076 GTT-----TCTTTGATGAGACTTAAGTACACTGATTTGCGAGTATGCGCAAAAT 1129
 DB 1006 GCTGACTCAATCTAGAGAAACATTAATACCTTCCCTTGGTATGAGACAGAGAA 1065
 QY 1130 GTGAGAAATCTCCCATGTTAAT 1153
 DB 1066 ATCAAGAACCAACTATTTGTTAAT 1089

RESULT 14
 US-09-641-806-3
 ; Sequence 3, Application US/09641806
 ; Patent No. 6395527

GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Freedman, Richard
 ; TITLE OF INVENTION: No. 6395527e1 motor proteins and methods for
 ; TITLE OF INVENTION: their use
 ; FILE REFERENCE: 1034
 ; CURRENT APPLICATION NUMBER: US/09/641,806
 ; NUMBER OF FILING DATE: 2000-08-17
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1011
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-641-806-3

Query Match 1.0%; Score 98; DB 4; Length 1011;
 Best Local Similarity 48.3%; Pred. No. 1.8e-14;
 Matches 346; Conservative 0; Mismatches 355; Indels 15; Gaps 2;

QY 359 TTGACAGGATATATGCAATATTTGATATGAGACAGACATCTTACAGCAAGCTTAC 418
 DB 214 TTGAGAGGCTTCAATGACATGCTCTTGTGATGTGACAGGCTCAGGAAAGCATAC 273
 QY 419 ACAATGATGGGAACACCAA-----ATTCAITGGGCATTAATCCCAAGCCATA 466
 DB 274 ACCATGGGAGGAGCCACCTCCCTCTGAGATGAGAGGAGCATTTGCCAGAGGCCATG 333
 QY 467 CAGAAATTTTAAATTTATTCAGAGATACCGAAGAGAGTTCTTTCAAGTTCT 526
 DB 334 GCCGAGGCTTCAACTATGATGAGAGACCACTGCTTGTCTCTGTATCATGTGCTC 393
 QY 527 TATATGATTTTACATGAAACTGTGAAAGACCTTCTGTGTATGACAGAAAGAAAG 586
 DB 394 TACTGGAAGGTATCAAGAGAGAGTCCGAACTGCTGAGTGGGCACTGCCAGCCGT 453
 QY 587 CCCTTGAATTTCCGAGGATTTTATATGAACCTGTATGTGCTGACCTGATCAAGAA 646
 DB 454 GACATCCAGCTCCGGAAGATGAGCGGGAATTTGTGTGTGCGGGTGAAGAGGTC 513
 QY 647 CTGTATGTTCTCTGAACATGTATACAGTGTATCAAAAAGGATGAAAAACAACAT 706
 DB 514 GACGTGAGGCTGTGATGAGGTCTGAGCTCCTGTGAGATGAGCAACGCGCGGAC 573
 QY 707 TATGAGAGACTAAATGAATGATCATGATGTGCTTACATCAATATTTAGATGATT 766
 DB 574 ACGGAGCAAGCACTCAACCACTGTCTAGCGGCTCACACAGGCTTCAACCGTACC 633
 QY 767 GTTAAAGCGAGACAGAAATGATCCCAAAATTCAGAGAACTGTATGAGAGCTGATG 826
 DB 634 CTGAGAGAGGCGGCGCGCCCGCAGCGCTTACCCGCGCGCGCGCGCGCTGCTC 693
 QY 827 GTATCTCACTTGAATTTGATGATCTTGTGCTGAGTGAAGAGCAAGCCAACTGAGCT 886
 DB 694 GTCTCAAGTTTCACTTGTGATCTGAGCTGCGGCTCAGAGAGGCTGCTCAAGCGGAC 753
 QY 887 GAAGGTGAGACTTAAAGAGGCTGCAATCAATCAACCGAGCTTGTATTTCTTGAACG 946
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 DB 814 GTCATGAGCGCCCTGAGGAGCCCTCAGCGCGGAGGAGCAATACCTTACCGGACTCC 873
 QY 1004 AAATCTCAGAAATTTCTCAAAATTTGATGAGAGAAATGCTTAAACGGTTATTAAT 1059
 DB 874 AAGATCAAGGATCTCAAGAGCTGCTGCGGAGGAGAGCGCAAGCGGTATGAT 929

RESULT 15
 US-09-723-129-3
 ; Sequence 3, Application US/09723129
 ; Patent No. 6551787

GENERAL INFORMATION:

APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6551787el motor proteins and methods for
their use
FILE REFERENCE: 1034
CURRENT APPLICATION NUMBER: US/09/723,129
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 09/641,806
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for windows Version 4.0
SEQ ID NO 3
LENGTH: 1011
TYPE: DNA
ORGANISM: Human
US-09-723-129-3

Query Match

1.0%; Score 98; DB 4; Length 1011;

Best Local Similarity 48.3%; Pred. No. 1.8e-14; Matches 346; Conservative 0; Mismatches 355; Indels 15; Gaps 2;

QY 359 TTGACAGGATATATATGACCAATATTTGATACGACAGACATCTTCAGGCAAGACGTAC 418
DB 214 TTGACAGGCTTCAATGCCACTGTCTTGCTATGTCAGACGGGCTCAGGGAAGACATAC 273
QY 419 ACAATATGGGAACACCA-----ATTCAATGGGATATATACCCCAAGCCATA 466
DB 274 ACCATGGGGAGGCCACCTCCCTCTTGAGATGACAGGGCAATTGTCCGAGGGCCATG 333
QY 467 CAGGAAGTTTAAATTTATTCAGAGATACGACAGAGATTTCTTAAAGATTTCT 526
DB 334 GCCGAGGCTTCAAGCTCATGAGAGACGACCTGCTTACCTGTCTGATCATGTGTC 393
QY 527 TATATGAGATTATCATGATGAATCTGTAAAGACCTACTGTGTATGACAGAGAAAG 586
DB 394 TACCTGGAAGTATGACAGAGAGAGAGTCCAGACCTGCTGAGGTGGGCACTGCCAGCCGT 453
QY 587 CCTTGGAAATTCGCGAGGATTTTAATAGAAAGCTGATGTTCTGACCTGACTGAAGA 646
DB 454 GACATCAGCTCCGGAGAGATGACCGCGGAATGTTGCTGTGCGGGGTGAAGAGATC 513
QY 647 CTTGTATGTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 706
DB 514 GACGTGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 573
QY 707 TATGAGAGACTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 766
DB 574 ACGGAGGCAAGCACTCAACCTGTGTAGCGGCTCAACAGGCTTCAACCGTGACC 633
QY 767 GTTAAAGCCGAGACAGAAATGATCCCAAAATTCAGAGAACTGTATGAGCTGTATG 826
DB 634 CTGGAGCAGCGGGGCGCGCCCGCCAGCTACCCCGCCCGCGGCGCAGCTGCTC 693
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DB 694 GTCTCAAGTTCCTGCTGAGCTGTGCGGGCTCAGAGGGGTGCTCAAGACGGGAGC 753
QY 887 GAAGGTGAGACTTAAGAGAGGCTGCAACATCAACCGCAGCTTGTATCTTGGACAG 946
DB 754 ACCGGGAGCGGCTCAAGAGAGATCCAGATCAACAGCGCTCTGCGGCTGGGCAAC 813
QY 947 GTTATTAGAAAGCTTAGCAGCGGCTGATGATTT--ATTAATACAGAGACAGC 1003
DB 814 GTCATAGGCGCCCTGGGGAGCCCTCAGCGCGGGGAGCCACATACCTTACCGGACTCC 873
QY 1004 AAACCTACCAAGATTTCCAAATTTCAATGGGAGAAATGCTAAACGTTATAT 1059
DB 874 AAGATCACCAGATCTCTCAAAAGACTGCTGGGCGGGAAGCCAAAGCGGTGATGAT 929

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Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620.4	6.4	8491	12 US-10-133-013-260	Sequence 260, App
2	620.4	6.4	8493	13 US-10-071-766-51	Sequence 51, App1
3	620.4	6.4	8503	14 US-10-037-270-130	Sequence 130, App
4	615.2	6.4	7992	11 US-09-893-519A-140	Sequence 140, App
5	206.6	2.1	581	9 US-09-833-790-351	Sequence 351, App
6	147.8	1.5	3505	12 US-09-814-353-21787	Sequence 155, App
7	146.6	1.4	501	9 US-09-833-790-167	Sequence 167, App
8	138.2	1.4	3753	12 US-10-116-712-668	Sequence 668, App
9	135.2	1.4	4348	12 US-10-116-712-661	Sequence 661, App
10	133.6	1.4	4348	12 US-10-116-712-667	Sequence 667, App
11	133.6	1.3	9240	14 US-10-198-846-13194	Sequence 13194, A
12	124.4	1.3	1726	12 US-10-133-013-263	Sequence 263, App
13	122.8	1.3	3366	10 US-09-938-842A-2651	Sequence 2651, App
14	117.6	1.2	4858	10 US-09-954-456-733	Sequence 733, App
15	95.8	1.0	29793	10 US-09-973-451-38	Sequence 38, App1
16	90	0.9	29793	10 US-09-973-451-38	Sequence 38, App1

17	85.6	0.9	501	9 US-09-833-790-329	Sequence 329, App
18	82	0.9	4775	14 US-10-146-473-81	Sequence 81, App1
19	81.2	0.8	6586	10 US-09-954-456-1115	Sequence 1115, App
20	81.2	0.8	6586	10 US-09-954-456-1790	Sequence 1790, App
21	81.2	0.8	6586	14 US-10-157-031-37	Sequence 37, App1
22	73.8	0.8	3348	10 US-09-954-456-90	Sequence 90, App1
23	73.8	0.8	3348	10 US-09-954-456-727	Sequence 727, App1
24	68.2	0.7	3376	13 US-10-071-766-80	Sequence 80, App1
25	68	0.7	5361	10 US-09-742-096-2	Sequence 2, App1
26	68	0.7	6152	10 US-09-742-096-1	Sequence 1, App1
27	67.8	0.7	5848	13 US-10-044-090-299	Sequence 299, App
28	67.6	0.7	3930	10 US-09-847-874A-2	Sequence 2, App1
29	66.6	0.7	410	14 US-10-106-698-2537	Sequence 2537, App
30	66.6	0.7	14006	12 US-10-311-455-1931	Sequence 1931, App
31	62.8	0.7	6668	12 US-10-311-455-1670	Sequence 1670, App
32	61.8	0.6	3673778	12 US-10-312-841-2	Sequence 2, App1
33	61	0.6	1171	14 US-10-198-846-12848	Sequence 12848, A
34	59	0.6	9539	12 US-10-240-845-54	Sequence 54, App1
35	59	0.6	9539	14 US-10-239-676-52	Sequence 52, App1
36	58.6	0.6	113515	12 US-10-311-455-2147	Sequence 2147, App
37	58.4	0.6	1002	10 US-09-879-536-442	Sequence 442, App
38	58.2	0.6	498	10 US-09-738-973-345	Sequence 345, App
39	58.2	0.6	498	10 US-09-854-133-345	Sequence 345, App
40	58.2	0.6	498	14 US-10-144-648A-345	Sequence 345, App
41	58	0.6	529	10 US-09-983-965-2109	Sequence 2109, App
42	57.4	0.6	446	10 US-09-960-352-3400	Sequence 3400, App
43	56.4	0.6	6668	12 US-10-311-455-1669	Sequence 1669, App
44	56.2	0.6	5750	12 US-10-311-455-1981	Sequence 1981, App
45	56	0.6	1395	12 US-10-161-051-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-133-013-260
Sequence 260, Application US/10133013
Publication No. US20030166903A1
GENERAL INFORMATION:
APPLICANT: Astromoff, Anna
APPLICANT: Bandman, Olga
APPLICANT: Cocke, Benjamin G.
FILE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
TITLE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133, 013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287, 067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SEQ ID NO 260
LENGTH: 8491
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20030166903A1 441283.5
US-10-133-013-260

Query Match	6.4%	Score 620.4	DB 12	Length 8491
Best Local Similarity	65.5%	Pred. No. 2	Se-131	
Matches 1001	Conservative	0	Mismatches 491	Indels 36
			Gaps	5
QY	69	GGCGCCAAAGGAGCTAAAGTACAGACAGAGAGCGGTGCTACCGATTTCAC	128	
DB	17	GGCGCTGAGAGCGCTGAAGTCCGCGCGAGAGGCTCCGCTTTGCTGGACAG	76	
QY	129	TAAATCGTCTCAAAATGTCGAGAGGATGCACTTAAAGTGTGTGAGGCTTCGCGCC	188	
DB	77	TTACGCTATATGATGAGGCGAGAGAGCCCTGCGCTGCGTGTGCGGCGCCG	136	
QY	189	TTATACAGAGAGAACAA-----GGGATCAAGCCCACTGCAATGGAAGCTGGAACA	242	

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Db      137 TGAACAGAGAGAGATCACTTGGAGAACTGCCAACTTTACTGGAAAACTGACAAATA 196
Qy      243 ACACCAATTTCCCAAGTTGATGAGCAAAAGTCTTTCAATTCGATCGTGTATTTAAATTC 302
Db      197 ATGTCAATTTATCAAGTTGATGAGAAATATCTTCAATTTTGTGTCTTTCATGTGA 256
Qy      303 ACAGATCAACAATCAAAATTTACCAAGAAATAGCAATCTTATCATAGATCAAGCTTGC 362
Db      257 ATGAAATCAACAAAATGTGTATGAAAGAAATAGCAACCAATCATCATGATTCGCATAC 316
Qy      363 AGGATATATAGGACAAATATTTGATACAGACAGATCTTCAAGCAAGCTACACAA 422
Db      317 AAGGCTACAAATGTATCTATATTTGCTATGACAGCTGCTTCAAGAAAAATATATCA 376
Qy      423 TGAATGGAACACCAATTTCAATTTGGCATATATCCCAAGCCATACAGAAAGTTTAA 482
Db      377 TGAATGGTTCAGAAAGATCATTTGGAGATTATACCAAGGCAATCATATCAATTTCCAA 436
Qy      483 TTATTCAGAGATACCGAACAGAGAGTTTCTTAAAGATTCTTATATGAGATTATCA 542
Db      437 AATTTAAGAAAGTTTCTGTATAGGAATTTCTTCTACGTATCTTACATGAAATATCA 496
Qy      543 ATGAAATCTGAAACCACTCTGTGTATGACAGAAAGAAAGCCCTTGGAAATTCGCG 602
Db      497 ATGAAACCAATTAACAATTTACTCTGTGCACCTCAAAAATGAAACCTTTATTTGAG 556
Qy      603 AGGATTTTAAATGAAACGTATATGTTGCTGACCTGACAGAAATCTTGTATGTTCTG 662
Db      557 AAGATGTCATATGAAATGTATGTGTGCTGATCTTCAAGAAAGATGTATATATCATCAG 616
Qy      663 AACATGTATACAGTGTATCAAAAAGGTGAAAAAACAACATTTATGAGAGACTAAA 722
Db      617 AATGTGCTTTAAATGATATCAAAAGGAGAAAGAGAGCAATTTATGAGAAACAAA 676
Qy      723 TGAATGATCATATGATAGTGTACATATCAATTTTAAATGATGTTGAAAGCCGAGACA 782
Db      677 TGAATCAAGAAAGAGTGTCTTCTATCAATCTTTAGATGATTTGAAAGCAGAGAGA 736
Qy      783 GAAATGATCCCAAAATTCAGAGAACTGTATGAGCTGATGATCTTCACTGAAT 842
Db      737 AGGCTGAACCTTTAAAT-----TGTAGAGATCTGTTAAGTATCCCATTTGAAT 787
Qy      843 TGTATGATCTTTGCTGAGAGTGAAGAACCAAGCCAACTGAGCTGAAGTGTGAGACTTA 902
Db      788 TGTGATCTTTGAGGAGTGAAGAGCTCTCAAAAGGCGCTGAGGCTGCGGCTCA 847
Qy      903 AGGAGGCTGCAATCAACGAGCTTGTATATCTTGGAGAGTATTTAAGAACTTA 962
Db      848 AGGAGGCTGTAATATATTAATCGAAGCTATTTTGGAGCAAGTATCAAGAACTTA 907
Qy      963 GCGAGCGCGAGCTGTGTGATTTATTAATCAAGAGACAGAACTCACAGAAATTC 1022
Db      908 GTATGAGCAAAAGTTGTGTGTTTCAATTAATATGAGATGACAAAGTTAACACAAATTC 967
Qy      1023 AAAATTCATTTGGAGAGAAATGCTAAAGAGTATTAATTTGACAAATTTAGCCAGTTTCT 1082
Db      968 AGAATTCCTTTGGAGAGAAATCCAAAGACATTTATTTGCACAATTTACTCCAGATCTT 1027
Qy      1083 TTGATGAGCTCTTAAGTACATTTCACTTTGCGAGTACTGCAAAATGAGAAATATCTC 1142
Db      1028 TTGATGAACTCTTACTCTCTCCAGTTTGCAGTACTGTAAATATATGAAATATCTC 1087
Qy      1143 CCCATGTAATGAGAGCTCGATGATGAAAGCTTGTATTAAGATGAGAAAGAAATCT 1202
Db      1088 CTTATGTTATAGAGATCAACTGATGAAAGCTCTCTGAAAGATATGAAAGAAATTA 1147
Qy      1203 TGGATTTAAGAAACAATTTAGAAATTTAGATCAATGCTGAAACAAAGCTCAAGAA 1262
Db      1148 TGGATCTTAAAAACAATTTAG-----GAGCTTTCTTTGAGAGCGGCTCAAGCAA 1201
Qy      1263 TGGCTAAGAGAGATACAGCTTGTAGCTGAATCAAAACAATCAACAAAGAGAG 1322
Db      1202 TGGAAAAAGACCAATTTGGCCCAACTTTTGAAGAAAAAGATTTGCTTCAGAAATGACGA 1261

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Qy      1323 AAGATAGATATGCACTTTGACAAATATTTGTTGTG---CTTATCCCAAGATCTCAAC 1379
Db      1262 ATGAGAAAAATGAAAAATTTAAACAGGATGCTGTGTGACCTTTCTTCCATCAGTTCAAC 1321
Qy      1380 AGGACAAAGAGTCAACAGAAACGAAGAGTTTCGTTGGGCGCCAGAGAAATATCAAAATA 1439
Db      1322 AGGATTTAAAGCTTAAAGAAAGAAAGAGAGTTTCTTGTGTGCTTGGCAAAATTAACAAA 1381
Qy      1440 GTTTACATGCTTCTGTGTGTTTCTGACTTTGATATGCTATTCAGATTAAGCTGGCAATTTTA 1499
Db      1382 TGAAGAA-----CTCAAACTATGACAGATCAATTTAATATACAAATATATA 1429
Qy      1500 GCAAGAGGCAAGATTTCTGACATGCTTCAATTTCCAGAAATTTGATGACTGTTGTA 1559
Db      1430 CACAAAAACACATATAGCTTTCTATTAATTTATTAAGAAATATGATGATGATCTGTCT 1489
Qy      1560 CAGATTTTCTGATTTTGTATGACGCGCT 1587
Db      1490 CAGAGTGTATGTTTCACTAACACTCT 1517

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RESULT 2

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US-10-071-766-51
; Sequence 51, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Huel-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071.766
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 51
; LENGTH: 8493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incycle ID No. US20020192678A1 441283.3
US-10-071-766-51

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Query Match      6.4%; Score 620.4; DB 13; Length 8493;
Best Local Similarity 65.5%; Pred. No. 2.6e-131;
Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;

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Qy      69 GCCGCAAAAAGGACTAAGTGAACAGAGACAGGAGCGGTGCTACCGATTTCTCCAC 128
Db      17 GCGGCTGTGAGCCCTGAAGTGCCTGCGGAGGCTCTGGCCATTTGTGTGGACAG 76
Qy      129 TAATGCTCTCAAAATGTCCGAGGAGATGCACTTAAAGTGTGTGAGAGTTGCGCGC 188
Db      77 TTGAGCTGTATGAGATGCGGAGAGAGAGCGCTGCGCTGTGCGAGTCCGCGCC 136
Qy      189 TTATACGAGAGAGAA-----GGGATCAAGCCAACTGCAATGAGAGCTGGAACA 242
Db      137 TGAACAGAGAGAGATCACTTGAGAAAGTCCCAAGTTTACTGAAAACTGACAAATA 196
Qy      243 ACACCAATTTCCCAAGTTGATGAGCAAAAGTCTTTCAATTCGATCGTGTATTTAAATTC 302
Db      197 ATGTCAATTTATCAAGTTGATGAGAAATATCTTCAATTTTGTGTCTTTCATGTGA 256
Qy      303 ACAGATCAACAATCAAAATTTACCAAGAAATAGCAATCTTATCATAGATCAAGCTTGC 362
Db      257 ATGAAATCAACAAAATGTGTATGAAAGAAATGACAGACCAATCATCATGATTCGCATAC 316
Qy      363 AGGATATATAGGACAAATTTGATACAGACAGATCTTCAAGCAAGCTACACAA 422
Db      317 AAGGCTACAAATGTATCTATATTTGCTATGACAGATGCTTCAAGAAAAATATATCA 376
Qy      423 TGAATGGAACACCAATTTCAATTTGGCATATATCCCAAGCCATACAGAAAGTTTAA 482

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Db 377 TGAATGAGTTCAGAGATCATTTGGAGTTATACCAGGCATTCAGCATTTTCCAAA 436
Qy 483 TTATTCAGAGATACCGAACAGAGATTTCTTAAAGATTTCTTATGAGATTTTACA 542
Db 437 AAATTAGAGATTTCTGATAGGAAATTTCTTACGATTTTACATGGAATATACA 496
Qy 543 ATGAACCTGGAAGAGCTACTGTGTATGACAGAGAAAGAGCCCTTGGAATTCGCG 602
Db 497 ATGAACCTGGAAGAGCTACTGTGTATGACAGAGAAAGAGCCCTTGGAATTCGCG 556
Qy 603 AGGATTTTAAAGAAAGTATGTTGCTGACCTGACCTGACCTGTAAGATTTGCTCG 662
Db 557 AAGATGTCATAGGAATGTATGTTGCTGATCTCAGAGAAAGTGTATATATACATG 616
Qy 663 AACATGTAATACAGTGTATCAAAAAGGGTGAAGAAAAACAGACTTTATGAGAGACTMAA 722
Db 617 AAATGGCTTTGAATGGATTTACAAAGGAGAAAGAGCGGCTTATGAGAAACAAAA 676
Qy 723 TGAATGATCATGATGATGCTGTCATACATATTTTGAATGATTTGTAAGCCGAGACA 782
Db 677 TGAATCAGAAAGAGAGCTGCTTCTCATACATCTTTAGATGATTTTGAAGAGAGAGA 736
Qy 783 GAAATGATCCACAAATTCAGAGAACTGTATGAGAGCTGTATGATCTCACTTGAAT 842
Db 737 AGGATGAACTTCTAAT-----TGGAAGATCTGTAAAGTATCCCATTTGAAT 787
Qy 843 TGTGATATTTTGTGCTGACAGTGAAGAGCAAGCACTGAGCTGAAGGTGTGACCTTA 902
Db 788 TGGTGTATTTTCAAGGAGTGAAGAGCTGCTCAAAAGAGGCTGAGAGTGTGCGGCTCA 847
Qy 903 AGGAAGGCTGCAACATCAACCGAGCTGTTTATCTTGTGACAGTGTATTAAGAACTTA 962
Db 848 AGGAAGGCTGTATATTAATTCAGAGCTTATTTTGGAGCAAGTATCAAGAACTTA 907
Qy 963 GCGAGCGGAGCTGTGTATTAATTAATCAAGAGCAAGCAACTCACAGATTTCTCC 1022
Db 908 GTGATGAGCAAGTGTGTGTTTCAATTAATGAGATGCAAGTAAACAGATTTCTTC 967
Qy 1023 AAAATTGATGGAGAAATGCTAAAGCGTTAATTTGACAAATTAAGCCATTTCTT 1082
Db 968 AGAATTCCTTGGAGAGAAATCCAAAGACAGTATTTCTGCACAATTAATCTCCAGTATCT 1027
Qy 1083 TTGATGAGACTTAAGTACATTTCAAGTTTCCAGTCTGCAAGCAAGTGAAGAAATCTC 1142
Db 1028 TTGATGAAACTTTACTGCTCTCCAGTTTGCAGTACTGCTAAATTAATGAAAGAAATCTC 1087
Qy 1143 CCCATGTTAATGAGCTCTGATGATGAGAGCGTGTAAAGAGTACAGAAAGAAATCT 1202
Db 1088 CTTATGTTATAGGATCACTGATGAGAGCTCTCTGAAAGATTAAGAAAGAAATTA 1147
Qy 1203 TGGATTTAAGAAACAATTAAGAAATTAAGTCACTGCTGAAACAAAGCTCAAGCA 1262
Db 1148 TGGATCTTAAAGAAACAATTAAG-----GAGGTTCTTTAGAGAGCGGCTCAAGCA 1201
Qy 1263 TGGCTAAGAAAGACATACAGTGTGCTGAAATCAAAACAACATCAAGAGAGAG 1322
Db 1202 TGGAAAGAACCAATTTGGCCCACTTTTGAAGAAAGATTTGCTTCAAGAAATACAGA 1261
Qy 1323 AAGATGATATGACCTGACAAATATTTGTTGTTG---CTTCATCCCAAGATCTCAAC 1379
Db 1262 ATGAGAAATTTGAAATCTTAACAGAGATGCTGTGACCTTCTTCTCCAGCTTCAAC 1321
Qy 1380 AGGACCAAGGCTCAAGCAAGAAAGTTCAGTGGCGCGAGAAATTCCAAAATA 1439
Db 1322 AGGAATTAAGGCTAAAGAAAGAAAGAGTTCAGTGGCGCGCAAAATTAACAAA 1381
Qy 1440 GTTTACATGCTCTGTGTTTCTGACTTGTATGATGATCCAGATCTGCGCAATTTTA 1499
Db 1382 TGAAGAA-----CTCAACTATGACAGATCAATTTAATTAATCAACAAATATTA 1429
Qy 1500 GCAGAGAGCAAGTCTCTGACATGCTTCAATTTCCAGAAATGATGATGCTGTTGTA 1559
Db 1430 CAACAAACACATATAGCTTTCTAATTTATTAATTAATGAGAAATGATGATCTGTCTGT 1489

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Qy 1560 CAGAGTTTCTGATTTTGTAGCGCCCT 1587
Db 1490 CAGAGTCTGATTTTTCAGTAACACTCT 1517

RESULT 3
US-10-037-270-130
; Sequence 130, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1ei Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 130
; LENGTH: 8503
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (91)..(8082)
; US-10-037-270-130

Query Match 6.4%; Score 620.4; DB 14; Length 8503;
Best Local Similarity 65.5%; Pred. No. 2,6e-131;
Matches 1001; Conservative 0; Mismatches 491; Indels 36; Gaps 5;

Qy 69 GCCGCCAAAGGAGCTAAAGTACAGAGACAGAGACGCGTGTGCTACCGATTTCTCCAC 128
Db 17 GCGGCGTGTGAGCCCTGAAAGTCCGCGCGGAGGCTCTGCGCAATTTTGGTGGAGCCAG 76
Qy 128 TTAATGCGTCTCAAAATGTCGAGGAGATGCTTAAGTGTGTGTGAGCGTTCCGCCCC 188
Db 77 TTCACCTGATATGATGCGGAGAGAGAGCGTGTGCGTCTGCGTGTGCGAGTCCGCCCC 136
Qy 189 TTATACAGAGAAACA-----GGGATCAAGCCAACTGCAATGGAAGAGCTGGAACA 242
Db 137 TGAACAGCAGAGAAAGATCACTTGAAGAAATGCCCCAGTTTACTGGAAGAACTGACAAATA 196
Qy 243 ACACATTTCCCAAGTGTGATGAGCAAGATCTTCAATTTGATGATGATTTAAATTTCTC 302
Db 197 ATGATATTTATCAAGTGTGATGAGAAATATCTTCAATTTGATGATGATGATGATGAT 256
Qy 303 AGCAATCAACAAAGTCAATTTTCAAGAAATGCGATCTATCATATGATCAAGCTTTGCG 362
Db 257 ATGAACACTACCAAAATGTATGAAAGAAATGCGAGCAACATTCATTCGATTCATAC 316
Qy 363 AGGATATATGCAACATATTTGATGATGCGAGCAGACATCTTCAGGCAAGAGCTACAAA 422

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317 AAGGTACATGCTCTATATTTGCTTGAAGACAGCTGCTTGCAGAAAAACATATCCA 376
423 TGATGGAAACCAAAATTCATTTGGGCAATATACCCAGCATGAGAGTTTAAAA 482
377 TGATGGGTTGAGAAATCATTTGGAGTTATACCCAGGCAATTCATGACATTTCCAA 436
483 TTATTCAGAGATTCGGAACAGAGATTTCTTAAAGATTTCTTATATGAGATTACA 542
437 AAATTAAGAGATTTCTGATAGGAAATTTCTTACCTGTATCTTACATGAAATATACA 496
543 ATGAACTGTGAAAAGCTTACTGTGTATGACAGAAAGAAAGCCCTTGGAAATTCGG 602
497 ATGAAACCATTAACGATTTACTGTGGCACTCAAAAAAGAAACCTTTAATTTATCG 556
603 AGATTTTAAATGAAAGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 662
557 AAGATGCTATGAGAAATGTTATGTTGCTGATCTCAGAGAAAGTTGTATATACATG 616
663 AACCTGTAATACAGTGTATCAAAAGGTTGAAAAAAGAGACATTAATGAGAGCTAAA 722
617 AAATGCTTTGAATGATTAACAAGGAGAAAAAGAGAGGCAATTAAGAGAAACAAAA 676
723 TGAATGATCAATAGTATCTTCTTCAATCAATTTTGAATGATGTTGAAAGCCAGACA 782
677 TGATCAAAAGAGAGCTGCTTCTCAATCCATCTTATAGATGATTTGAAAGCAGAGAGA 736
783 GAAATGATCCCAAAATTCAGAGAACTGTGATGAGCTGTATGATCTTCACTTGAAT 842
737 AAGGTGAACTTCTAAT-----TGTGAAGATCTGTAAAGTATCCCATTTGATTT 787
843 TGGTATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
788 TGGTATGATCTTTCAGAGAGAGTGAAGAGCTGCTCAAAAGAGGCTGAGAGTGGGCTCA 847
903 AGGAAGCTGCAACATCAACAGAGCTGTTTATCTTGAACAGTATTAAGAGCTTA 962
848 AGGAAGCTGTAATTAATTAAGAGCTTATTTATTTGGGACAGATGATMAAACTTA 907
963 GCGAGCGCCAGGCTGTGAGATTTTAACTACAGAGACAGAACTCAACAGAAATCTCC 1022
908 GTGATGAGCAAGTTGGTGGTTTCATTAATTAATGAGATGACAAAGTATTCCTTC 967
1023 AAAATTCATTTGGAGAAATGCTTAAACGGTTAATTTGCAATTAATGCGCAATTTCTT 1082
968 AGAATTCCTTGGAGAAATCCAAAGACGTTATTTGCACAATTAATTCAGATCTT 1027
1083 TTGATGAGCTCTTAAGTACACTTCAAGTTTGCAGTACGCAAAACATGAGAAATCTC 1142
1028 TTGATGAACTCTTACTGCTCTCCAGTTTGCAGTACTGTAAATATATGAGAAATCTC 1087
1143 CCCATGTTAATGAGTCTGTGATGAGAGCTTGTAAAGGTTACAGAAAGAAATCT 1202
1088 CTTATGTTAATGAGTATCACTGATGAAGCTTCTCTGAAAGGTTAGAAAGAAATTA 1147
1203 TGGATTTAAAGAAACATTAAGAAATTTAGATCAATGCTGTAACAAAGCTCAAGCA 1262
1148 TGGATCTTAAAGAAACATTAAG-----GAGGTTCTTTAGAGCGGGCTCAAGGCA 1201
1263 TGGCTAAAGAGACATACAGATTTGCTGTAAGTAAATCAAACTACAAAGAGAG 1322
1202 TGGAAAGAGACAAATTTGGCCCACTTTTGGAGAAAAAGATTTCTTACAGAAATTA 1261
1323 AAGATGATATGAGCACTTGAACAAATATTTGTTG---CTTCAATCCCAAGAAATCTCAC 1379
1262 ATGAGAAATTTGAAATTTAAACAGGATGCTGTGAGCTCTTCTTCTTCAAGTGCAC 1321
1380 AGGACCAAGGCTCAAGAAAGAGAGATTAAGTGGGCGCCAGAGAAATCAAAATA 1439
1322 AGGATTTAAGGCTTAAAGAAAGAGAGATTAAGTGGGCTTGGCAAAATTAACAAA 1381
1440 GTTATACATGCTTCTGTTGTTCTGACTTTGATATGATCAATTAATCTGCGCAATTTTA 1499

Db 1382 TGAAGAA-----CTCAACTATGACATCAATTTAATATCAACAAATATAA 1429
Qy 1500 GCAAGAGGCAAGATTTCTGACATGCTTCAATTCAGAAATGATGACTGTTTGA 1559
Db 1430 CAACAAAACACATTAAGCTTTCTATTAATTTATTAAGAGAAATGATGATCTGCTGT 1489
Qy 1560 CAGATTTTCTGATTTTGTATGAGCGCCCT 1587
Db 1490 CAGAGTCTGATGTTTTCAGTAACACTCT 1517

RESULT 4
US-09-893-519A-140
Sequence 140, Application US/09893519A
Publication No. US20030027243A1
GENERAL INFORMATION:
APPLICANT: ANADYS PHARMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BUURMAN, Ed T.
APPLICANT: BRADLEY, John
APPLICANT: DESILVA, Thamara
APPLICANT: HARRIS, Sandra
APPLICANT: KOMARNITSKY, Svetlana
APPLICANT: MENDILLO, Marc
APPLICANT: MCCOY, Melissa
APPLICANT: SANDERSON, Karen
APPLICANT: HAO, Farig
APPLICANT: ZHU, Shuhao
APPLICANT: LONG, Fan
APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTI-FUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/1G548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.1
SEQ ID NO 140
LENGTH: 7992
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER:
DATABASE ENTRY DATE: 1993-01-10
RELEVANT RESIDUES: (1)..(7992)
US-09-893-519A-140

Query Match 6.4%; Score 615.2; DB 11; Length 7992;
Best Local Similarity 66.7%; Pred. No. 3.9e-130;
Matches 970; Conservative 0; Mismatches 448; Indels 36; Gaps 5;

Qy 143 ATGTCCGAGGAGATGCAATTAAGTGTGTGAGGTTGGCGGCTTATACAGAGAA 202
Db 1 ATGGCGGAGAGAGAGCGGTGGCGGTCTGGGTGAGGTGGCGGCTGAACACAGAGAA 60
Qy 203 CAA-----GGGAGTCAAGCCACCTGCATTTGAGAGGCTGGAACAACACATTTCCAA 256
Db 61 GAATCACTTGGAGAACTGCCCAAGTTTACTGAAAACTGACAAATATGTCAATTAACA 120
Qy 257 GTGATGGGCAAAAGTTTTCATTTTCGATCGTTATTTAATTTCTACAGAAATCAAGT 316
Db 121 GTTATGAGATTAATCTTCAATTTTGAATCGTCTTTCAATGTAATGAATACCAAA 180
Qy 317 CAAATTTACCAAGAAATAGCAGTACTATCATACATGCTTTGAGAGATATATGTC 376
Db 181 AATGTGATGAAGAAATATGAGCAGCAATCATGATTCGCCATCAAGGCTACAAATGT 240
Qy 377 ACAATATTTGATGAGAGACATCTTCAGGCAAGAGTACACAAATGATGAGAAACACCA 436

Db 241 ACTATATTTTCCCTATGACAGACTGCTTCAGGAAAAACATATACATGATGGGTTTCAGA 300
Qy 437 AATTCATTTGGGCAATAATACCCCAAGCCATACAGAAAGTTTAAATTTATTCAGAGATA 496
Db 301 GATCATTTTGGAGTTATACCCAGGGCAATTCATGACATTTTCCAAAAATTAAGAAGTTT 360
Qy 497 CCGAAGAGAGAGTTTCTTCTAAGAGTTTCTTATATGAGATTTTACAATGAAGTGTGAAA 556
Db 361 CCGATAGGGAATTTCTTCTTACGTATCTTACATGAAATTAACAATGAAGCATTACA 420
Qy 557 GACCTACTGTGTATGACAGAAAGAAAGCCCTTGGAAATTTGCCAGATTTTAAATAGA 616
Db 421 GATTTACTCTGTGACACTCAAAAAATGAAACCTTTATTTTGGAGAGATGTCATAGG 480
Qy 617 AACGTGTATGTGTGCTGACCTGACTGATAAGAACTTGTATAGGTTCTGTACATGTATACAG 676
Db 481 AATGTGTATGTGTGCTGATCTCAGAGAAAGTTGTATATACATCAGAAATGCGCTTGAAA 540
Qy 677 TGGATCAAAAAGGTTGAAAAAAGACACATTTATGAGAGACTAATAATGATCATAGT 736
Db 541 TGGATTTACAAAGGAGAAAAAGACAGGCAATTTAGAGAAACAAAAATGAATCAAGAGC 600
Qy 737 AGTCGTTACATCAATATTTAGATGATGTGAAAGCCGAGACAGAAATGATCCACA 796
Db 601 AGTCGTTCTCATRCCATCTTTAGAGATGATTTGAAAAGCAGAGAGAGGTTGAACTTCT 660
Qy 797 AATTCAGAGAACTGTATGAGAGCTGTATGTATCTCACTTGAATTTGGTATGATCTTGT 856
Db 661 AAT-----TGTAGAGATCTGTAAAGTATCCCATTTGAATTTGGTATGATCTTGCA 711
Qy 857 GGCAGTGAAGAGCAAGCCAACTGAGCTGAAAGGTGTGAGATTTAAGAAAGCTGTCAAC 916
Db 712 GGCAGTGAAGAGCTGCTCAAGAGGCTGACAGGTGTGAGGCTCAAGAGAGGCTGTAAAT 771
Qy 917 ATCAACCGAGCTGTTTATTCCTTGGACAGGTATTAAGAAAGTTTGGCAGCGCCAGGCT 976
Db 772 ATTAATCGAAGCTTATTTATTTTGGAGCAAGTATCATCAAGAACTTATGTATGACAAAGT 831
Qy 977 GGTGATTTATTAATACTACAGAGACAGCAAACTGACAGAAATTTCCAAAATTCATTGGGA 1036
Db 832 GGTGATTTATTAATACTACAGAGATGACAAAGTTTCAAGAAATTTCTTCAAGATTTCTTGGA 891
Qy 1037 GGAATATGCTAAAAAGGTTATATTTGACAAATTAAGCCAGTTCTTTTGTATGAGACTCTTA 1096
Db 892 GGAATATCAAAAGCAAGTATTAATCTGACAAATTAATCTCAAGTATCTTTGTATGAAACTCTT 951
Qy 1097 AGTACACTTCAGTTTCCAGTACTGACCAAAATCATGTGAGAAATCTCCCACTGTTAATGAG 1156
Db 952 ACTGCTCTCAAGTTTCCAGTACTGCTTAATATATGAGAAATCTCTTATGTATATGAG 1011
Qy 1157 GTCTGATGATGAAAGCGTTGTCTTAAAGAGTACAGAAAGAAATCTTGTGATTTAAAGAA 1216
Db 1012 GTATCAACTGATGAAGCTCTCTGAAAAGGTATAGAAAAGAAATTAATGATCTTAAAGAAA 1071
Qy 1217 CAATTTAGAGATTTAGAGTATGCTGAAAACAAAAGCTCAGCAATGCTTAAAGAGAG 1276
Db 1072 CAATTTAGAG-----GAGGTTTCTTTAGAGACCGGGGCTCAGGCAATGGAAGAACCAA 1125
Qy 1277 CATACACAGTTGCTACTAGTAAATCAAAACAACTACAGAAAGAGAGAAAGTATGAATATG 1336
Db 1126 TTGGCCCAACTTTTGAAGAAAAAGATTGCTTCAAGAAATGACAGATGAGAAATTTGAA 1185
Qy 1337 CACTTGACAAATATTTGTTGT---TGCTTCAATCCCAAGAAATCTCAACAGAGCAAAAGGCT 1393
Db 1186 AACTTAAACAGAGATGCTGTGAGACTCTTCTTCTTCAAGTGAACAGAAATTAAGGCT 1245
Qy 1394 AAAAGAAAAGAGGTTACGTGAGGCGCCAGAGAAAAATCCAAATATGTTTACATGCTTCT 1453
Db 1246 AAAAGAAAAGAGGTTACGTGAGGCGCCAGAGAAAAATTAAGAAATTAAGAAATTAAG 1305
Qy 1454 GGTGTTTCTGACTTTATATGCTATCAGATTAATCTGGAATTTTGAAGAAAGGAGAG 1513

Db 1306 TATGACATCAATTTAATATACACA-----AATATAACAAACAAACAT 1353
Qy 1514 TTCTGACATGCTTCAATTTCCAGAAATTTGATGACTGTTGTACAGAGTTTCTGAT 1573
Db 1354 AACCTTTCAATAATTTAATTAACAGAAATTAAGAAATGAGAAATGCTGTCTGATGATTT 1413
Qy 1574 TTGATGACGCTT 1587
Db 1414 TTCAGTAACTCTT 1427

RESULT 5
US-09-833-790-351
; Sequence 351, Application US/09833790
; Patent No. US2002068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tonglong
; APPLICANT: Secret, Heather
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Indriase, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-790-351

Query Match 2.1%; Score 206.6; DB 9; Length 581;
Best Local Similarity 68.4%; Pred. No. 5.8e-37;
Matches 333; Conservative 0; Mismatches 144; Indels 10; Gaps 3;

Qy 955 GAACTTACGACGCGGAGCTGTGATTTATTAATTAACAGAGACAGAACTCACAG 1014
Db 72 GAACTTACGATGAGCAAGTTGTGTTTCAATTAATTCAGATAGCAAGTTACAG 131
Qy 1015 AATTCCTCAAAATTCATTTGGAGAAATGCTAAACGGTTATATTTGCACATTAAGCC 1074
Db 132 AATTCCTCAAAATTCCTTGGAGAAATGCAACACGTATATTCGACAAATTAATCTC 191
Qy 1075 AGTTCTTTGATGAGACTCTTAAGTACCTCAGTTTGCAGTACGCAAAATCATGTGAG 1134
Db 192 AGTATTTTGTATGAGAAACCTTAAGTCTTCCAGTTTGCAGTACGCTAAATATGAA 251
Qy 1135 AATATCTCCCATGTTAATGAGTCTGATGATGAAGGCTGCTTAAAGAGTACAGAA 1194
Db 252 GAATACTCTTATGTTAATGAGATTAACAAGTATGAAAGCTTCTGAAAGGATAGAA 311
Qy 1195 GGAATCTTGAATTTAAGAAACAAATTAAGAAATTTAGTATGCTCTGAAACAAAGC 1254
Db 312 AGAAATTAATGATCTTAAAGAAACAAATTAAG-----GAGGTTTCTTTAGAGACGCGGCG 365
Qy 1255 TCAAGCAATGGCTTAAAGAGAGATACACAGTTGCTAGTGAATCAACAACTACACA 1314
Db 366 TCAAGCAATGAGAAAGAACCAATTTGCCCACTT-TTGAAGAAAAAGATTTGCTTACAA 424
Qy 1315 AGAGAGAGAGATAGATATGACACTTGAACAATATGTTGT---TGCTTCAATCCCAAGA 1371
Db 425 AGTACGATGAGAAATTTGAAACCTTAACAGAGATGCTGTGACCTCTTCTTCCCTCAG 484
Qy 1372 ATCTCAACGAGACCAAGGCTCAACGAAACGAAAGATTTAGTGGGCGCCAGAGAAAT 1431
Db 485 GTTGACACGAGATTAAGGCTTAAAGAAAGAAAGAAAGAGATTTAGTGTGCTTGCAGAAAT 544
Qy 1432 CCAAAAT 1438

Db 545 ACCAAT 551

RESULT 6

US-10-175-523-155

/ Sequence 155, Application US/10175523

/ Publication No. US20030096264A1

/ GENERAL INFORMATION:

/ APPLICANT: Brockman, Jeffrey

/ APPLICANT: Evans, David

/ APPLICANT: Hook, Derek

/ APPLICANT: Klimczak, Leszek

/ APPLICANT: Laeng, Pascal

/ APPLICANT: Paley, Michael

/ APPLICANT: Rajan, Pritchi

/ TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)

/ FILE REFERENCE: 3235/10795-US3

/ CURRENT FILING DATE: US/10/175,523

/ PRIOR FILING DATE: 2002-06-18

/ PRIOR APPLICATION NUMBER: US 60/299,151

/ PRIOR FILING DATE: 2001-06-18

/ PRIOR APPLICATION NUMBER: US 60/317,828

/ PRIOR FILING DATE: 2001-09-07

/ PRIOR APPLICATION NUMBER: US 60/325,150

/ PRIOR FILING DATE: 2001-09-25

/ PRIOR APPLICATION NUMBER: US 60/333,047

/ PRIOR FILING DATE: 2001-11-14

/ PRIOR APPLICATION NUMBER: US 60/349,936

/ PRIOR FILING DATE: 2002-01-18

/ PRIOR APPLICATION NUMBER: US 60/361,834

/ NUMBER OF SEQ ID NOS: 197

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 155

/ LENGTH: 2109

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-10-175-523-155

Query Match 1.5%; Score 147.8; DB 14; Length 2109;

Best Local Similarity 51.8%; Pred. No. 4.2e-23;

Matches 530; Conservative 0; Mismatches 452; Indels 41; Gaps 7;

QY 234 CTGGAACCAACACCAATTTCCCAAGTTGATGAGCAAAAGTCTTCAATTCGATCGGTAT 293

Db 140 CTGTACATAGACATGATTTCTTCCATGAACTCCAAAGACATTTACTTTGATCTGTTT 199

QY 294 TTAATTCGACGATCAACAGTCAATTTTCAAGAAATAGAGTACTTATCATAGAT 353

Db 200 TTGGACCAAGAGTAAACCACTTGATGTTTAACTTAAGTCACTGACCACTTATTTGATT 259

QY 354 CAGCTTGCAGGATATATGACAAATTTTGCATACGAGACATCTTCAGGCAAGA 413

Db 260 CTGTACTGGAAGCTCAATGAGCACTTTTTCATATGACAAACGGAAGGCAAGCA 319

QY 414 CGTACCAATGATGGG-----AACACCAATTCATGGGCATATATACCCCAAGCA 464

Db 320 CTTTACCACTGAAAGGTTCGAGCTATTCGAACTTGAAGAAATATCCCAATTCAT 379

QY 465 TA---CAGGAGTTTAAATATATCAGAGATACCGAACAAGAGTTTCTTCAAG 521

Db 380 TTGCTCAATATTTGCTCATATTTGCAAAAGCGAGGTGATCAAGGTTTGGTTGAG 439

QY 522 TTTCTTATATGAGATTTTCAATGAAACTGTGAAAGACCTACTGTGTGACAGAGAA 581

Db 440 TGTCTTATTTGAAATATATATATGAAGAGTTCGAGACCTTTTGGGCAAGATCGAC 499

QY 582 AGAAGCCCTGGAATTCGCGAGGATTTTAAATAGAAAGCTGTATGTCGACCTGACTG 641

Db 500 AAGAG---TTACCGGTTAAAGAAAGCCGATGTGGAGTTTATATCAAAAGATTATCAG 556

QY 642 AAGAACTGTATATGTTCTCTGAAACATGTATATACAGTGTATCAAAAGGTTAAAAAACA 701

Db 557 CTTATGTGTAATAATGCTGATGATATGATAGATTAAGACCTAGGCCACAAAATC 616

QY 702 GACATTTATGAGAGACTTAAATGAATGATCATATGATGCTGTTCAATATTTAGAA 761

Db 617 GTTCTGTGTGTGCACTTAATATATGAAAGCAATAGTTCCTGTTCCATGCTTTACAA 676

QY 762 TGAATGTTGAAGCCGAGACAGAAATGATCCCAAAATTCAGAACTGTATGAGCTG 821

Db 677 TTACTATAGATGCACTGA-----AAAGGACATTTGATGTAATCATGACATG 721

QY 822 TCATGTTATTCATCTTGAATTTGATGATCTTGTGAGAGTAAAGAGACCCAACTG 881

Db 722 TCAGATGAGGAGAGCTTCACTTGTGATCTTGTGATCTTGTGATCAAGAGAGCAAAACTG 781

QY 882 GAGCTGAGGTGTGAGACTTAAGAGAGGCTGCAATCAACCGCAGCTTTGTTATCTTG 941

Db 782 GAGCTTCTGAGACGCGCTTAAAGAGAGCTTCAAAATCAATCTTCACTTCCACCTTG 841

QY 942 GACAGGTTATTAAGAGCTTACGAGCGGCGAGCTGTGATTTTAAACTACAGAGCA 1001

Db 842 GTATGTATTTCTGCTTGTGATGATAAAGACATCA---TGTGCTTATGCTAACT 898

QY 1002 GCAAACTCACGAAATTTCCAAAATTAATGAGAGAAATGCTTAAACGCTTATATTT 1061

Db 899 CTAACTGACTGCTTCTTTCAGGATCTTAAAGAGAAATTCAAAACCATGATGTGTG 958

QY 1062 GCACATTAAGCCAG-----TTCTTTGATGAGACTCTAGTACTTCACTTGTGCA 1115

Db 959 CAAATATTTGGGCGACACATTAATGATGATGAACTATGATGATGATGATGATGCA 1018

QY 1116 GTACTGCCAACAATGTGAAATTAATCTCCCATGTTAATGAGTCTGTGATGATGAGCT 1175

Db 1019 ATCGCTAGAGATTTTAAATTAAGCTTAAGATTAATGAGATCAAAAGATCTTTGC 1078

QY 1176 TGTAAAGAGTACGAAAGAAATCTTGATTTTAAAGAAATTAAGATTTAGAT 1235

Db 1079 TGC--GTACGTTCCAGAAAGAAATGAAAGCTGAAAAAGAGCTTAAAGAGTGAAGA 1136

QY 1236 CAT 1238

Db 1137 AAT 1139

RESULT 7

US-09-814-353-21787

/ Sequence 21787, Application US/09814353

/ Publication No. US20030165831A1

/ GENERAL INFORMATION:

/ APPLICANT: Lee, John

/ APPLICANT: Thompson, Pamela

/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

/ FILE REFERENCE: MRI-006B

/ CURRENT APPLICATION NUMBER: US/09/814,353

/ PRIOR FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: US 60/191,031

/ PRIOR FILING DATE: 2000-03-21

/ PRIOR APPLICATION NUMBER: US 60/207,124

/ PRIOR FILING DATE: 2000-05-25

/ PRIOR APPLICATION NUMBER: US 60/211,940

/ PRIOR FILING DATE: 2000-06-15

/ PRIOR APPLICATION NUMBER: US 60/216,820

/ PRIOR FILING DATE: 2000-07-07

/ PRIOR APPLICATION NUMBER: US 60/220,661

/ PRIOR FILING DATE: 2000-07-25

/ PRIOR APPLICATION NUMBER: US 60/257,672

/ PRIOR FILING DATE: 2000-12-21

/ NUMBER OF SEQ ID NOS: 22037

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 21787

/ LENGTH: 3505

TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 3503, 3505
 OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-21787

Query Match 1.5%; Score 146.6; DB 12; Length 3505;
 Best Local Similarity 51.1%; Pred. No. 1.1e-22;
 Matches 523; Conservative 0; Mismatches 459; Indels 41; Gaps 6;

234 CTGGAACAACACACATTTCCCAAGTTGATGGACAAAGCTCTTCAATTTGATGCTGAT 293
 303 CTGTACATAGACTGATTTCTTCCATGACCTCCAAAGACATTTACTTTGATACGT 362
 294 TTAATTCCTCAGATCAACAGTCAATTTACCAAGAAATAGACATCTATCATAGAT 353
 363 TTGACACAGAGATTAACAATTGATGTTATTAATTAATTAATTAATTAATTAATTA 422
 354 CAGCTTGCAGGATTAATGACCAATTTGCTATCGACAGACATCTTCAGGACAGA 413
 423 CTGTACTTGAAGGCTCAATGAGCTAATTTTGCATATGACCAACCGAAGGACGAAA 482
 414 CGTACCAATGATGGGAACCAATTCATTGGCATATATCCCAAGCATACAGAG 473
 483 CTTTTCATGAAAGGTGTTGAGCTATCTCTGAATTAAGGATTAATTTCCCAATTCAT 542
 474 TTTTAAATTTATTCAGAGATACCGAACAGAG-----TTTCTTCAAG 521
 543 TTGCTCAATATTTGGCATATTTGCAAAAGCGGGGTATACAAAGTTTTTGGTTCAG 602
 522 TTTCTTATATGAGATTTACATGAACTGTGAAGCCTACTGTGTGATGACAGAA 581
 603 TGCTTATTTGAAATATATATATGAAAGAGTCTGCTTTTGGGCAAGATCAGAC 662
 582 AGAGCGCTTGAATTCGGAGGATTTTATATGAAACGTATGTTGCTGACCTGAC 641
 663 AAAAG--TTAGCGTTAAAGAAAGACCTGATGGAGTTTATATCAAAATTTATCAG 719
 642 AAGAACTTGAATGTTCTCTGAACATGTAATACATGATCAAAAAGGTTGAAAAAACA 701
 720 CTATATGTAATATATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 779
 702 GACATATGAGAGACTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 761
 780 GTTCTGTGCTGCACTAATATATGACCAATGATGATGATGATGATGATGATGATGATG 839
 762 TGAATTTGAAGCCGAGACAGAAATGATCCCAATTCAGAGAACTGTGATGAGCTG 821
 840 TTAATTAAGATGACATGA-----AAAAGCATTTGATGATGATGATGATGATGATG 884
 822 TCATGATCTCACTTGAATTTGTTGATGATGATGATGATGATGATGATGATGATGATG 881
 885 TCGAGATGGGAGAGCTTCATCTTGTATGATGATGATGATGATGATGATGATGATGATG 944
 882 GAGCTAAGGTGTGAGACTTAAGAAAGCTGCAACATCAACCGACGTTGTTATCTG 941
 945 GAGCTACTGAGACGCGCTTAAGAGAGCTCAAAAATCAATCTTTCACTTTCCACCCTG 1004
 942 GACAGTTATTAAGAACTTAAGCAGCGCGGAGCTGTGATTTTATTAATTAACAGAGA 1001
 1005 GTATATTAATTTTGCCTTGTGATGAGAAAAAGCACTA--TGTCCTTATCTGTAAT 1061
 1002 GCAAACTACAGAAATTTCTCAAAATTCATTTGGAGAAATGCTAAACGGTATATAT 1061
 1062 CTAACTGACTGCTCTTCTTCAAGATTCCTTAAGAGAAATTCAAAAACATGATGCTG 1121
 1062 GCACAAATTACGACG-----TTTCTTTGATGAGACTTAAGTACATTCAGTTTGCCA 1115
 1122 CAATATTTGGGCGACAGATTAATCAATTAATGATAAATCATACATCTACGTTGATGCCA 1181
 1116 GTACTGCCAAACATGTGAGAAATATCTCCCATGTTAATGAGTCTCGATGATGAAGCT 1175

1182 ATCGTCTAAGATATTTAAATAAAGCTAGATTAATGAAATCCAAAGAGCTTTGC 1241
 1176 TGCTAAAAAGTACAGAAAGAAATCTTGATTTAAAGAAACAATTAAGATTAAGT 1235
 1242 TGC--GTCACTTCAGAAAGAAATAGAAAGATGAAAAAGAGCTTGAAAGGTGAAGA 1299
 1236 CAT 1238
 1300 AAT 1302

RESULT 8

US-09-833-790-167
 ; Sequence 167, Application US/09833790
 ; Patent No. US200206828BA1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Wang, Tonglong
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Mohamath, Raedoh
 ; APPLICANT: Inditias, Carol Y.
 ; APPLICANT: Fan, Liqun
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.512
 ; CURRENT APPLICATION NUMBER: US/09/833.790
 ; CURRENT FILING DATE: 2001-04-11
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 167
 ; LENGTH: 501
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-833-790-167

Query Match 1.4%; Score 138.2; DB 9; Length 501;
 Best Local Similarity 57.7%; Pred. No. 2.7e-21;
 Matches 266; Conservative 0; Mismatches 193; Indels 2; Gaps 1;

2844 AATGGAAGCTGATTTGCAAAAGAGTTCGCAAGTCTTTAATGAGATTAAGTACTTAA 2903
 1 AATGCAAGTATGATCGGAAAGAAATTAACAATCTGTTAATGATTAACAAACTCA 60
 2904 ATGCGCTTCTGCGAGAAAGTCCCAAGATTTGCTTTCTGCTGTTGAATGAGAAAA 2963
 61 CTCCTTATATGATGCAAAAGTTCAAAAGATTTGCTGTATTTGGAATTTGGAAGGAA 120
 2964 AGGTTCTGAGCTTCAAGACAGCTTGAGAAAGCA--TTGGAAGAAAAAATGCTTGA 3021
 121 AGATTAATGATCTTCAAGAAAGAACTAAATTAAGAAAGTTGAAAGAAATGAACTTTGCG 180
 3022 GAATGAAGTACTTGGCTATCAGAAATACAAATTTTGGCAATGAAGTGAATGCTTGA 3081
 181 GGAAGAGATCTTTTGGCTTCAAGATTTGAATCTTTTACCTTCTGAAAGTGAAGGCTGAG 240
 3082 AATATGATCAAGCAAGCTTCTGAAGATATATGTTATTAAGCAAGAAAGAGACATTC 3141
 241 GAAAGAGATACAGAACAAATCTGAAGAGCTCCATATATATCAAGAAAAAGATAATT 300
 3142 TGATATATTAAGCAACAGATTAATCAATGACAGAGCAATCTGACAGATTTTACA 3201
 301 GTTTTGAAGTATGTTCAATAGAGAGTGAAGTTCAAGTTTACTTGAAGAAATTTGGGA 360
 3202 ACTGATGAGAGTACACACACAGTCAAAAGTGCAGACAGTGAAGAGCAATCTT 3261
 361 AAGAAAGATGACTGACACATCAAGTGAATTTAAAGCACTGATTAAGATTTCCA 420
 3262 GAGATGAAGAAATGCAATGATGATCTTTTGAAGATTA 3302
 421 AATTTCAAAACCTTCATATGAGCTTTGAGCAAAAGATTA 461

RESULT 9
US-10-116-712-668
; Sequence 668, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 668
; LENGTH: 3753
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-668

Query Match 1.4%; Score 135.2; DB 12; Length 3753;
Best Local Similarity 50.6%; Pred. No. 4.7e-20;
Matches 468; Conservative 0; Mismatches 408; Indels 48; Gaps 4;

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OY 257 GTTGATGGACAAGTCTTTCAATTGCGATGTTAATTCTCAAGATCAACAAGT 316
DB 154 GTTGATGACAGATTAATCCTTCACTACGATTTTGATTGATCCCTCACTGAACAGGA 213
OY 317 CAATTTACCAAGAAATGACAGTACCTATCATAGATAGCTTTGCGAGGATATATGCG 376
DB 214 GAAGCTTCAATACAGCGATGAGCGGCTCACTAATAAGGTGATTTAAAGATATTAATGCA 273
OY 377 ACAATATTGCAATACGACAGACATCTTCAGCGAAGAGTACACATGATGGGAACCA 436
DB 274 ACGGTCCGCGCTATGGGACAGATGCGCTGTGAAAAACCTATCAAGGAGGCTGATAT 333
OY 437 AATTCATTG-----GGCATATACCCCAAGCCATACAGAAATT 475
DB 334 ACTCGACAGCAAGAAATGAACCAAGTTGGGGTTATCTTGGGTAATACAACTGCTC 393
OY 476 TTTAAATTTATTCAGAGATACCGACAGAGATTTCTTCAAGATTTCTTATAGAG 535
DB 394 TTCAAGAAATGATTAAGAAAGAGTCTTGGAATTTACTTGAAAGTGTCTTATCTTAGAG 453
OY 536 ATTACAAATGAATCTGAAAGACCTACTGTGTGATGACAGAAAGAAAGCCCTTGAA 595
DB 454 ATTACATGAAGAAATTTTGATCTTCTATGCCCATCTGTGAGAAAGCTCAATTAAT 513
OY 596 ATTGCGAGGATTTTAATGAACGTGTATGTGCTGACCTGACCTGAACATCTGTATG 655
DB 514 ATACGAGAGGATCTTAAGAAAGGATTAAGATTTGTGGACTCACTGAGAAAGACTGTTTG 573
OY 656 GTTCTGGAACATTAATACAGTGTGATCAAAAAGGTGAAAAAAGACGATATGAGAG 715
DB 574 GTTGCTTGATATCTGTTCTGTTTGGAAAGGGGCAACACTAGAGCTGTGCTCC 633
OY 716 ACTAATATGAATGATAGTAGTCTGCTCAATACATATTTTGAATGATTTGAAAGC 775
DB 634 ACGGCTATGATCTCCAGTGTGCTGATCTGATGCTATCTTACAT--CTCCTTAGAGC 691
OY 776 CAGACAGAAATGATCCCAAAATTCAGAAAGCTGATGAGCTGTATGATGATCTAC 835
DB 692 AAAGAAAGAAAGTACAGAAATAGAG-----CTTTCGCTCCAG 732
OY 836 TTGAATTTGATGATCTTCTGCTGAGTGAAGAGCAAGCAAACTGAGCTGAAGGTG 895
DB 733 CTGCTCTTTGATGACCTGCTGATCAGAAAGACAGAAAGAAACCAAGGCTGAGGGAT 792
OY 896 AGACTTAAAGAGCTGCAACATCAAGCGCTGTTATCTTTGAGACAGTATTAAG 955
DB 793 CGTAAAAAGAGGATTAATTAATTAACGAGGCTCTTATGCTTGGGAAATGATATCAGT 852
OY 956 AAGCTTAGCAGCGGCGAGGCTGTGATTTAATACTACAGAGACAGCAAACTCAGCA 1015
```

RESULT 10
US-10-116-712-661

; Sequence 661, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 661
; LENGTH: 4348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-661

Query Match 1.4%; Score 133.6; DB 12; Length 4348;
Best Local Similarity 50.5%; Pred. No. 1.2e-19;
Matches 467; Conservative 0; Mismatches 409; Indels 48; Gaps 4;

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OY 257 GTTGATGGACAAGTCTTTCAATTGCGATGTTAATTCTCAAGATCAACAAGT 316
DB 187 GTTGATGACAGATTAATCCTTCACTACGATTTTGATTGATCCCTCACTGAACAGGA 246
OY 317 CAATTTACCAAGAAATGACAGTACCTATCATAGATCAAGCTTTGCGAGGATATATGCG 376
DB 247 GAAGCTTCAATACAGCAGTAGGCGCATCAATAAAGTGTATTTAAAGATTAATGCA 306
OY 377 ACAATATTGCAATACGACAGACATCTTCAGCGAAGAGCGTACACATGATGGGAACCA 436
DB 307 ACGGTCCGCGCTATGGGACAGATGCGCTTGAAAAACCTATTCATGAGAGTGCATAT 366
OY 437 AATTCATTG-----GGCATATACCCCAAGCCATACAGAAATT 475
DB 367 ACTCGACAGCAAGAAATGAACCAAGTTGGGGTTATCTTAGGATTAATACACTGCTC 426
OY 476 TTTAAATTTATTCAGAGATACCGAACAGAGTTCCTTGAAGTTCCTTATAGAG 535
DB 427 TTCAAGAAATGATTAAGAAAGAGTGAATTTGAAATTTACTGTAAGAGTGTCTTAAAG 486
OY 536 ATTACAAATGAATCTGTAAGAAAGCTACTGTGTGATGACAGAAAGAAAGCCCTTGAA 595
DB 487 ATTACATGAAGAAATTTTGATCTTCTATGTCATCTGAGAAAGCTCAATTAAT 546
OY 596 ATTGCGAGGATTTTAATGAACGTGTATGTGCTGACCTGACTGAAGAACTGTATG 655
DB 547 ATACGAGAGATCTTAAGAAAGCAATAAGATTTGGGACCTACCTGAGAAAGCTGTTTG 606
OY 656 GTTCTGGAACATGATATCAGTGTGATCAAAAAGGTGAAAAAAGACGATTAATGAGAG 715
DB 607 GTTGCTTGATATCTGTTCTGTTTGGAAAGGCAACACTTAGAGCTGTGAGGCTCC 666
OY 716 ACTAATATGAATGATAGTAGTGTGTTACATCAATATTTAGATGATTTGAAAGC 775
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Db 667 ACGGCTATGAACTCCAGTGTGCCGATCTCATGCCATCTTTACAAT--CTCCTTAGAGC 724
Qy 776 CGAGACAGAAATATATCCCAAAATTGAGAGACTGTGAGCTGTGATATCTCAC 835
Db 725 AAGGAAAGAAAGTGAACAAGATAGCAG-----CTTTCGCTCCAG 765
Qy 836 TTGAATTTGGTATCTGTGTGAGAGAAAGCAAGCCAACTGGAGCTGAAGGTG 895
Db 766 CTGCATCTTGTAGACCTCGCTGATCAGAAAGACAGAAACCAAGCTGAAGGGAT 825
Qy 896 AGACTTAAGGAAGGCTGCAACATCAACCGAGCTTGTATCTTGGACAGTTAATAAG 955
Db 826 CGCTTAAGAGAGGATTAATTAATTAACGAGGCTCTATGCTGGAAATGTAATCAGT 885
Qy 956 AAGCTTAGGACGCGCAGGCTGTGATTAATACTACAGACAGCAAACTCACCAGA 1015
Db 886 GCTCTTGAGATGACAAAAAGGTGGCTTGCGCCCTACAGAGATTCCAAGTTGACTCGA 945
Qy 1016 ATTCTCCAAATTCATTGGAGGAATGCTAAACGGTTAATTTGCAATTAAGCGCA 1075
Db 946 CTGCTTCAAGATTCTCTAGAGGTAATAGCCATATCTTATGATAGCTGTGAGTCTT 1005
Qy 1076 GTT-----TCTTTGATGAGACTTAAGTACACTTCAGTTGCCAGTACTGCCAAACAT 1129
Db 1006 GCTGACTCCATTTAGAGAAACATTAATACCCTTCGCTATGCTAGACAGCAAGAAAA 1065
Qy 1130 GTGAGAAATACCTCCCATGTTAAT 1153
Db 1066 ATCAAGAACAAACCTATTGTTAAT 1089
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RESULT 11
US-10-116-712-667
; Sequence 667, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116.712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 667
; LENGTH: 4348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-712-667
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Query Match 1.4%; Score 133.6; DB 12; Length 4348;
Best Local Similarity 50.5%; Pred. No. 1.2e-19;
Matches 467; Conservative 0; Mismatches 409; Indels 48; Gaps 4;
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Qy 257 GTTGATGGACAAAGTCTTCAATTCATGATGTAATTTAATCTGACGAATCAACAAGT 316
Db 187 GTTGATGACAGATTAATCTTCACTCACTGATTTGATTTGATCCCTCACTGAACAGAA 246
Qy 317 CAAATTTACCAAGAAATAGCAGTATCTATATCGATCAGCTTTCAGAGGATTAATGGC 376
Db 247 GAAGTCTTAATAACACAGAGGCGCACTCATTAAGGTTAATTAAGATTAATATGA 306
Qy 377 ACNATTTTGCATACGAGACGATCTTTCAGCAAGCGTACGATGATGGAGAACCA 436
Db 307 ACGGTCTGCTTATGAGGAGCTGCTGAGAAAACTTATTCATTTGAGAGGTGATAT 366
Qy 437 AATTCATTG-----GGCATATACCCCAACCATACAGAAATT 475
Db 367 ACTGACAGACCAAGATGAAACCAACAGTTGGGTTATTCCTAGGTAATCAACTGCTC 426
Qy 476 TTTAAATTAATTCAGAGATACCGAAACAGAGTTCTTCTTAAGATTCTTATATGAG 535
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Db 427 TTCAAAGAAATGATTAAGAGAGTACTTTGATTTACTGTGAAGATGCTTACTAGAG 486
Qy 536 ATTTACAAATGAACCTGTGAAGACCTACTGTGTGATGACAGAAAGAAAGCCCTTGAA 595
Db 487 ATTTACAAATGAAGAAATTTTGATCTTCTATGCTCATCTCTGAGAAAGCTCAAAATAT 546
Qy 596 ATTGCGAGAGATTTTAATGAACGCTATGTTGCTGACCTGACCTGAGAACCTGTATATG 655
Db 547 ATTCGAGAGATCTTAAGAAAGGATTAAGATTTGGACTCACTAGAAAGTGTGTTTG 606
Qy 656 GTTCTGAAACATGTAATATACAGTGTATCAAAAAGGTTGAAAAAAGACATTAATGAGAG 715
Db 607 GTTGCTTGATATCTGTTTCCTGTTTGAACAGGGCAACACATTAAGACTGTGGCTCC 666
Qy 716 ACTAAATGAATGATATATAGTATGCTGCTTACATACATATTTTGAATGATTTGTAAGC 775
Db 667 ACGGCTATGAATCCAGAGTGTCCGATCTCATGCCATCTTACAAAT--CTCCTTAGAGC 724
Qy 776 CGAGACAGAAATGATCCCAAAATTCAGAGAACTGTGATGAGCTGTCAATGATCTCAC 835
Db 725 AAGGAAAGAAAGTGAACAAGATAGCAG-----CTTTCGCTCCAG 765
Qy 836 TTGAATTTGGTATGATCTTCTGCACTGCAAGCAAGCCAACTGAGCTGAAGGTGTG 895
Db 766 CTGCATCTTGTAGACTCGCTGATCAGAAAGCAGAAAGAAACCAAGCTGAAGGGAT 825
Qy 896 AGACTTAAGGAAGGCTGCAACATCAACCGAGCTGTTTATCTTGGACAGGTTAATAAG 955
Db 826 CGCTTAAGAGAGGTAATTAATTAACGAGGCTCTATGCTGGGAATGTAATCAGT 885
Qy 956 AAGCTTAGGACGCGCAGGCTGTGATTAATACTAGAGACAGCAAACTCACCAGA 1015
Db 886 GCTCTTGAGATGACAAAAAGGTGGCTTGCGCCCTACAGAGATTCCAAGTTGACTCGA 945
Qy 1016 ATTCTCCAAATTCATTGGAGGAATGCTAAACGGTTAATTTGCAATTAAGCGCA 1075
Db 946 CTGCTTCAAGATTCTCTAGAGGTAATACCATATCTTATGATAGCTGTGAGTCTT 1005
Qy 1076 GTT-----TCTTTGATGAGACTTAAGTACACTTCAGTTGCCAGTACTGCCAAACAT 1129
Db 1006 GCTGACTCCATCTAGAGAAACATTAATACCCTTCGCTATGCTGACAGCAAGAAAA 1065
Qy 1130 GTGAGAAATACCTCCCATGTTAAT 1153
Db 1066 ATCAAGAACAAACCTATTGTTAAT 1089
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RESULT 12
US-10-198-846-13194
; Sequence 13194, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198.846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13194
; LENGTH: 9240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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LOCATION: 1, 9240
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13194

Query Match 1.3%; Score 124.4; DB 14; length 9240;
Best Local Similarity 50.3%; Pred. No. 2.5e-17;
Matches 438; Conservative 0; Mismatches 396; Indels 36; Gaps 4;

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QY 321 TTACCAAGAAATGACGATCTTATCATAGATGAGCTTTGACAGGATATTAATGGCA 380
DB 273 TTTTCAAGTGCTTTGGAGAGATATCTCGAAGATGCTTTGATGAGCTTACAAATGATGTA 332
QY 381 TATTGCAATGAGACAGACATCTTCAGCAAGAGCTACAGATGATGGAAACCAAT 440
DB 333 TCTTGCTATGAGACAGCTGGCTGTGAAATCTTATACATGATGGGACAGCTGACC 392
QY 441 CATTGGCATTAATCCCAAGCCATACAGAACTTTTAAATTTATTCAGAGATACCGA 500
DB 393 AACCTGATTAATCCCAAGCTTTCAGTGAAGCTTTGAAACGAAGCTCAGAAAGAGAAA 452
QY 501 ACAGAGG-----TTCTTCTAAGAGTTCTTAATGAGATTTTAAATGAAGCTGCA 554
DB 453 ATGAAAGACAGAGTTTAAAGTGAAGTGTCTACATGAAATTTATTAATGAAAGTTTC 512
QY 555 AAGACCTACTGTGTGATGACAGAAAGAAAGCCCTTGAATTCGCGAGATTTTAAATA 614
DB 513 GAGACCTCTTGTATCCCAAGAAAGCCGTGAGAGCTTGAAGTCAAGAGCATATGTGT 572
QY 615 GAAACGTATGTTGCTGACCTGACGAAACCTTGTATGTCTTCTGAAACATGTAAATC 674
DB 573 TGGAGCTTATGTGAGAGGCTTCTTAACTGTGCTGACCAAGCTACAAAGATATTGAGT 632
QY 675 AGTGATCAAAAAGGAGGTAAGAAAGACATTAATGAGAGACTTAAATGAATGATCATA 734
DB 633 CGTTGATGTGTGAGGTAACAAATCTGCACTGTGCTGCAACCAATGAAGAGAGAG 692
QY 735 GTAGTGTGTACATACAAATTTAGATGATTTGTAAGCCGAGACAGAAATGATCCCA 794
DB 693 GTAGCGATCCCATGAGGTTCTCAAAATCACCT-----CACGATACCTCT 740
QY 795 CAATTCAGAGAACTGTGATGAGCTGTCAATGATCTCACTTGAATTTGTGATCTTG 854
DB 741 ACGATCGAAGTGTGAGCATCTGAGAGAAAGTGGCAAACTCAGCTGTGTGATTTAG 800
QY 855 CTGGCAGTGAAGAGCAAGCAAACTGAGCTGAAGTGAAGTGAAGTGAAGTGAAGTGA 914
DB 801 CTGGCAGTGAAGAGCAAGCAAGCAAGCGCTGACAGGAGCAGAGCTGAAGAGAGAGCA 860
QY 915 ACATCAACCGCAGCTTTTATCTTGGACAGGTTATTAAGAACTTGAAGCAGGCGCAG 974
DB 861 ACATTAACAAGTCCCTCACAACTCGGTCTGTGTTATCTCACTTTGACAGATCAGAGT 920
QY 975 CTGG-----TGATTTATTAATCAAGACAGAACTTCACCAATTTCTC 1022
DB 921 CTGGCAAAAACAAAGATTAATTTGTTCATATGTAATCAATTCACCTTGTGCTGCTCA 980
QY 1023 AAAATTCATTGGGAGAAATGTCTAAACGTTTAAATTTGCAATTAAGCCAGTTTCT- 1081
DB 981 AAGACAGCTCGGGGGTAAACAGACAGACCGCCATGGTGTACTGTGATCTTCACGCTG 1040
QY 1082 -----TTGATGAGACTCTAAGTACACTTCAGTTTCCAGTACTGCGCAAACTGTGAGAA 1136
DB 1041 ATTAATGATGAGAAACCTCTCACTCTGCGGTATCAGATGAGAGCAAGCATTTGTA 1100
QY 1137 ATACTCCCATGTTATGAGGTCCTGAGAG 1166
DB 1101 ACCAGCGTGTGTGATGAGAGACCTTAATG 1130

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RESULT 13
US-10-433-013-263
Sequence 263, Application US/10133013
Publication No. US2003016903A1

GENERAL INFORMATION:
APPLICANT: Astromoff, Anna
APPLICANT: Bandman, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
PRIORITY FILING DATE: 2002-04-25
PRIORITY FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SEQ ID NO 263
LENGTH: 1726
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US2003016903A1 441283.4
US-10-133-013-263

Query Match 1.3%; Score 122.8; DB 12; length 1726;
Best Local Similarity 45.6%; Pred. No. 2e-17;
Matches 685; Conservative 0; Mismatches 787; Indels 30; Gaps 6;

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DB 213 GAGCAATTAACCCAGAGATTACGACCTAATGAGATGAATGAAATGCTCGGATTG 272
QY 4709 TCTAACAACTTGAAATCCTTCAGAAAGATGAGAGCGTCCGTTCTATTAAGATGAC 4768
DB 273 TCCAAAGACTTCAAGAAAGTATGATGAATGAATCTGTGCTTAAGAGAAAGATGAC 332
QY 4769 CTGCAACAGAACTGAAAAGCTTGTGAGTGAACATTAATTTTAAAGAAATTTGAC 4828
DB 333 CTACAGAGGCTCAAGAAAGTTCTTCAATCTGAAAGTCAAGCTCAAGAAACATTA 392
QY 4829 ACAACCTTAACATCATTCAGATCTCAAGCTCAGCTGCAAGAAACAGCAAGATGA 4888
DB 393 GAAATTTGATGCTTAACACCTGGAACCTGAAGAGAACTTAAGTTGCTCATTTGCTG 452
QY 4889 CAGTTGCTAAGATCTTGCATCGCTGCTTGAACAAATGTCATTAATCAAGAAAG 4948
DB 453 -----AAGAACAGAGAACTATTATAGTTAAGTGAATCTTTCAGAGAG 503
QY 4949 GAAACCTCTGCAATTTGTGTGATCTCTGGAAGAAAGATTTGTTAATCTGAAGAA 5008
DB 504 GAAACTGAATATCAACCATTCMAAAGCAGTTAGAGCAATCAATGATTAATTCAGAAC 563
QY 5009 TTGCATCAAAAACATTAAGACAGGAAATTTACTACATGAAGAAAGATGAAGCTTGA 5068
DB 564 AAGATCCAAAGATTTATGAGAAAGAGAA-----CAATTAATTAACCAATTTAGTGA 620
QY 5069 GCTCAGTTGAGCTAAAGTGCAGAGTGAACATCTGATGAAGAGATGATGAATGGAAG 5128
DB 621 GTTCAGGAAAAAGTGA-----TGAATGAACATTCAGAGGATCCGAAAGCCAGAGAT 677
QY 5129 TCTTACTTGTAGTCTTGTGACAGATGAAGAAATGATACTGAACAAACCTTCTGCTTT 5188
DB 678 TCAGACATTAACAAGTATGAAAGTAAAGTGTGCTGATGACCAACAGACTTCAAGAAAGT 737
QY 5189 AAACAGCAGATGCAAGTATGATCAAGAAAGAAAGAGCTGCAACAAACCATGAACAC 5248
DB 738 CAGAGAAATTAACAAATTTATATTAAGAAAGAAAGAGAAATGAAGAAAGTCAAGAGGCC 797
QY 5249 TTAACAGCTGAGTGAAGCACTTAAGAGAAATGTGAATTTGGTTGAATTTTAAAT 5308
DB 798 CTTCAGATGAGAGAGCACTGAAGAAACCTTAAGAAATTTGTGCTTAATATGAAA 857
QY 5309 GAAAGGAGCAAGAGCACTTAAGAGAAATGTCTGCTTAATGAGATTAAGAACTTGAAG 5368
DB 858 GAAATCTCAAGAAAGAAATATCAGTTTCTTAAGATGACAGCTGCTCAATGAGACTCAGAG 917

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/ APPLICANT: Young, Paul
/ TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
/ FILE REFERENCE: 689290-76
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: US/09/954,456
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: US/60/233,617
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: US/60/234,052
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: US/60/234,923
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: US/60/235,134
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: US/60/235,637
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US/60/235,638
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US/60/235,711
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US/60/235,720
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US/60/235,840
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: US/60/235,863
/ NUMBER OF SEQ ID NOS: 2276
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 733
/ LENGTH: 4858
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-954-456-733
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Query Match      1.0%; Score 95.8; DB 10; Length 4858;
Best Local Similarity 53.5%; Pred. No. 6,2e-11;
Matches 286; Conservative 0; Mismatches 222; Indels 27; Gaps 3;
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DB 734 AAAAGGGGCGACGAAAGGACAACTGAGCTCTGATGAAATGACATCTAGTGT 793
OY 744 CACATACATATTAGATGATGTTGAAAGCGAGACAGAAATGATCCCAAAATTGAG 803
DB 794 CCCACTGAGTTTCTCTGTTACATACATATGAAGA-----AACTACGA 838
OY 804 AGAAGTGTGATGAGCTGTATGATCTCACTGAAATTTGTAGATCTTGCGCAGTG 863
DB 839 TTGATGAGAGAGAGCTGTGTAATCGAAAGTTGAACCTTGATCTTGCGAGAGTG 898
OY 864 AAAGAGCAAGCCAACTGAGCTGAGAGGTGAGACTTAAAGAGGCTGCAACATCAC 923
DB 899 AAAACATGCGCCGTTCTGAGCTGTGATAGAGAGCTCGGAAAGCTGAAATATAATC 958
OY 924 GCAGCTTTGTTATCTTGACAGGTATTAAAGAGCTTAGCGAGCGCGCTGGTGAT 983
DB 959 AATCCCTGTTGACTTTGGGAGGGTCATTACTGCTTGTAGAAAGAACCTCATG--- 1015
OY 984 TTATAACTACAGAGACAGAACTGACAGAAATTTCCAAATTCATTGGGAGAAATG 1043
DB 1016 ---TTCTTATCGAGATCTAAACTAGTAGAATCTCCAGGATTCCTTTGAGGGCGTA 1072
OY 1044 CTAAAGCGTTATTAATTGACAAATTCAGCCAGTTTC-----TTTGTAGAGACTTAA 1097
DB 1073 CAAGAACATCTTAATTTGCAACATTTCTCCGATCTCTCATCTTTAGAGAACTCTGA 1132
OY 1098 GTACCTTCAAGTTGCACTACTGCGCAACATGTAGAAATACCTCCCATTTAATGAG 1157
DB 1133 GTACATTTGAAATATGCTCTAGAGCAAGAACATTTGAATAGCCTGAAGTGAATCAG 1192
OY 1158 TCTTGATGATGAGCGTTGCTAAAGGTACAGAAAGAAATCTTGATTTAA 1212
DB 1193 AACTCACCAAAAGCTCTTATTAGAGATATAGGAGAGATGAACGTTTAA 1247
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Job time : 2254 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 22, 2003, 19:44:52 ; Search time 308 Seconds
(without alignments)
4233.265 Million cell updates/sec

Title: US-09-724-584-1
Perfect score: 14769
Sequence: 1 MSEGDAVAVCVRRVRLPIORE.....QAENWYEAKKETAECKTS 2954

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3615.5	24.5	8257	4	US-09-595-684B-30
2	3613.5	24.5	8503	4	US-09-620-312D-130
3	1153	7.8	10136	1	US-08-353-700-2
4	1153	7.8	10136	5	PCR-US95-16216-2
5	1061	7.2	8789	1	US-08-328-254-5
6	1051	7.1	4757	4	US-09-572-191-1
7	1051	7.1	4757	4	US-09-723-262-1
8	1051	7.1	4757	4	US-09-723-219-1
9	941.5	6.4	4348	4	US-09-595-684B-22
10	941	6.4	4127	4	US-09-592-054-7
11	915.5	6.2	4176	4	US-09-722-139-1
12	915.5	6.2	4176	4	US-09-721-832-1

13	915.5	6.2	4176	4	US-09-721-689-1	Sequence 1, Appl
14	909.5	6.2	4308	4	US-09-592-054-1	Sequence 1, Appl
15	867.5	5.9	3572	2	US-08-713-815A-2	Sequence 2, Appl
16	866	5.9	30549	4	US-09-134-001C-322	Sequence 322, App
17	848	5.7	6773	4	US-09-166-350-27	Sequence 27, Appl
18	841.5	5.7	3837	4	US-09-724-517-1	Sequence 1, Appl
19	841.5	5.7	3837	4	US-09-641-807A-1	Sequence 1, Appl
20	841.5	5.7	3837	4	US-09-723-096-1	Sequence 1, Appl
21	828	5.6	580073	4	US-08-545-528D-1	Sequence 1, Appl
22	776	5.3	8848	4	US-09-643-597-119	Sequence 119, App
23	776	5.3	8848	4	US-09-480-884A-119	Sequence 119, App
24	776	5.3	8948	4	US-09-542-615A-119	Sequence 119, App
25	776	5.3	8948	4	US-09-606-421B-119	Sequence 119, App
26	769.5	5.2	11091	4	US-09-1134-001C-2243	Sequence 2243, App
27	759	5.1	3319	1	US-08-006-676B-2	Sequence 2, Appl
28	759	5.1	3319	1	US-08-282-845-1	Sequence 1, Appl
29	759	5.1	3319	2	US-08-428-414A-4	Sequence 4, Appl
30	759	5.1	3319	5	PCR-US94-0034-2	Sequence 2, Appl
31	758.5	5.1	3709	3	US-09-541-782-7	Sequence 7, Appl
32	758.5	5.1	3709	4	US-09-723-820-7	Sequence 7, Appl
33	758	5.1	7501	4	US-09-620-312D-249	Sequence 249, App
34	756.5	5.1	4911	4	US-09-718-852-1	Sequence 1, Appl
35	756.5	5.1	4911	4	US-09-718-852-1	Sequence 1, Appl
36	756.5	5.1	4911	4	US-09-718-852-1	Sequence 1, Appl
37	755	5.1	7453	4	US-09-620-312D-248	Sequence 248, App
38	754	5.1	13977	4	US-09-484-970B-60	Sequence 60, Appl
39	748.5	5.1	6306	1	US-08-195-487-3	Sequence 3, Appl
40	748.5	5.1	6306	5	PCR-US93-06160-3	Sequence 3, Appl
41	744.5	5.0	6306	1	US-08-466-390-3	Sequence 3, Appl
42	744.5	5.0	6306	1	US-08-470-950-3	Sequence 3, Appl
43	744.5	5.0	6306	1	US-08-467-781-3	Sequence 3, Appl
44	744.5	5.0	6306	2	US-08-483-924-3	Sequence 3, Appl
45	742	5.0	19307	3	US-08-836-022A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-595-684B-30
; Sequence 30, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Bernad, Christophe
; APPLICANT: Oshahi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytop036
; CURRENT APPLICATION NUMBER: US/09/595, 684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295, 612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8257
; TYPE: DNA
; ORGANISM: Human
US-09-595-684B-30
Alignment Scores:
Pred. No.: 8.67e-283
Score: 3615.50
Percent Similarity: 50.34%
Best Local Similarity: 31.97%
Query Match: 24.48%
DB: 4
US-09-724-584-1 (1-2954) x US-09-595-684B-30 (1-8257)
Matches: 996
Conservative: 572
Mismatch: 932
Indels: 615
Gaps: 86


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QY 1 MetSerGluGlyAspAlaValLysValCysValArgValArgProLeuIleGlnArgGlu 20
Db 91 ATGGCGGAGGAGGAGCGCGTCTGCGTGCAGTGCAGCGCGCTGAAACAGCAGAGAA 150
QY 21 Gln-----GlyAspGlnAlaAsnLeuGlnThrLysValGlyAsnAsnThrIleSerGln 38
Db 151 GAATCAGCTTGAGAACTGCCCAAGTTTACTGGAAAGCTGACAAATATATCTCATTTATCAA 210
QY 39 ValAspGlyThrLysSerPheAsnPheAspArgValPheAsnSerHisGluSerThrSer 58
Db 211 GTTGAAGGAGAAATCTTCAATTTGATCGTCTTCAATGATGATGAAAGTAACTCAAA 270
QY 59 GlnIleTyrGlnGlnIleAlaValProIleIleAsnSerAlaLeuGlnGlyTyrAsnGly 78
Db 271 AATGTGTATGAAGAAATAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 330
QY 79 ThrIlePheAlaTyrGlyGlnThrSerSerGlyLysThrTyrThrMetMetGlyThrPro 98
Db 331 ACTATATTTGCTTATGACAGACTGCTCAGGAAACATATACATATGCTGCTTCAAA 390
QY 99 AsnSerLeuGlyIleIleProGlnAlaIleGlnGlnValPheLysIleIleGlnGlnIle 118
Db 391 GATCATTTGGAGATATACCCAGGCAATTCATGACATTTTCCAAAAATTAAGAAGTTT 450
QY 119 ProAsnArgGluPheLeuLeuArgValSerTyrMetGluIleTyrAsnGlnThrValLys 138
Db 451 CCGTAGGGAATTTCTTACGCTGATCTTACATGAAATATACATGAAATGAAATGAAATGAA 510
QY 139 AspLeuLeuCysAspAspArgLysLysProLeuGlnIleArgGluAspPheAsnArg 158
Db 511 GATTACTCTGTGGCACTCAAAATGAAACCTTATATTCGAGAAAGTGCATATAG 570
QY 159 AsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGlnHisValIleGln 178
Db 571 AATGTGATGTGCTGATCTCAGAGAAAGTGTATATACATCAAGAAATGCTTTGAAA 630
QY 179 TrpIleLysGlyGlyLysAsnArgHisTyrGlyGlnThrLysMetAsnAspHisSer 198
Db 631 TGGATTCAAGAGGAGAAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690
QY 199 SerArgSerHisThrIlePheArgMetIleValGlnSerArgAspArgAsnAspProThr 218
Db 691 AGTGTCTCTCATACATCTTTAGATGATTTTGGAAAGCAGAGAGAGAGGCTTAACCTTCT 750
QY 219 AsnSerGluAsnGlyAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAla 238
Db 751 -----AATGTGAGAGATCTGTTAAGTATCCCATTTGAATTTGCTTATCTTCA 801
QY 239 GlySerGluArgLysSerGlnThrGlyAlaGluGlyValArgLeuLysGlyGlyCysAsn 258
Db 802 GGCAGTGAAGAGCTGCTCAACAGCCTGCGAGGCTGCGGCTCAAGAGAGGCTGTAT 861
QY 259 IleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAla 278
Db 862 ATTAATCGAAGCTTATTTATTTGGACAGATGATCAAGAACTTGAAGTGAAGCAAGTT 921
QY 279 GlyGlyPheIleAsnTyrArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGly 298
Db 922 GGGGTTTCATATTAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 981
QY 299 GlyAsnAlaLysThrValIleIleCysThrIleThrProValSerPheAspGluThrLeu 318
Db 992 GGAATTCAGAAAGACGCTATATCTGCACATTTCTCCAGATCTTTTGTATGAAACTCTT 1041
QY 319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValAsnGlu 338
Db 1042 ACTGCTCTCCAGTTGCTCCAGTACTGCTAAATATATGAAGAAATCTCTTATGTTATGAG 1101
QY 339 ValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGlnIleLeuAspLeuLysLys 358
Db 1102 GTATCAACTGATGAAGCTCTCTGAAAGATATGAAAGAAATATATGAGTCTTAAAAA 1161
QY 439 GlnLeuGluAsnLeuGluSerSerGluThrLysAlaGlnAlaMetAlaLysGluGlu 378

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Db 1162 CAATTAGAG-----GAGTTTCTTTAGAGAGCGCGCTCAGGCAATGAAAGAACCA 1215
QY 379 HisThrGlnLeuLeuAlaGluIleLysGlnLeuHisLysGlyValArgGluAspArgIleTrp 398
Db 1216 TTGGCCCAACTTTTGGAGAAAGAAAGATTTGCTTCAAGAAAGTACAGAAATGAGAAATGAA 1275
QY 399 HisLeuThrAsnIleValAlaLysSerGlnGlnSer-----GlnGlnAspGlnArgVal 417
Db 1276 AACTTAAACGAGATCTGCTGATCTTCTTCCCTCAGCTTGCACAGAAATTAAGGCT 1335
QY 418 LysArgLysArgArgValThrTrpAlaProGlyLysIleGlnAsnSerLysLysLys 437
Db 1336 AAAAGAAAGAGAGGTTACTTGTGCTTGGCAAAATTAACAAATGAAAGAACTCAAC 1395
QY 438 GlyValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysValLys 457
Db 1396 TATGACAGATCAATTTAAT-----ATACCAACAAATATTAACCAACAAACACAT 1443
QY 458 PheSerAspMetProSerPheProGlnIleAspAspSerValCysThrGluPheSerAsp 477
Db 1444 AAGCTTTATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1503
QY 478 PheAspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGluThrPheAsnLeuAla 497
Db 1504 TTCAAGTAACTCTTGTATACATTAAGT-----GAGATGAAATGAAATGAAATGAAATGAA 1551
QY 498 SerLysValThrHisArgGlyLysThrSerLeuHisGlnSerMetIleAspPheGln 517
Db 1552 ACAAAGCTACTTAATCAAGAG-----GAGATGAAATGAAATGAAATGAAATGAAATGAA 1572
QY 518 IleSerAspSerValGlnPheHisAspSerSerLysGluAsnGlnLeuGlnThrLeuPro 537
Db 1572 ----- 1572
QY 538 LysAspSerGlyAspMetAlaGluCysArgLysAlaSerPheGluLysGluIleThrSer 557
Db 1572 ----- 1572
QY 558 LeuGlnGlnLeuGlnSerLysGluGluGlyLysGluLeuValGlnSerPheGlu 577
Db 1572 ----- 1572
QY 578 LeuLysIleAlaGlnLeuGlnGlnLeuSerValLysAlaLysAsnLeuGluMetVal 597
Db 1573 -----AATATGAAAGTGAAG 1587
QY 598 ThrAsnSerArgGlnHisSerIleAsnAlaGluValGlnThrAspValGluLysGluVal 617
Db 1588 TTGAATCTCA----- 1596
QY 618 ValArgLysGluMetSerValLeuGlyAspSerGlyTyrAsnAlaSerAsnSerAspLeu 637
Db 1596 ----- 1596
QY 638 GlnAspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGlnHis 657
Db 1596 ----- 1596
QY 658 ArgLysMetLeuGlnGlnLysIleValAspLeuGlnGluPheIleGluAsnLeuAsnLys 677
Db 1596 ----- 1596
QY 678 LysSerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeu 697
Db 1596 ----- 1596
QY 698 CysGluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAsp 717
Db 1597 -----CTTGCTGCT 1605
QY 718 AsnPheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuGlu 737

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Db 1606 GACTGATGATATCTGTTATAGACTATGAAACAAGTACGAAAGAAAGAAAGAAATGGA 1665
Qy 738 ArgSerLeuLysGluAsnGlnGluThrAsnGluPheGluIleLeuGluLysGluThrGln 757
Db 1666 TTGAATATTAAAGAAAGAAAGAAATTTGGATGAAATTTGAGGCTCTGAAAGAAAGAAAGCTAAA 1725
Qy 758 LysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLysLeuValGluAsn 777
Db 1726 AAAAGATCAAGAGATGCACTAAATTCATGAAATTTGCAACTTAAAGAAATTTAGTTAGTAC 1785
Qy 778 AlaGluMetTyrAsnGlnAsnLeuGluGluAspLeuGluThrLysThrLysLeuLys 797
Db 1786 CGAGAGATATATATCAAGATCTTGAGATGAACTGAGTCAAAAGTAAAGTACGCTTAA 1845
Qy 798 GlnGlnGluIleGlnLeuAlaGluLeuArgLysArgAlaAspAsnLeuGlnLysVal 817
Db 1846 GAAAAGGAAAGACCAATTAAGAGCTACAGAAATACATGACTCTCAAAAGCTAGAAAT 1905
Qy 818 ArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeuGluGluIlePhe 837
Db 1906 ATAAAATGAGACTTGTCTATACCTCATTG-----GAAAGCATTGAAAGACCCAAA 1953
Qy 838 GlnLeuLysGlnSerLeuSerAspAlaGluAlaValThrArgAspAlaGlnLysGluCys 857
Db 1954 CAAATGAAGCAGACTCTGTTTATGCTGTAAGCTGAGCCCTTGATGCCAAGAGAGATCA 2013
Qy 858 SerPheLeuArgSerGluAsnLeuGluLeuLysGluLysMetGluAspThrSerAsnTrp 877
Db 2014 GCCTTCTTAGAAGTGAAATCTGGAGTTGGAAGAGAAATGAAGAACTTGCAACTACA 2073
Qy 878 TyrAsnGlnLysGluLysAlaAlaSerLeuPheGlnLysGlnLeuGluThrGluLysSer 897
Db 2074 TACAAGCAAAATGGAATGATATTCAGTTATCAAGGCCAATTTGAGGCAAAA----- 2127
Qy 898 AsnTyrLysMetGluAlaAspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIle 917
Db 2128 -----AGAAATGCAAGTTGATCTGCGAAAGAAATTTCAATCTGCTTTTATGAGAA 2181
Qy 918 AsnTyrLeuAsnGlnLysLeuAlaGlyLysValProArgAspLeuLeuSerArgValGlu 937
Db 2182 ACAAAATCACCTCCCTTATAGATGGCAAAAGTTCCAAAAGATTTGCTCTGTAATTGGA 2241
Qy 938 LeuGluLysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGlnGluLysAsn 957
Db 2242 TTGGAGGAAAGATTAAGTATCTTCAGAAAGAACTAAATTAAGAAATTAAGAAATGA 2301
Qy 958 AlaLeuGluAsnGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGlu 977
Db 2302 GCTTTCGGGAAGAGTCAATTTGCTTTCAGAAATTTGAAATCTTTACCTTCTGAGTAGAA 2361
Qy 978 CysLeuLysAsnGlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGlnGlu 997
Db 2362 AGCGTAGAGAAAGATTCACAAACAATCTGAAGAGCTCCATATATATACATCAGAAAA 2421
Qy 998 GlnHisSerAlaSerIleLeuSerLysGlnGluIleIleMetGlnGlnGlnSerGlnGln 1017
Db 2422 GATTAATTTGTTTCTGAGTACTTTCATAGAGAGAGTAGAGTCAAGGTTTACTTGAGAA 2481
Qy 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnGlnThrGlnGlu 1037
Db 2482 ATTGGGAAAAACAAGATGACCTTAGCACTACACGTCGAATTAATTAAGACCTGATCA 2541
Qy 1038 GlnTyrLeuGluMetLysLysMetHisAspAspLeuPheGluLysTyr----- 1053
Db 2542 GAATTCCAAATTTCCAAACCTTCATATGACCTTGAGCAAAAGATTAAGATGCTCT 2601
Qy 1054 -----TleArgAsnLysSerGluAlaGluAspLeuLeuArgGluMetGluAsnLeu 1070
Db 2602 GAGGAGATGAGAGATGATCAGGAAATAGTTAATCTCTTAAGAAAGCCCAAAATTT 2661
Qy 1071 LysGlyThrMetGluSerValGluValLysIleAlaAspThrLysIleGluLeuGlnGlu 1090
Db 2662 GATTGAGATTGGTGCTTGAAGACCGAGCTTTCTTACAAAGCCCAAGAACTTCGAG 2721

Qy 1091 ThrIleArgAspLysGluGlnLeuLeuHisGluLysLysTyrPhePheGlnAlaMetGln 1110
Db 2722 AAACACGTGAGCTTCAAGAAAGACTTAAATGATGAGAAACAGCTGAGAGCAATTAAGA 2781
Qy 1111 ThrIlePheProIleThrProLeuSerAspSerLeuProProSerLysLeuValGluGly 1130
Db 2782 AAT-----AGAGATTTCCCTCGCAACCTGAGAAAGGAGAAACACTGATTTCTGAG 2835
Qy 1131 AsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
Db 2836 AAATGCGAGCAAACTTTAGAA-----GAGATTAAGAACTTTAATCAAGAAAGAAATGAT 2889
Qy 1151 ArgAsnAsnIleMetValCysLeuGluLysGluValArgAsnSerLeuLysGluGlnVal --- 1169
Db 2890 CTAAACCACTCAAGAAAGCTTGCAAAATTTGAGAGGAGACCAACTCAAAATGATATTCAC 2949
Qy 1170 -----TleAspLeuAsnThrGlnLeuGln-----SerLeuGlnAlaGln 1182
Db 2950 GATCTGTTAATCATGATATATGATATCTCAAGAACATTAAGAAATGCTTGAGCTCTG 3009
Qy 1183 SerIleGluLysSerAspLeuGlnLysProLysGlnAspLeuGluGluGluValLys 1202
Db 3010 AAACAACATCAAGAAACATTAATATACATTAATGCAAAATTTCTGAG---GAGTTTCC 3066
Qy 1203 LeuLeuLeuGluMetGluLeuLeuLysGlyHisLeuThrAsp-----SerGln 1218
Db 3067 AGCAATTTGCATATGAGAGAAATACAGAGAGAACTAAAGATGAATTTCCAGCAAAAGATG 3126
Qy 1219 LeuSerIleGluLysLeuGlnLeuGluLysAsnLeuGluValThrGluLysLeuGlnThrLeu 1238
Db 3127 GTTGCATATGATTAAGAAACAG-----GATTTGGA---GCTAAATTAACCAACACTCA 3177
Qy 1239 GlnGluGluMetLysAsnIleThrIle----- 1247
Db 3178 ACTGCAGATGTTAAGATATGATATGATATGAGCAACAAGAGAGATATTTCTTTAATA 3237
Qy 1248 ---GluArgAsnGlnLeuGlnThrAsnPheGlnAspLeuLysAlaGlnHisAspSerLeu 1266
Db 3238 CAGGAGAAAGAAATGAACTCCACAAATGTTAGAGAGTGTATAGCAAGAAAGAAACAAATTTG 3297
Qy 1267 LysGlnAspLeuSerGluAsnIleGluGlnSerIleGluThrGlnAspGluLeuArgAla 1286
Db 3298 AAGACTGACCTTAAGAGAAATATTTGAATGACCATTTGAAACACAGAGAAATTAAGACTT 3357
Qy 1287 AlaGlnGluLeuArgGlnGlnLysGlnLeuValAspSerPheArgGlnLeuLeu 1306
Db 3358 CTTGGGAGATGAATTAAGAAAGCAACAGAGATGTTGCAACAAGAAAGAACATGCGATA 3417
Qy 1307 AspCysSerValGlyTyrLeuSerSerProAsnHisAspAlaValAlaAsnGlnGluLysVal 1326
Db 3418 AAG---AAAGAGGAGAGCTTTCTAGGACCTGTGACAGCTGCGAGAAATTTGMAAGAA 3474
Qy 1327 SerLeuGluGluValAsnSerLeuGlnSerGluMet-----LeuArgGly 1341
Db 3475 CTAAGGAAAGAAAGAGCCAGCACTCCAGAGAAACAGCAACAACTTTAATGTTACAGAA 3534
Qy 1342 GluArgAspGluLeuGlnThrSerCysLysAlaLeuValSerGluLeuGluLeuLeuArg 1361
Db 3535 GAGATGAGTGAATGACAGAAAGAG-----ATTAATGAATTAAGAAATTTAAG 3582
Qy 1362 AlaHisValLysSer-----ValGluGluGluAsnLeuGluIle 1374
Db 3583 AATGATTTAAGAAACAAAGAAATTTGACATTTGGAACATATGAAACAGAGAGCTTGAGTTG 3642
Qy 1375 ThrLysLysLeuAsnGlnLysGluLysGluIleLeuGluLysSerGluGlnSerGluVal 1394
Db 3643 GCTCAGAAACTTAATGAAATTTATGAGAGAGTGAATCTATATACCAAGAGAAAGAAAGTT 3702
Qy 1395 LeuLysSerMetLeuGluAsnLeuLysGluAspAsnAsnLysLeuLysGluGlnAlaGlu 1414
Db 3703 CTAAGGAAATTAACAAGATCATTTGAACAGAGAGACCACTTAAGAGATAT----- 3756

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OY 1415 GluTyrSerSerLysGluAsnGlnPheSerLeuGluGluValPheSerGlySerGlnLys 1434
Db 3757 -----ATAGAGAAATGAGCTACAGGCTACAA 3786
OY 1435 LeuValAspGluIleGluValLeuLysAlaGlnIleuValAlaGluGluLysLeu 1454
Db 3787 ACCAAGAGAACTAAATAATGCTCATATTACCTTAAAGAACACCAAGAAACTATGAT 3846
OY 1455 IleLysAspArgAspTyrPheGlu--LeuValGlnThrAlaSerThrAsnLeuValGlu 1473
Db 3847 GAACTAAGAAAGAGCCATCTGAGAGACAGCTCAAAATATAAATACCTGAGACTTAA 3906
OY 1474 GlyLysLeuGluIleThrProLeuGlnAlaAsp-----HisGlnGluAsp----- 1487
Db 3907 ---AATCCCATTCACAAATTACAGAGAGATCCAGTGCCTTCATGAGAGAAACAAGATTA 3963
OY 1488 -----SerIleAspArgArgSerGluGluMet-----GluIleLysValLeu 1501
Db 3964 CTGCCTAATGTGAAAAAGTCACTGAGACTCAGAAACATGAACTGAGATTA 4023
OY 1502 GlyGluLys--LeuGluArgAsnGlnTyrLeuLeuGluArgLeuGluGlnLysLeu 1520
Db 4024 ACAGAACAGTCCACAAACAGGACTCAACACCTGGCAGAAATAGAAATGAAAGGCTC 4083
OY 1521 GluLeuSerAsnLysLeuGluIleLeuGlnLysGluMetGluThrSerValLeuLys 1540
Db 4084 AGTTGATGAAAAAATTTCCAGAAAGTCAAGAAAGATTAATCTTACCAAGAAAGA 4143
OY 1541 AspAspLeuGlnGlnLysLeuGluSerLeuSerGluAsnIleIleLysGluAsn 1560
Db 4144 GACAACTTAAAGACATTAAGAAAGCCCTTCAGTAAACATGACCCAGTGAAGAAACAT 4203
OY 1561 IleAspThrThrLeuLysHisIleSerAspThrGlnAlaGlnLeuGlnLysThrGln 1580
Db 4204 ATTAGAGAACTTG-----GCTAAATTCAGAGGCTCTCAAC 4242
OY 1581 GluLeuGlnLeuAlaLysAsnLeuAlaIleAlaLysSerAspAsnLysProIleThrGln 1600
Db 4243 AAACAAAGACAGCTTAAATATGAAAGAAAGAAACATGAATCTCCAAATCTGAGAT 4302
OY 1601 GluLysGlu-----ThrSerAlaAspCysValHisProLeuGlnGluLysIleLeu 1617
Db 4303 GAGATGAGCAATTCAAAACCCAAAGATTCAGCACTCTAAGGATTAATAATAATGCTC 4362
OY 1618 LeuLeuThrGluGluLeuHisGlnLysThrAsnGlnGlnLysLeuLeuHisGlnLys 1637
Db 4363 GATTTGCCAAAGAGCTTCAAGAAAGTCAATGAAATGAATCTGTACTAAGAGAA 4422
OY 1638 AsnGluLeuGlnGlnAlaGlnValGluLysCysGluValGlnHisLeuMetLysSer 1657
Db 4423 GATGACTTACAGAGCTCAAGAAAGTCTTCAATCTGAATGAAAGTCACTC----- 4473
OY 1658 MetIleGluSerLysSerLeuGlnSerLeuGlnHisGluLysHisAspThrGln 1677
Db 4474 -----AAAGAAACATTAAGAAATTTAGTAAACACCTGGAACCTGAAAG 4521
OY 1678 GlnLeu-----LeuAlaLeuLysGlnMetGlnValAlaThrGlnLys 1693
Db 4522 GAATTAAGAGTTCATGCTGCTGCTGAAGAAACAGAGAACTATTAAGATTAAGA 4581
OY 1694 LysGluLeuGlnGlnThrHisGlnHisLeuThrAlaGlnValAspHisLeuLysGluAsn 1713
Db 4582 GTGAATCTTTCAGAGAAAGAA-----ACTGAATATATCAACCATCAAAACAG 4629
OY 1714 IleGlu--LeuGluLeuAsnPheLysAsnGluAlaGlnGlnLysThrThrLysGluGln 1732
Db 4630 TTAGAGCAATCATGATTAATTAACAGAAACAGATCCAGAGATTTATGAAAGAGAA 4689
OY 1733 CysLeuLeuAsnGluAsnLysGluLeuGlnSerGlnHisAlaGluLeuGlnCysGluIle 1752
Db 4690 CAACCT-----AATATTAACCAATTAAGAGGCTTACAGAAACGGAAT--GAAC 4740
OY 4753 GlnGluLeuMetLysSerLeuLysAspLysGluSerAlaLeuGluThrLeuLysGluSer 1772

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Db 4741 AAACAATTCAAGAGAGATGCAAAAGCCAGAGATTACAGCACTCAAGATTA----- 4791
OY 1773 GlnGlnLysValIleAsnLeu-----AsnGlnGluMetGluMet 1785
Db 4792 GAAAGTAAAGATGCTGCAAGTTGACCAACAGACTTCAAGAAAGTCAAGAAATCAAT 4851
OY 1786 ValMetLeuGluMetGluLysLeuLysAsnSerGlnArgThrValIleAlaGluArgAsp 1805
Db 4852 ATGATTAAGAAAGAAAGAGAAATGAAGAAAGATGACAGAGGCCCTTCAGATGAGAGAG 4911
OY 1806 GlnLeuGlnAspAspLeuArgGluSerValGluMetSerIleGluThrGlnAspLeu 1825
Db 4912 CAATGAAAGAAACCTTAAGAAATTTGACTTAATTAAGAAAGATCTCAAGAA----- 4965
OY 1826 ArgLysAlaGlnGluAlaLeuGlnGlnLysAspArgValGlnLysLeuThrSerGln 1845
Db 4966 AAAGAAATACAGTTTCTTAAGATGACAGCTGCTCAATGAGACTCAGGAAATGTTGAA 5025
OY 1846 IleSerValLeuGlnGlnLysIleSerLeu-----LeuGluAsn----- 1858
Db 5026 ATAGAAACCTTAAGAGAGCAATTTGAGAACCCAGAACTTAACCTGAAAAATAGAAAC 5085
OY 1859 -----GlnMetLeuTyr--AsnValAlaThrValLysGluThrLeu 1871
Db 5086 GAGATATTAAGCTTGACTCAGATCTCATGAAACCTTGAAGAAATGAGATCTGTAACA 5145
OY 1872 SerGluArgAspArgLeuAsnGlnSerLysGlnHisLeuPheSerGluIleGluThrLeu 1891
Db 5146 AAAGAAAGAGTGAAGCTTGAAGAGTGTGAGAGAGACTCTCAAGTAAAGAGAGAGCCAG 5205
OY 1892 SerLeuSerLeuLysGluLys--GluPheAlaLeuGlnAlaGluLysAspLys-- 1909
Db 5206 AAGAAAACTTGAAGAAACATTAAGTAAAGCTTGAAGAAACAGAGAGCTTAATAAT 5265
OY 1910 -----AlaAspAlaAlaArgLysThrIleAspIleThrGluLysIleSerAsn 1925
Db 5266 GTTCACATGATCTGAAGAGACACCAAGAACTATGAT-----AAACTAAGAGGG 5316
OY 1926 IleGluGlnGlnLeuLeuGlnGlnAlaThrAsnLeuLysGluThrLeu--TyrGluArg 1944
Db 5317 ATTGTTTCAGAGAAACAAATGAATATCAATATGCAAAAGAGCTTGAACACTCAAT 5376
OY 1945 GluSerLeu-----IleGlnCysLysGlnGlnLeuAlaLeuAsnThrGlnHis 1960
Db 5377 GATGCTTAAAGACACAGAGATCGAAATATCAAGAGAGAACTGAAGATTCCTCAGTCAT 5436
OY 1961 LeuArgGluThrLeuLysSerLysAspLeuAlaLeuGluLysMetGluGlnArgAsp 1980
Db 5437 CTCAAAAGACACAGAGAACTTATGACAAACTCAGAGAAATGTTTCTGAGAGACAGAT 5496
OY 1981 GluAlaAlaAsnLysValIleAlaLeuThrGluLysMetSerSerLeuGlnGlnIle 2000
Db 5497 AAACATATCAATATATGCAAAAGATTTAGAAAATTCAAATGCTTAATATTCAGAAAGAT 5556
OY 2001 AsnGluAsnValThrThrLeuLysGluGluGluGluLysGluThrPheTyrLeuGln 2020
Db 5557 CAAGAA-----CTTAAGCAAAATGACATCACTTATTAAGTAAAAAAGAT 5604
OY 2021 ArgProSerLysGlnGlnSerSerGlnMetGlnGlnLeuArgGluSerLeuLysThr 2040
Db 5605 GTCAATGAGACACAGAAAGAGTCTGCAATGAGAGCACTTAAGAAACAAATTAAGAG 5664
OY 2041 LysAspLeuGlnLeuGluGluAlaGlnLysGluIleSerGluAlaThrAsnGluIleLys 2060
Db 5665 CAAGCTTAACCTCGAGTAATTA-----GAAATAGAG 5697
OY 2061 AsnLeuThrAlaLysIleSerSerLeuGlnGluGluIleLeuGlnAsnAlaSerIleLeu 2080
Db 5698 AATTTA-----AATTGGCTCAAGAACTTATGAAACCTTGAAGAAAG 5742
OY 2081 AsnGluAlaValSerGluArgLysAsnLeuArgHisSerLysGlnGlnLeuValSerGlu 2100

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Db 5743 AAATCTGTAATGAAAGAAAGATAATCTAAGAAGAGTAGAGAGACACTCAAACTGAG 5802
Qy 2101 LeuGluGlnLeuSerLeuThrlLeu-----LysSerArgAspHisAlaPheAlaGln 2117
Db 5803 AGAGACCAATCAAGGAAAGCCCTGCAAGAAACCAAGCTAGAGATCTGGAATACAAACAG 5862
Qy 2118 -----SerLysArgGluLys-----AspGlnAlaVal 2126
Db 5863 GAACTAAAACTGCTGCTATGCTATCAAAAAGAACACAAAGAAACTGTTAACTTAGA 5922
Qy 2127 AsnLysIleAlaSerLeuAlaGluGlnIleLysIleLeuThrlLysGlnMetAspGlnPhe 2146
Db 5923 GAAAAAATTTCAAGAAAGACAAATTCAAATTTTCAGACATTCAAAGAGATTAGATAA--- 5979
Qy 2147 ArgAspSerLysGlnSerLeuGlnGlnGlnSerHisLeuSerGlnLysCysThr 2166
Db 5980 -----TCAAAAGATCAATTCAGAAAAAGATCCAAAGACTTCAG----- 6018
Qy 2167 TyrLysThrGlnLeuGlnMetLeuLysGlnGlnLysGlnAspIleAsnLysLeuAla 2186
Db 6019 ---AAAAAGAACTTCACTGCTTAGA---GTGAAGAAAGATGTCAATATGACT---CAT 6069
Qy 2187 GlnLysValLysGlnValAspGlnLeu----- 2195
Db 6070 AAAAAAATTAATGAATGAGACAGATTGAGAAAGCAATTGAGCCAAACTATCTAGCAAG 6129
Qy 2196 -----LeuGlnHisLeuSerSerLeuLysGlnGlnLeuAspGlnIleGln 2210
Db 6130 TGTGAGATGATTAACCTCCAGTTGACTTAAGAAACCTTCAGAAAGCTTCAGAAATAAGA 6189
Qy 2211 MetGlnLeuArg---AsnGlnLysLeuArgAsnTyrGlnLeuCysGlnLysMetAspIle 2229
Db 6190 ATTGAAGCTTAAGAAAGACATGAGCTTAGAGAGATTAAGAAATCTCTCAAAATGGA--- 6246
Qy 2230 MetGlnLysGlnIleSerValLeuArgLysMet-----Gln 2241
Db 6247 AGGACCAATTCATGACCAACCTTAAGGAAATGATGACTAGAACCCGACAGAACCCAA 6306
Qy 2242 AsnGlnProGlnGlnGln-----GluAspAspValAlaGlnArgMetAspIleLeuGln 2259
Db 6307 GTAAAAACCTGAAAAAGGTTACTTAAGTGAACAACAGACCTTAATGAAAGCCGTGAGA 6366
Qy 2260 SerArgAsnGlnGlnIleGlnGlnLeuMetGlnLysIleSerAlaValLysSerGlnGln 2279
Db 6367 GAAAGTGTCTAGAAATAAAGACTTTGAAGAGACTCTCAGAGATG---GATATCAT 6423
Qy 2280 HisThrLeuSerLeuSerSerGlnLeuGlnLysGlnIleThrlGlnAlaHisLysHis 2299
Db 6424 TATGAGTGTGTAATGATTTGCTCTTGACTTGAGAGAAATTTGAATTCACAGAA--- 6480
Qy 2300 CysMetLeuAsnIleLysGlnSerLeuSerThrLeuSerArgSerPheGlnSerLeu 2319
Db 6480 ----- 6480
Qy 2320 GlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
Db 6481 -----ATCATGAAGAACTGGAAGTAT 6501
Qy 2340 Val-----TyrArgThrAlaAlaValLysGlnAspHisSerLeuIleLysAspTyrGln 2357
Db 6502 GTGTTAAGCTATGTTAACAATAAAGAAAGAAACAACATGATGCATCAATAAATTTGAA 6561
Qy 2358 LysAspLeuAlaAlaGlnGlnLysArgHisAspGlnLeuArgLeuGlnLeuGlnCysLeu 2377
Db 6562 ATGGAATTTTATGATGAAGTGAAGAAAGCAAAAGCAATTCCTAATTAATAACAGACCTT 6621
Qy 2378 GlnGlnHisGlnArgLysTyrSerAspSerAlaSerGlnGlnLysPheCysGlnIle 2397
Db 6622 CAACAGAGAT-----TGTGATGTACCATCAGAGAAATTAAAGGATCTCAAAATG 6669
Qy 2398 GlnPheLeuAsnGlnLeuLeuPheLysValAsnIleIleGlnSerValGlnAspAsp 2417
Db 6670 AACCAAGATATGATGCTA-----CATATTGAGGAATTTCTCAAGAT 6711

Qy 2418 PheSerGlnValGlnValPheLeuAsnGlnValGlnSerThrLeuGlnGlnLeuGln 2437
Db 6712 TTCTCAAGAAAGTAGAG-----TTCCCTAGCAATAAAGACTGAATTTCAACAGACTAAGT 6765
Qy 2438 HisLysLysGlnPheMetGlnThrPheGlnGlnGlnPheGlnLysAspLeuHisValAspAlaLys 2457
Db 6766 AATAGAAAGAAATGACACAGTTTGTGGAAAGTGSTTAATATACGTTTGTGATATAGA 6825
Qy 2458 LysLeuSerGlnGlnMetGlnGlnGlnLeuAsnArgGlnIleAlaSerThrIleGlnLeuLeu 2477
Db 6826 AAGCTTAATAAATGGGATGCAGAAAGAAATGATAGGATTTGTCAAGTGAATTAATCTTTT 6885
Qy 2478 ThrLysArgLeuLysAlaValAlaGlnSerLysIle-----GlnArgGlnLysThr 2494
Db 6886 AATTAACAGAAATATATGCTAATAATGAATATACACAGACTTTGAGAAAGAAAGTCTTACC 6945
Qy 2495 ValTyrLeuAsnGlnPheGlnAlaLysLeuGlnGlnLysLysGlnGlnAsnLysGlnLeu 2514
Db 6946 ATA---TCCAAAGAGTGGGAACAGACCTGAAATCAGTGAAGAAAGAAATGAATAACTA 7002
Qy 2515 MetArgArgMetGlnHisIleGlnProSerAlaSerValMetGlnGlnGlnAlaArg 2534
Db 7003 TTTAAAACTACCAAAACATTGAAAGACTTCCTTGCGATCTGGTCCAGATTAT----- 7056
Qy 2535 LeuLeuGlnIleLeuLysThrValGlnAspGln-----SerLysLys 2548
Db 7057 -----CTTACACACAGACAAATAAGAAATCTCATGTTACATCAAGACT 7101
Qy 2549 LeuGln-----SerArgIleLysMetLeuGlnGlnGlnLeuAsnLysValLysAsp 2565
Db 7102 ACACAGTTAACCACAGAAATAATTCAGAGCTGGAAATTCAGTCCAGAACTAAAGAA 7161
Qy 2566 AspAlaMetHisLysGlnLysValAlaIleLeuGlnAspLysLeu---LeuSerArg 2584
Db 7162 AGTGTATGATTAAGAAAGCAAGATTTAAAGATGCAAGAAAGAACTTGAGGTGACTAAT 7221
Qy 2585 AsnAlaGlnAlaGlnLeuAsnAlaMetGlnValLysLeuThrLysLysGlnAspAsnLeu 2604
Db 7222 GACATTAATGCAAAACCTT-----CAAGCCAAAGTTCAATGAATCAATTAATGCTT 7272
Qy 2605 GlnAlaAlaMetLysGlnIleGlnAsnLeuGlnLysMetValAlaLysGlnValAlaPro 2624
Db 7273 GAAAAAACAAGACAAATTCAGACTTCAAGCAAAAGTTGCTTGAAGACTAAGCA 7332
Qy 2625 TyrLysGlnGlnIleAspAsnLeuLysThrLysValAlaLysIleGlnMetGlnLysIle 2644
Db 7333 TATAAAGAAAGAAATGAAAGATCTCAAAATGAAGCTTGAAAAATGAGACTAGAGAAATG 7392
Qy 2645 LysTyrSerLysAlaThrAspGlnGlnIleAlaTyrLeuLysSerCysLeuGlnAspLys 2664
Db 7393 AAAAATGCCAAAGAAATTTGAAGAAAGCAATCGTGTACAAAAGCCATGTGAATATGAA 7452
Qy 2665 GlnGlnGlnLysArgArgLeuLysGlnGlnLeuArgArgAlaGlnAlaAspAsnAspThr 2684
Db 7453 AAGGAATTAATAGGCTATTTGAGAAATACTCAGAAAGATCAACAGCCCAAGATACC 7512
Qy 2685 ThrValCysValProLysAspTyrGlnLysAlaSerThrPheProValThrCysGlnGly 2704
Db 7513 TCAGATGATATGAAACATATGATCTCAGGCTTCAAATAAACCTTAATCTTGTCAGAGT 7572
Qy 2705 GlnSerGlnIleValGlnSerThrAlaMetLeuValLeuGlnSerGlnLysAlaLysLeu 2724
Db 7573 GGCACGGCATTTGTAACAAACAAAGCTCTTTATTTGAAAGAGAAACATATAGGCTA 7632
Qy 2725 GlnArgGlnLeuSerHisTyrLysLysLysTyrHisIleLysSerArgThrMetSerSer 2744
Db 7633 GAAAGAAATTTCTAATTAATGAAGCAAAATGAACAGCTA----- 7674
Qy 2745 SerGlnAspArgLysLysThrLysAlaLysSerAspAlaHisSerSerHisThrGlnSer 2764
Db 7675 -----ATAAACAAAGAAATGAAATGTTAAGCAATATATCAGACTCTT 7716

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QY 2765 SerHisArgGlySerProHisIleuThrGluThrArg-----HisGlyProVal 2781
Db 7717 TCCTAATGAGTCAAACTTGCAGAGAAAGAACCTTTAAAGAGAGCGCTCACAAAACAAGTA 7776
QY 2782 ThrProGluArgSerGluMetProSerIleuHisLeuGlySerProIleuSerGluSer 2801
Db 7777 ACTGCTGAG-----AATCTCTCAAG----- 7797
QY 2802 SerThrIleuArgValIleuSerProAsnArgSerGluIleuSerGluIleuValMetSer 2821
Db 7798 -----TCT 7800
QY 2822 ProGlyLysThrGlyMetHisIleuSerProSerIleuValGlyLeuHisIleu 2841
Db 7801 CCTAAAGTCACTGCAACA-----GCTCTTAAA 7827
QY 2842 LysArgAlaLeuSerProAsnArgSerGluMetProThrGluHisValIleuSerProGly 2861
Db 7828 AAGAAACCAATTACACC----- 7845
QY 2862 LysThrGlyLeuHisIleuSerProHisIleuThrGluSerThrLeuPheAspAsnLeuSerPro 2881
Db 7846 -----TCTCA 7851
QY 2882 CysLysGlnGlnLysValGlnGlnLeu-----AsnSerProLysGlyLysLeuPhe 2899
Db 7852 TGCAGAGACGCAATTACAGATCTCTGTCGCAAGAACCAACCAAAATCTGTTT 7911
QY 2900 AspValLysSerLysSerMetProTyr---CysProSerGlnPhePheAspAsnSerLys 2918
Db 7912 GATAGCCGATCAAACTCTTACAGATCCTCATCATCGCTTTCGCTTTTGAATCACTAGT 7971
QY 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnLysSerGlnAlaGluAsn 2938
Db 7972 TTAGCCCTTTGCCAGAGTGCAGAAATGCAAGACAGAGTGTGATTCCTCAGCCAGGT 8031
QY 2939 TrpTrpTyrGluAlaLysLysGluThrAlaProGluCysLysThr 2953
Db 8032 CCTTGACAGCGCTCTCTCAGGCAAGATGCTGAGTCAAACT 8076

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RESULT 2

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US-09-620-312D-130
Sequence 130, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Aseundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aildong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Dundi
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
TITLE OF INVENTION: Dmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0

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; SEQ ID NO 130
; LENGTH: 8503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130

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Alignment Scores:

Pred. No.:	Score:	Length:
1,31e-282	3613.50	8503
Percent Similarity:	50.34%	Matches: 996
Best Local Similarity:	31.97%	Conservative: 572
Query Match:	24.47%	Mismatches: 932
DB:	4	Indels: 615
		Gaps: 86

US-09-724-584-1 (1-2954) x US-09-620-312D-130 (1-8503)

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QY 1 MetSerGluGlyAspAlaValLysValCysValArgValArgProIleuIleGlnArgGlu 20
Db 91 ATGGCGAGAGAAAGAGCGCGTGGCTGCGAGTGGCGGCTGAAACAGACAGAGAA 150
QY 21 Gln-----GlyAspGlnAlaAsnLeuGlnTrpLysAlaGlyAsnAsnThrIleSerGln 38
Db 151 GATTCATCTGAGAAAGAACTGCCCAAGTTACTGGAAACAGCAATATGCTCATTTATCA 210
QY 39 ValAspGlyThrLysSerPheAsnPheAspArgValPheAsnSerHisGluSerThrSer 58
Db 211 GTTATGAGAGTAAATCTCTCATTTTGTATCGCTTTTCAAGTAAAGTAACTCAAA 270
QY 59 GlnIleTyrGlnGlnIleAlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGly 78
Db 271 AATGATGATAAAGAAATAGACAGCAATCATGCAATTCGTCATCAAGTAAAGTAACTCA 330
QY 79 ThrIlePheAlaTyrGlyGlnThrSerSerGlyLysTrpTyrThrMetMetGlyThrPro 98
Db 331 ACTATATTCGCTATGACAGACTGCTTCAGAAACATATACCATGATGGTTCCGAA 390
QY 99 AsnSerLeuGlyIleIleProGlnAlaIleGlnGlnValPheLysIleIleGlnGlnIle 118
Db 391 GATCATTTGGAGATTATACCCAGGCAATTCATGATCTTCCAAAAATTAAGAAGTTT 450
QY 119 ProAsnArgGluPheLeuLeuArgValSerTyrMetGluIleTyrAsnGlnThrValLys 138
Db 451 CCGATAGGGAATTTCTTACGTATCTTACATGGAATATACAAATGAACCATTACA 510
QY 139 AspLeuLeuCysAspAspArgArgLysLysProLeuGluIleArgGluAspPheAsnArg 158
Db 511 GATTTACTCTGTGGCACTCAAAAATGAACCTTTAATTGAGAGAGATGTCATAGG 570
QY 159 AsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGluHisValIleGln 178
Db 571 AATGCTATGTTGCTGATCTACAGAAAGTTGATATACATCAAAAATGCGCTTGA 630
QY 179 TrpIleLysLysGlyGlnLysAsnArgHisTyrGlyGlnThrLysMetAsnAspHisSer 198
Db 631 TGGATTACAAAGGAGAAAGAGAGAGCATTAAGCAAAACAAATATGATCAAGAAC 690
QY 199 SerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnAspProThr 218
Db 691 AGTCGTTCTATACCACTTTAGATGATTTTGGAAAGAGAGAGAAAGGCTCACTTCT 750
QY 219 AsnSerGluAsnCysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAla 238
Db 751 -----AATGTAAGAGATCTTTAAGTATCCCATTTAATTGCTTATCTTCA 801
QY 239 GlySerGluArgAlaSerGlnThrGlyAlaGluGlyValArgLeuLysGlnGlyCysAsn 258
Db 802 GCGAGTGAAGAGCTCTCAACAGCGCTGCAAGTGTGCGCTCAAGAGAGGCTGTAT 861
QY 259 IleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAla 278

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Db	862	ATTAATTCGAAGCTTATTTATTTTGGACAAGATCAGAAACTTAATGATGACAAGTT	921
OY	279	GIYGIYPHEILEASNTYRARGAPSERLYLEUTHRARGILEUGLNAASERLEUGLY	298
Db	922	GGTGGTTTCATTAATTTATGAGATGACAAATTACACGAATCTTCAGAAATTCCTGGGA	981
OY	239	GLYASNAIALYETHVALILEILECYSTHRIETHRPROVALSERPHEASPGLUTHRLEU	318
Db	982	GGAAATCCAAAGACACGATATTATTCGACAAATTACTCCGATTCCTTTGATCAAACTCTT	1041
OY	319	SERTHLEUGINPHEALASERTHRILALYSHISVALARGASPTHPROHISVALAENGIL	338
Db	1042	ACTGCTTCACGTTTGCCAGTACTCTCTAAATATTAAGAATAATCCCTTATTTAATGAG	1101
OY	339	VALLEUAERASPGLUALALEUDEUYBARGTYRARGLYSGULILEUASPREUYLSYS	358
Db	1102	GTATCAACTGATGAAGCTCTCTCGAAAAGTATACAAAAGAAATATGATCTTTAAAAA	1161
OY	359	GLNLEUGLUAENLEUGLUSERSESERGLUTHRYLYSALAGLNAIMETCALYSGLUGLU	378
Db	1162	CAATTAGAG-----GAGGTTTCTTTAGAGACGGCGGCTCAGCGCATGGAAAAACCA	1211
OY	379	HISTHRGILNLEUHALAGLUILEYSGILNLEUHSILYSGUIARGLUASPRGLIETPR	398
Db	1216	TTGGCCCACTTTTGGAGAAAAAGATTGCTTCAGAAAAGTACAGAAATGAGAAATTGAA	1271
OY	399	HISLEUTHRAENILVALVALASERSEINGLUSER---GLINGLNAESPGLNARGVAL	417
Db	1276	AACTTAAACAGGATCTGTGTGACCTCTTCTCCACGCTTGCAACAGAAATTAAGCT	1331
OY	418	LYSARGLYSARGARGVALTHRTYRILAAPROGLYLSILEGLNANSEIRLEUHSILASER	437
Db	1336	AAAAAGAAACGAGAGTACTTGCGCTTGCGCAAAATTAACAAATGACAAACCTCAAC	1391
OY	438	GLYVALSERAPRPHASPMETLEUSERXARGLEUPROGLYASNPHERSEIRLYBYVALAYS	457
Db	1396	TATGCAGATCAATTTAAT-----ATACCAACAAATATACACAAACAAACACAT	1441
OY	458	PHESERAPMECPROSERPHERPROGLUILEAPRAPERVALCYETHRGUPHERASPR	477
Db	1444	AAGCTTTCTATTAATTTATTCAGAAATTTGATGATCTGTCTTTCAGAGCTGATGTT	1501
OY	478	PHEASPRAPALALEUSERMETECASPRSERANGILYILEASPRALAGLUTRYAPNLEU	497
Db	1504	TTCAAGTACACGCTTGATACATTAGT-----GAGATGAAATGGAATCCACGA	1551
OY	498	SERLYSVALTHIRHISARGGLULYTHIRSERLEUHSILEGINSEMERILESPRHEGLYN	517
Db	1552	ACAAAGCTACATAAAACAGAG-----	1572
OY	518	ILESERASPRSERVALGNPHEIRHAPRSEIRLYSGUIAENGLLEUGLITYLEUPRO	537
Db	1572	-----	1572
OY	538	LYASPRSERGLYASPMETALAGLUCYSARGLYSALASERPHEGLULYGLULIETHRSE	557
Db	1572	-----	1572
OY	558	LEUGINGLGNLEUGLNSERLYSGULUGLULYLYSGULUENVALGLNSERPHEGLU	577
Db	1572	-----	1572
OY	578	LEUYSILLEALIGLLEUGLUGLUGLNLNUSERVALYLYSALYASNPHEUGLUMETVAL	597
Db	1573	-----	1573
OY	598	THIRANSEARGLUNHIESERILEASNALAGLUALGINTHIRAPRVALGLULYSGULVAL	617
Db	1588	TTGAACCTCA-----	1591
OY	618	VALARGLYSGULUMETSERVALLEUGLYASPRSERGLITYRASNALASERASNPHERLEU	637
Db	1596	-----	1596

QY	638	GINaSPeSerSeValaSPGILyVaRgLeuSerSeRHaSPGILCySIlleGIuHs	657
Db	1536	-----	1596
QY	658	ARGLyMeTLeuGIuGlnIySerIleValaSPeGIuGIuPheIlleGIuAnLeuAnLyS	677
Db	1536	-----	1596
QY	678	LySPeGIuAnSPLyGLInLySPeSeRGIuAnSPHeMeTGIuSeRIleGIuLeu	697
Db	1536	-----	1596
QY	698	CySGILuAlaIlleMeTAlaGIuLyVaLaSPeAlaLeuGIuGIuLeuAlaLeuMeTARgAp	717
Db	1537	-----CTTGCTGCT	1605
QY	718	AsnPHeaSPeAsnIleIleLeuGIuAnSPInThRLeuLySPARyGILyAlaLaSPeGIu	737
Db	1606	GACATATGATTAATCTGCTATTAGACTATGACATACACACTGACGAGAAAAAATGGGA	1666
QY	738	ARgSeRLeuLySGILyAnSPInGIuThRAnSPInPheGIuIlleLeuGIuLySGILuThRGI	757
Db	1666	TTGAATTTAAAAAGAAAGAAATGATTTGGATGATTTGGCTTGAAGAAAGAAATCTAA	1726
QY	758	LySGILuHsAGILuAlaGIuLeuIlleIleGIuIlleGIySeRLeuLySGILyLeuAlaGIuAn	777
Db	1726	AAAGATCAAGACATGCACTAATTTATGAAATTTGGAACTTAAAGAAATTTACTTAACAT	1786
QY	778	AlaGIuMeTYRAnSPInAnLeuGIuAnSPeGIuThRLeuLySPeThRLeuLeuLyS	797
Db	1786	CGAGAAATATTAATCAAGATCTTGAGAAATGAACTCAGTTCAAAAGTAGAGCTGTAGA	1846
QY	798	GIuGIuGIuIlleGIuLeuAlaGIuLeuARySaRgAlaSPeAnLeuGIuLySVal	817
Db	1846	GAAAAAGAAACCAAGATTAAAGAGCTAACAGAAATCATAGACTCTCAAAAGCTTAAGAAAT	1906
QY	818	ARgAnSPeAnSPeSeRSeValSeMeTGIyAPSeRGIuLySPeCySGILuIllePhe	837
Db	1906	ATAAAATGGACTGTCTACTACTCATG-----GAAAGCATTTGAAGACCCAAA	1956
QY	838	GIuLeuLySGILySeRLeuSeRAspAlaGIuAlaValThRaRgAspAlaGIuLySGILyS	857
Db	1954	CAAAAGAAAGCAGACTCTTTGATGCTGMAACTGTAAGCCCTTGAAGCCAGAGAAATCA	2014
QY	858	SeRPhLeuARySeRGIuAnSPeGIuLeuLySGILySPeMeTGIyAPSeRSeRAnThR	877
Db	2014	GCTTTCTTGAAGTGAATCTGGAGTTGAAGGAAATGAAGAACTTGCAACTGCACTCA	2073
QY	878	TYRAnSPInLySGILyValaLaSeRLeuPheGIuLySGILyGIuThRGIuLySeR	897
Db	2074	TACAAGCAAAATGAAAAATGATATTACAGTTATTATCAAAACCAATTGGAGCAAAA-----	2127
QY	898	AsnTYRlySPeMeTGIuAlaSPeGIuAnSPeGIuLeuGIuInSeRAlaPheAnSPInIle	917
Db	2128	-----AAGAAAAATGCAAGTTGATCTGGAGAAAGATTACATCTGCTTTTAATGAGTA	2187
QY	918	AsnTYRLeuAnSPInLyLeuLeuAlaGIyLySValPRoTARgAspLeuLeuSeRARGValGIu	937
Db	2182	ACAAAACCTCACCTCCCTTATAGATGGCAAAATTTCCAAAAAGATTTGCTGTGAATTTGGA	2241
QY	938	LeuGIuLySValSeRGIuPheSeRlySGILyAnSPInGIuLyValaLeuGIuGIuLySAn	957
Db	2242	TTGGAAAGAAAGATTACTGATCTTCAGAAAGAACTAAATTAAGAAAGTTGAAAGAAATGA	2301
QY	958	AlaLeuGIuAnSPInValThRSeRLeuSeRGIuTYRlySPeLeuPRoAnSPInValGIu	977
Db	2302	GCTTTGCGGGAAGATCATTTTGGCTTTCAGAAATGGAAATCTTTCCTTTCGAAAGTAGA	2361
QY	978	CySeLeuLySPeAnSPInIleSeRlyAlaSeRGIuGIuIlleMeTLeuLeuLySGILyGIu	997
Db	2362	AGGCTGAGGAAGATGATCAAGAAATCTGAAGGCTCCATTAATTAATCACTGAGAAAA	2421


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Qy 998 GluHisSerAlaSerIleIleSerIleGlnIleIleMetGlnGlnGlnSerGlnGln 1017
Db 2422 GATTAATTGTTTCTGAAGTACTTCAATAGAGAGATGAGATTCAAGGTTTACTGAGAA 2481
Qy 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerIleValGlnGlnThrGln 1037
Db 2482 ATTGGGAAAACAAAGATGACTACCAACTACACGCTGCAATTAATAAAGCAGCTGATCA 2541
Qy 1038 GlnIleLeuGlnMetIleIleSerHisAspAspLeuPheGlnIleIleIle 1053
Db 2542 GAATTCCTCAAAATTCCTCAATGATGACTTGAAGGCTTGAAGGCTTGAAGGCTTGAAG 1054
Qy 1054 -----IleArgAsnIleSerGlnIleGlnIleGlnIleGlnIleGlnIle 1070
Db 2602 GAGGAGATGAGAGATGATGATGAGAAATGATTAATCTCTCAAAAGAGGCTTGAAGGCTT 2601
Qy 1071 LysGlnIleMetGlnSerValGlnValIleValIleAspThrIleIleGlnIleGln 1090
Db 2662 GATTCGAGTGGGGCTTGAAGACGAGCTTCTTCAAGACCCCAAGAACTTCAAGAG 2721
Qy 1091 ThrIleArgAspIleGlnIleLeuIleHisGlnIleIleIleIleIleIleIle 1110
Db 2722 AAAACAGCTGAGCTTCAAGAAAGCTAATGATGATGAGACAGCTGAGAAAGCAATTAAGA 2781
Qy 1111 ThrIlePheProIleThrProLeuSerAspSerIleProProSerIleValIleGln 1130
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Qy 1131 AsnSerGlnAspProIleGlnIleAsnAspIleHisAsnIleIleIleIleIleIleIle 1150
Db 2836 AAACCTGACGCAAACTTAGAA-----GAGTAAAAACTTAACTCAAGAAAGATGAT 2889
Qy 1151 ArgAsnAsnIleMetValCysLeuGlnIleGlnIleGlnIleGlnIleGlnIle 1169
Db 2890 CTTAAACAACTCCAGAAAGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2949
Qy 1170 -----IleAspLeuAsnThrGlnIleGlnIle-----SerLeuGlnIleGln 1182
Db 2950 GATACCTGTTAAACATGATATGATATGATCAAGAAACATTAAGAAATGCTTGAAGTCTG 3009
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Db 3010 AAACAACTCAACAAACATTAATATGATCACTAAATTCGAAATTTCTGAG-----GAGTTC 3066
Qy 1203 LeuLeuLeuGlnIleMetGlnIleLeuIleIleIleIleIleIleIleIleIle 1218
Db 3067 AGGAATTTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3126
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Db 3238 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3297
Qy 1267 LysGlnIleSerIleSerGlnIleIleGlnIleIleGlnIleIleGlnIleIle 1286
Db 3298 AAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3357
Qy 1287 AlaGlnIleGlnIleLeuArgGlnIleGlnIleGlnIleValIleAspSerPheArgGlnIle 1306
Db 3358 CTTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3417
Qy 1307 AspCysSerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnIleVal 1326
Db 3418 AAG-----AAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3474
Qy 1327 SerLeuGlnIleValIleAsnSerLeuGlnIleMet-----LeuArgGly 1341
Qy 3475 CTTAAAGAAAAGAGCCAGCACTCCAGAGAAAACCAACAACTTAAATGATCAAGAA 3534
Db 1342 GluArgAspGlnIleGlnIleIleIleIleIleIleIleIleIleIleIleIle 1361
Qy 3535 GAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3582
Db 1362 AlaHisValIleSer-----ValIleGlnIleGlnIleIleIleIleIleIle 1374
Qy 3583 AATGATTTAAAGAAACAAAGATTTGACATTTGAAACATTAAGAAACAGAGAGCTTGAAG 3642
Db 1375 ThrIleIleValIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1394
Qy 3643 GCTCAAACTTAAAGAAATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3702
Db 1395 LeuIleSerMetLeuGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1414
Qy 3703 CTTAAAGAAATTAACAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT----- 3756
Db 1415 GluIleSerSerIleGlnIleGlnIleIleIleIleIleIleIleIleIleIle 1434
Qy 3757 -----ATTAAGAAATTAAGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 3786
Db 1435 LeuValAspGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1454
Qy 3787 ACCAAAGAAAGAAATTAAGATTTGATGATGATGATGATGATGATGATGATGATGAT 3846
Db 1455 IleIleAspArgAspIleIleIleIleIleIleIleIleIleIleIleIleIle 1473
Qy 3847 GAACTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3906
Db 1474 GlyIleIleGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1487
Qy 3907 -----AAATCCCATTAACAAATTAACAAAGAGATGCCAGTCTTATGAGAAACAGCTTA 3963
Db 1488 -----SerIleAspArgArgSerGlnIleMet-----GlnIleIleValIle 1501
Qy 3964 CTGCGTAAATGTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4023
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Qy 4024 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4083
Db 1521 GluLeuSerAsnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1540
Qy 4084 AGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4143
Db 1541 AspAspLeuGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1560
Qy 4144 GACAACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4203
Db 1561 IleAspThrThrLeuIleIleIleIleIleIleIleIleIleIleIleIleIle 1580
Qy 4204 ATTAAGAAACTTTG-----GCTAAATTCAGAGAGCTTCAAGC 4242
Db 1581 GluLeuGlnIleValIleAsnIleValIleIleIleIleIleIleIleIleIle 1600
Qy 4243 AAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4302
Db 1601 GluIleGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1617
Qy 4303 GATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4362
Db 1618 LeuLeuThrGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1637
Qy 4363 GATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4422
Db 1638 AsnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 1657
Qy 4423 GATGAGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4473
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Db 4474 -----AAGAAAAACATTAAGAAATTTAGCTAAACACCTGGAAACTGAGAG 4521
Qy 1678 GlnLeu-----LeuAlaLeuYsgInGlnMetGlnValValThrGlnGln 1693
Db 4522 GAACTTAAGAGTTCCTCATTTGCTGCTGAAGAACAGAGAACTATTAATGAGTTAAGA 4581
Qy 1694 LysGlnLeuGlnGlnThrHisGlnHisLeuThrAlaGlnValAspHisLeuYsgIn 1713
Db 4582 GTGAATCTTTCAGAGAGAA-----ACGGAATATCAACCTTCAAAAGCAG 4629
Qy 1714 IleGln--LeuGlnLeuAsnPhelysAnglnAlaGlnGlnLysThrThrLysGln 1732
Db 4630 TTAGAAGCAATCATATGATTAATTACAGAACAGATCCAGAGATTATGAGAAAGAGAA 4689
Qy 1733 CysLeuLeuAsnGlnAsnLysGlnLeuGlnInserGlnHisArgLeuGlnCysGln 1752
Db 4690 CAACCTT-----AATATAAACAAATTAAGTGAAGTTTCAGAAAAAGTGAT--GAACG 4740
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Db 4741 AAACATTCAGAGAGATCCGAAAGCCAGATTCAGCATCAAAAGTATA----- 4791
Qy 1773 GlnGlnLysValIleAsnLeu-----AsnGlnGlnMetGln 1785
Db 4792 GAAAGTAAGATGCTCGAGTTGACCAACAGACTTCAAGAAAGTCAAGAAATATCAAT 4851
Qy 1786 ValMetLeuGlnMetGlnGlnLysLysAsnSerGlnArgThrValIleAlaGlnArg 1805
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Qy 1806 GlnLeuGlnAspAspLeuArgGlnSerValGlnMetSerIleGlnThrGlnAspLeu 1825
Db 4912 CAACGTAAGAAAGAACTTAAGAAATTTAGCTAAATTAAGAAATCTCAAGAA----- 4965
Qy 1826 ArgLysAlaGlnGlnAlaLeuGlnGlnGlnLysAspLysValGlnGlnLeuThrSerGln 1845
Db 4966 AAAGATATCACTTTCTTAAGATGACAGCTGCATATGACAGAGAGAAATGCTGAA 5025
Qy 1846 IleSerValLeuGlnGlnLysIleSerLeu-----LeuGlnAsn----- 1858
Db 5026 ATAGAACACTTGAGAGAGCAATTTGAGACCAGAACTTAACCTGGAAGAACTAGAAAG 5085
Qy 1859 -----GlnMetLeuTyr--AsnValAlaThrValLysGlnThrLeu 1871
Db 5086 CAGAAATATATAGGTTGATCTGATTACTTAAGTGAAGAACTTGAAGAAATGATCTGAAGA 5145
Qy 1872 SerGlnArgAspAspLeuAsnGlnSerLysGlnHisLeuPheSerGlnIleGlnThrLeu 1891
Db 5146 AAAGAAAGAGATGACCTTAGAGAGTGGAGAGAGACTTCAAAAGTGAAGAGAGAGAGAG 5205
Qy 1892 SerLeuSerLeuLysGlnLys--GlnPheAlaLeuGlnGlnAlaGlnLysAspLys-- 1909
Db 5206 AAGGAAACCTTAGAGAAACTTAATTAAGAGAGCTGAGAAAGAAAGAGAGAGCTTAAAG 5265
Qy 1910 -----AlaAspAlaAlaArgLysThrIleAspIleThrGlnLysIleSerAsn 1925
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Db 5317 ATTGTTTCAGAGAAACAAATGAATATCAAAATATGCAAAAGAGACTTGAACACCTCAAT 5376
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Db 5377 GATGCTTAAAAAGCAGAGATCTGAATAATTAACAAGAGAACTAAGATTCCTCAGATGAT 5436
Qy 1961 LeuArgGlnThrLeuLysSerLysAspLeuAlaLeuGlnLysMetGlnGlnGlnArg 1980
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Qy 2001 AsnGlnAsnValThrThrLeuYsgInGlnGlnGlnGlnLysGlnValThrPheThrLeuGln 2020
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Qy 2021 ArgProSerLysGlnGlnSerSerGlnMetGlnGlnLeuArgGlnSerLeuYsrThr 2040
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Qy 2041 LysAspLeuGlnLeuGlnGlnAlaGlnLysGlnIleSerGlnAlaThrAsnGlnLys 2060
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Qy 2061 AsnLeuThrAlaLysIleSerSerLeuGlnGlnGlnIleLeuGlnAsnAlaSerIleLeu 2080
Db 5698 AATTTA-----AATTTGCTCAAGAACTTCATGAAACCTTGAAGAAATG 5742
Qy 2081 AsnGlnAlaValSerGlnArgLysAsnLeuArgHisSerLysGlnGlnLeuValSerGln 2100
Db 5743 AATCTGTATATGAAGAAAGAGATATATCAAGAGAGTGAAGAGACACTCAAACTGAG 5802
Qy 2101 LeuGlnGlnLeuSerLeuThrLeu-----LysSerArgAspHisAlaPheAlaGln 2117
Db 5803 AGAGACCAACTCAGAGAAAGCCCTGCAAGAAACCAAGCTAGAGATCTGGAATATACAGAG 5862
Qy 2118 -----SerLysArgGlnLys-----AspGlnAlaVal 2126
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Db 6190 ATTGTAGCTAAAGAAAGAGATGCTTAAGAGAGATTAAGAAATCTCTCAAAATGGA-- 6246
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Qy 2300 CysMetLeuAsnIleLysGlnSerLeuSerThrThrLeuSerArgSerPheGlnSerLeu 2319
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QY 2320 GlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
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 QY 2358 LysAspLeuAlaAlaGluGlnLysArgHisAspGlnLeuArgLysGlnLeuGlnCysLeu 2377
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 QY 2822 ProGluLysThrGlyMetHisLysHisIleLeuSerProSerLysValGlyLeuHisLys 2841
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 QY 2919 LeuGlyAspPheSerGlnLeuAsnThrAlaGlnSerAsnAspLysSerGlnAlaGlnAsn 2938
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 RESULT 3
 ; US-08-353-700-2
 ; Sequence 2, Application US/08353700
 ; Patent No. 559919
 ; GENERAL INFORMATION:
 ; APPLICANT: YEN, TIMOTHY J.
 ; APPLICANT: RATNER, JEROME B.
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
 ; TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: DANN, DOREMAN, HERRELL AND SKILLMAN
 ; STREET: 1601 MARKET STREET, SUITE 720

CITY: PHILADELPHIA
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0,
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/353,700
 FILING DATE: 09-DEC-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: REED, JANET E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10136 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: HUMAN

QY 571 uLeuValGlnSerPheGluLeuLysLeuAlaGluLeuGluGluLeuSerValLysAl 591
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 QY 591 aLysasnLeuGluMetValThrAsnSerArgGluHisSerLeu 605
 Db 1803 -----AAACAGCAAGAAAAAACCCTTGTAGAAAAACTGAA 1840
 QY 606 -----AsnAlaGluValAlaThrAspValGluLysGluValValArgLysGlu 621
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Qy 1158 uGluThrGluArgAsnserLeuLygIuInValIleAspleuAnthrGlnleuInse 1178
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Qy 1230 uValThrGluLyseuGlnInthrleuGlnleuGluMetLyseuAnIlethrIleGluArg 1250
Db 4388 ATTCCAAGAGAAATTTATCTTATCTTACAAAGTGAACAAATTTTACATGATGACACACTG 4447
Qy 1250 nGluLeuGlnInThraAspPhegluAspleuLygIuInIleAspserLeuLygIuAsple 1270
Db 4448 TCACATGAGCTCTAAATATGTCAGAGCTGCACACCTATGTCATATTAAAG----- 4499
Qy 1270 uSerGluAsnIleleuGlnserIleGluThrGlnAspleuLeuArgAlaIagInglu 1290
Db 4500 -GCCGAAATTTGCTTGTCA-----ACGAATCTGAGAAATCTTCAAGGTGA 4546
Qy 1290 uLeuArgGluInlysgInleuValAspserPheargInleuLeuAspCyserVa 1310
Db 4547 CTGTGTGAAGAGATGACAGCTG-----GGCTTGAGAGAGGGCTGTTCATCCCTGTGC 4600
Qy 1310 lGlyIleaserPheAsnIleAspAlaValAlaAsnGlnIuLyseuValserLeuGly 1330
Db 4601 ATCTCTTTGTGCTGCCTGACAGCTCTAGTCTTAC-----AGTTGGAGGA 4645
Qy 1330 uValAsnserLeuGlnserGluMetLeuArgGlyIuArgAspleuLeuGlnInthrSerCy 1350
Db 4646 C--TCTCTTTTACAGAGCTCTTTAGAA-----CAGACGAGGA 4684
Qy 1350 slyAlaIeuaIAspserGluLeuGlu----- 1358
Db 4685 TATGTCTCTTTTGAATAATTAGAGGGGCTTTTACAGCAACCAAGTCAGTATGATGA 4744
Qy 1359 -----LeuLeuArgAlaIleValIleSerValGluGluGluAsnleuGlu 1374
Db 4745 AGTATTTTGCAGAGCTGCAGAGCTATGTGACATTAAGGCCGAAATTTTGTCTT 4804

Qy 1374 eThrLyseuAsnGlnleuGluLygIuIleuGlnLyserGlu-----G 1391
Db 4805 GTCAACGATCTGCAAACTTTCAAGGTGACTGTGTGAAGAGATGACGCTGGCTTGA 4864
Qy 1391 uSerGluValleuLyseuMetLeuGlnAsnleuGluAspAsnAnIleuLyse 1410
Db 4865 GGAGGCGCTGTTCCATCTCTGTATCTCTTGTGTGCTCAGACCTCTAGCTTACGAG 4924
Qy 1411 -----GluGlnaIagIuIlySer----- 1417
Db 4925 TTTGGAGACTCTCTTTTACAGAGCTTTTGAACAGCAGAGGATATGCTCTTTT 4984
Qy 1418 -----SerLygIuAsnGlnPheSerleuGluIuValIlePhe----- 1429
Db 4985 GAGTATTTAGAGGGGTGTTTTCAGCAAAACAGTGCAGTGTGATGAATTTTTCAG 5044
Qy 1430 -----SerGlySerGlnLyseuVa 1436
Db 5045 CAGTCTGCAGAGAGAACTGACCCAGAAAGAAACCCCTTCGGCCAGGGAAGCTGT 5104
Qy 1436 lAspGluIle-----GluValleuLyseuIleuLyseuAlaIagIuArg 1452
Db 5105 TGAAGAGCTGAGTCCCTGTGTGAGGTGTACCGGAGTCCCTCGAAGCTAGAAAGAA 5164
Qy 1452 gLeuGlu-----IleLyAspArgAspTyrPhegluLeuValGlnThrlAs 1468
Db 5165 AATGGAAGCTGAGGAGTATGAAATATAGAAATTAAGAGCTCGACAGATTATTAAG 5224
Qy 1468 nThraAsnleuValGlu---GlyLyseuGluThrProleuGlnaIAspIleGlu----- 1485
Db 5225 TTTGGAAGGCAAGCTTGAAGCTGCTTGAAGAGAGATTTTGCAGAAATGAAACAGTG 5284
Qy 1486 -GluAspserIleAspArgAspserGluGluMetGluIleuLyseuValleuGlyGlu 1505
Db 5285 GCAACAGAGCTGCAAGAGCTGAGTGTGAGATGATGATGATGATGATGATGATGATGAT 5344
Qy 1505 uGluArgAsnGlnIlyrleuLeuGlu-----ArgleuGlnGluLyseuGlu 1521
Db 1521 uLeuSerAnlyseuGluIleuGlnLygIuMetGluThrSerValleuLeuLyse 1541
Qy 1541 pAspleuGlnInlyseuGlnserLeuLeuSerGluAsnIleleuLyseuGluAsnI 1561
Db 5432 CGACACAGAGATGCTATTCAAGC-----CGAAATGAGAGCTG 5470
Qy 1561 eAspThrThrleuLyshIleAspserPheGlnaIagInleuGlnlyse 1577
Db 5471 TGACATATCAAAAGAACTACTTCAGAAACTTCAAGAAAGAACACCAAGCATGATGTCA 5530
Qy 1578 -----ThrGlnGlnleuGlnleu-----AlaLy 1586
Db 5531 TCAGATTTGTATAAGATGCTCAGCAGAGCTCAATTAACATTTGAGAAATTAAGTGA 5590
Qy 1586 sAsnleuAlaIleAlaIeAspAspAspProIleThrGlnIuLygIuThr----- 1604
Db 5591 GACTGTGCTGAGTGAACCCAGAGAGAGTCTCGGGCAACAGTCCCAAGATTAACAAATTA 5650
Qy 1605 -----SerAlaAspCyValIleProleu----- 1612
Db 5651 TGAGCTTCAGGGAAGATTAACCCAGGCTTTTCAAGATTTCTGAATTTGTCAATT 5710
Qy 1613 -----GluGlyLyseuLeu 1618
Db 5711 TTTGCTCTAATGCTTTGTGTAAGTCTTCTGAGGGAATCAGGAATATTCATA 5770
Qy 1618 uLeuThrGluIuLeuHiegluInlyrthraAsnGluGlnIuLyseuHiegluLyse 1638
Db 5771 TCTTCAACTGGGGTAAAGAGACATCAATGAGATTTAGATTAATTGATGATGA 5830

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QY      1638  ngluleugluhlaaglnvalgluleuyscysgluvalgluhileuMetLysSerMe 1658
Db      5831  GGACCCGTGACAGA-----AAAGTTGAAAGTTCTTAAGCAAT 5869
QY      1658  tllleugluserLysSerSerleucluserleuGlnhileuglulysHlaSPThrGluGlnG1 1678
Db      5870  GAAGAATTGACTCAAAACTC-----CATTTACAGAGAGTACA 5908
QY      1678  nleuleuAla-----LeuysglnGlnMetGlnValIleAlaThrG1 1691
Db      5909  ACTTAATGACCAAAATTTGAAGCATGATAGATTTGAAAAAATGTTGGGAACTTAAGAA 5968
QY      1691  nglulysLysGluLeuGlnGlnThrHileuglulysleuThrAlaGluValaSPHileuLy 1711
Db      5969  AGAAAACTCAAGATTTAGTGAATAAATTGAAATATTTCTTGATGATCACAGAGTACT 6028
QY      1711  sglulsnllegluLeu-----GlyLeuAsnPhelysasnGluAlaGln---Glnlysth 1728
Db      6029  CCAGAGAGTGAAGAACTTCTGAAGGCTCATTTCTGATTTAGAAATGCGATGCAATTAATC 6088
QY      1728  rthlysglulncysleuleuAsnGluAsnLys----- 1739
Db      6089  ATCAGCTGAAGATATTGAGATTAATGTGCCAGAGTGAATGACAGCTGAAGAGAGATTT 6148
QY      1740  ---GluLeuGluGlnSerGlnHileuysglnGlnCysGlu----- 1751
Db      6149  TCTTGATGTGGAATAATGCTGAGTACGATCAGATCGAGAAAGCTAGCATTTGACATGA 6208
QY      1752  ---llegluLeuMetLysSerleuLysAspLysAspLysglulserAlaLeuGlnThr 1768
Db      6209  AGCCCTTACTGAGGCTGACCTTAAGAGTATGTTCAACAAGAGAGCTATGTTAGAAA 6268
QY      1768  rleuLysglulserGluGlnLysValIle---AsnLeuAsnGlnGluMetLysValIle 1787
Db      6269  AGACAAATGAATAATAGAGAAAGTTATTGCTGCTTGAAGAACTCTGAGTGTGTAC 6328
QY      1787  tleuGlnMetGluGluLeuLysasnSerGlnArgThrValIleAlaGluArg----- 1804
Db      6329  AAGTAGAGAAACAGCTTCTGTGAGAAATTAGATATGATCTATGCTCAAAAAACACGCACT 6388
QY      1805  -AspGlnLeuGlnAspAspLeuArgLysValIleGluMetSerIleGluThr----- 1821
Db      6389  GGATCAGTTCTCGAAAAATGAAAGAGAAACACAA---GAAGCTGAGTCTCATCAAAAG 6445
QY      1822  -----GlnAspAspLeuArgLysValIleGlnGluAlaIle 1832
Db      6446  TGAGTGTCTCCATTGCATTCAGGTGCGACAGGAGGAGGAAAGAAAGCGAACTCTCT 6505
QY      1832  uGlnGlnGlnLysAspLysValIleGlnLysleuThrSerGlnIleSerValIleGlnGluLy 1852
Db      6506  TCGACTTTGTCTCTGATGTGAGTGAGTGTGTTAAAGACAAAACTCATCTCCAGAAA 6565
QY      1852  slleSerLeuLeuGlnAsnGlnMetLeuLysasnValIleThrValLysGluThrLeuSe 1872
Db      6566  GCTGCAGACTTTGAAAAAGAGCTCACAGCACTGCTTGACAAATGATGAGCTGGAAA 6625
QY      1872  rgluArgAspAspLeuAsnGlnSerLysGlnHileuPheserGluIleGluThrLeuSe 1892
Db      6626  CCAATTTGACACACATTAAGAAAGAGAAAGAAATGCTTCTCAAGAACTCAAAAGCTGCA 6685
QY      1892  rleuSerLeuLysGluLysglulPhe-----AlaLeuGlnGlnAl 1905
Db      6686  GCCCAGACTGAGTAATCAGATTATGAAGAAAGCTGAATGCTCCAAAGCTGGAGGCGGC 6745
QY      1905  agluLysAspLysAlaSPAlaIleArgLysThrIleAspIleThrGluLysIleSerAl 1925
Db      6746  ACTGTGGAAGAAAGGTGAGTTCGATTGAGGCTAGCTCAACACAGAGAGAGATGATCA 6805
QY      1925  nile-----GluGlnGlnLeuSe 1931
Db      6806  GCTGAGAAAGAGCATCGAAAACTGAGAGTTCGATTGAGGCGGAGTAAAGAAAGAGCT 6865
QY      1931  uGlnGlnAlaIleThrAsnLeuLysglulThrLeuTyGluArgLysSerLeuIleGlnCysLy 1951

Db      6866  GCACATCGACAGAAACTGAAAGAACCGGAGCGGAGATGATGATCTT-----AA 6916
QY      1951  sglulGlnLeuAlaLeuAsnThrGlnHileuArgGluThrLeuLysSerLysAspLeuAl 1971
Db      6917  GATTAAGTTTGAAACCTTGAAGAGGAATTTGAGATGTCAGAGAAACCAAGAGCTAGT 6976
QY      1971  aleuGlyLysMetGluGlnGluArgAspGluAlaIleAsnLysValIleAlaLeuThrG1 1991
Db      6977  GATTT-----CTTGATGCCGGAATTCCAAGCA----- 7004
QY      1991  ulysMetSerSerLeuGluGlnGlnIleAsnGluAsnValIleThrLysglulGlyG1 2011
Db      7005  -GAAGTAGAGACTTAAACAAACAAATGAAGAGATGCGCAGAGCTGAAGATTTTGA 7063
QY      2011  v-----GlyLysLysGluThrPhelyrLeuGlnArgProSerLy 2024
Db      7064  ATTAGACCTTGTCACGTTAAGTCTGAAAAAGAAATCTGACAAACAAATACAGAAAA 7123
QY      2024  sglulnserSerSerGlnMetGluGluLeuArgLysSerLeuLysThrLysAspLeuG1 2044
Db      7124  ACAAGTCACTTGTTCAGAACTAGACAAGTTACTCTCTTCAATTTAAAACTGTAGAAAG 7183
QY      2044  nleuGlnGluAlaGluLysglulLysSerGluAlaThr----- 2056
Db      7184  AAAGAGCAACACAGATCAGATCAAGAAAGAAATCTTAACCTGAGAGATGCTTCA 7243
QY      2057  -AsnGluLleLysAsnLeuThrAlaLysIleSerSerLeu-----GluGlnGluThr 2074
Db      7244  GAATCAGTTAAAGAGCTTAATAGAGCAGTACAGCTTGTGTGTCGACCAAGAAATAT 7303
QY      2074  uGln---AsnAlaSerLleLeuAsnGlnAlaValIleSerGluArgLysAsnLysIse 2093
Db      7304  GAAGCCACAGAACACAGATTTAGAACCAACCAATAGAGAAAGCATCAGCTTGAATAG 7363
QY      2093  rLysGlnGlnLeuValSerGluLeuGlu-----GlnLeuSerLeuThrLe 2108
Db      7364  CATTGAAAGACTGAGACCGCTTGAAGCTAGATGAAAGAAAGAGCTCTGTGTTACA 7423
QY      2108  ulysSerArgAspAsnAlaIleAlaGlnSerLysArgLysAspGluAlaValaLysLy 2128
Db      7424  ACAACAGAAAG-----GAAAGTAGCATCATGACGATTTACTTAAGCTAG 7468
QY      2128  slleAlaSerLeuAlaGluGluLleLysIleLeuThrLysGluMetAsp----- 2144
Db      7469  AGTGGAGAACTTGAAGAGAGCTAGAGATGCCAGACAAACCAAGCATGCACTCT 7528
QY      2145  -GluPheArgAspSerLys-----GluSerLeuGlnGlnIleSerSerHileuSe 2161
Db      7529  TCGAGCAGAAATTTCAAGAGAGAGATGAGACCTTAACCAAAATATAGAAAGGATGAC 7588
QY      2161  rglulGluLeuLysThrTyLysThrGluLeuGlnMetLeuLysGlnGlnLysGluAspI1 2181
Db      7589  CCAAGTCTGAGAGCTGGAATTAGATGTTACTTAAGTCAAGAAAGAAATCT 7648
QY      2181  eAsnLeuLysleuAlaGluLysValLysGluValaSPGluLeuLeuGlnHileuSerSe 2201
Db      7649  GACAAATGAAATTTCAAAAAAGAGCAAGCCGAATATCTGAATTA----- 7691
QY      2201  rleuLysglulnleuAspGlnIleGlnMetGluLeuArgAspGluLysleuArgAnty 2221
Db      7692  -----GAAATATATTAATTCATCATTTAAATAT 7718
QY      2221  rglulLeuLysglulysMetAspIleMetGluLysglulLysSerValLeuArgLeuMetG1 2241
Db      7719  -----ATTTGCAAGAAAAAGA 7735
QY      2241  nAsnGluProGlnGlnGlnGlnAspAspValaIleGluArgMetAspIleLeuGlnSerAr 2261
Db      7736  GCAAGAGAAAGTACAGATGAAGAAATACACACATGCCATGAGATCTTCAACA-- 7793
QY      2261  gAsnGlnGluIleGlnGlnLeuMetGluLysIleSerAlaValIlySerGlnGlnHileTh 2281

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Db 7794 -----CAATTAAGAAGCTCATATGAGAGTGGACGCTCATTAATGACCAAGAAGC 7846
 Qy 2281 rleuLeuser-----SerLeuSerSerGluLeuGlnLysGluThrGlnAlaHisIle 2298
 Db 7847 CTGAAGGCCCAAGAGCAGAAATCTTAGTCAAGTAGAG----- 7886
 Qy 2288 HisGlyMetLeuAsnIleLysGluSerLeuSerSerThrLeuSerArgSerPheGly 2318
 Db 7887 -----TGCTT-----GAACTTGAGAAAGCTCAGTTGCTACCAAGCCTTGAGCA 7930
 Qy 2318 rleuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPhe 2338
 Db 7921 GGCCAAAATATATATGTTGTTTGCATCTTCAGTGAAGGCTCATTCAGAA----- 7985
 Qy 2338 sValValLysrThrAlaValLysGluAspHisSerLeuIleLysAspTyrGly 2358
 Db 7986 -----CTAGAAAGATGGCAACA 8002
 Qy 2358 sAspLeuAlaLysGlnLysArgHisAspGluLeuArgLeuGlnLysGlnCysLeu 2378
 Db 8003 GAAATGGAGAAAGATGAAAGAAATCATGACTGAAATAATCAAAATTCAGACCAAGA 8062
 Qy 2378 uGlnHisGlyArgLysTyrSerAspSerAlaSerGluGluLeuLysPhe----- 2394
 Db 8063 GCAGCTTCTCTAACTGTCCAGGTGGAAGAGAGACCAACTTTGGAAGAGCAAAA 8122
 Qy 2395 -CysGluIleGluPheLeuAsnGlnLeuLeuPheLysLysAlaAsnIleIleGlnSer 2414
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 Qy 2414 IGlAspAspPheSerGluValGlnValPheLeuAsnGlnValGlnSerThrLeuGln 2434
 Db 8183 AAATGCTCTTTCGACGACACATTAGAACTGACAGCTTCTTAAGAAATCTTAGAA 8242
 Qy 2434 uGlnLeuGlnLysHisLysLysGlyPheMetGlnTrpLeuGlnGluPheGly----- 2450
 Db 8243 TGAGCTTGAATTGACAAATAATGACAAATATGCTCTTGTGTAAGAAAGTAAACAAATGAC 8302
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 Qy 2479 sArgLeuLysAlaValGlnSerLysIleGlnArgGluIleThrValTyrLeuAsn 2499
 Db 8423 AGAAATTAAGAC-----AGCAAGATCA----- 8447
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 Db 8448 -----TTGAAGAGAGCTCACACTGAAATAATAGTGAATTGAGAGA----- 8486
 Qy 2519 uHisHisGlyProSerAlaSerValMetGlnGlnLysAsnAlaArgLeuLeuGlyIle 2539
 Db 8487 -----AGCTTAGATTGCATGCACAAACCAAGGTGGAAGAAAGAGG----- 8528
 Qy 2539 uLysThrValGlnAspGlnSerLysLysLeuGlnSerArgIleLysMetLeuGln 2559
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 Qy 2559 uLeuAsnLeuValLysAspAspAlaMetHisLysGlyLys-----ValAlaIle 2577
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 Db 8600 TTGGAC-----ACAAACAAACAGTATGAAGTAAATCCAGACATCCAGAGAAAT 8653
 Qy 2597 uThrLysLysGlnAspAsnLeuGlnAlaAlaMetLysGlnIleGlnAsnLeuGlnLys 2617
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Qy 2617 cValAlaLysGlyAlaValProTyrLysGlnGluIleAspAsn----- 2631
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 Qy 2632 -----LeuLysThrLysValLysIleGlnMetGlnLysIleLysTyr----- 2646
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 Db 8810 GAAGAGGAAATGAACTGCCCGGAGGAAATGAAGTTGTTGATCAAAATCTGTAAACA 8869
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 Qy 2680 sAspAsnAspThrThrValCysValProLysAspTyrGlnLysAlaSerThrPhePro 2700
 Db 8930 GAAGCAGAAACA----- 8942
 Qy 2700 IThrCysGlyGlyGlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSer 2720
 Db 8943 -----GGTACTGTTATGATGATCAAGGTCGATGAATTAACAATGA 8983
 Qy 2720 u-----LysAlaAlaLeuGln-----ArgGluLeuSerHisTyrLys 2733
 Db 8994 GATCAAGAACTGAAAGAACTTTGAAGAAACCAAGAGCAGCATGAATACTTGA 9043
 Qy 2733 sLysTyrHisHisLeuSerArgThrMetSerSerSerGlnAspArgLysThrLysAla 2753
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 Qy 2753 sLysSerAspAlaHisSerSerHisThrGlySerSerHis-----Arg 2768
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 Qy 2768 ySerProHisLysThrGlnThrTyrArgHisGlyProValThrProGlnLysSerGln 2788
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 Db 9197 CCTTTCTTACTGAAAGAGATTATCATCTGCGCCAAATTAAGCTTACGACAGAGCA 9256
 Qy 2799 rGlnSerSer-----ThrLysArgValLysSerProAsnArgSerGluIle 2815
 Db 9257 AAGATCCAGTGAAATGAGAAATGTAAGAGAACCAACACTGCTACCCAGAGAGCTT 9316
 Qy 2815 rSer-----GlnLeuValMetSer-----ProGly-LysThrGlyMet 2828
 Db 9317 TTCTAAAAAAGCAAGAAAGATCATGATGATTCACCTGCGCAAGACA----- 9369
 Qy 2828 iLysHisIleLeuSerProSerLysValGlyLeuHisLys-----LysArgAlaLys 2846
 Db 9370 -----CGAAGGTACTAGTTTGAGCCAGAGGACTTCCAAAGTTGTAAAGAAAGGTTTGC 9427
 Qy 2846 eProAsnArg-----SerGlnMetProThrGlnHis 2857
 Db 9428 TGACATCCCGACAGAAAGACTAGCCCATATATCTCGGAGAAACAAACATGAGCA----- 9483
 Qy 2857 aLlIleSerProGlyLysThrGlyLeuHisLysAsn-----LeuThrG 2871
 Db 9484 -----CTCGAGCCAGCCCGCTGCTGCAAGAAAGTTAGCGGTATCCCGCATGAGCTTGC 9541
 Qy 2871 iLysThrLeuPheAspAsnLeuSerSerProCysLysGlnGlnLysValGlnLysAsn 2891
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 Qy 2891 euAsnSerProLysGlyLysLeuPheAsp-----ValLysGln 2904
 Db 9587 CAGATCACAAAAGTCAAAAGTTGCTCAGCGGAGCCAGTATTCAGGACCATCTCTCG 9646

QY 2904 ysserMetPrcTyrCysProSerGln-----PhepheAspAsnSerLyLeuGlyA 2921
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QY 2921 sPheSerGluLeuAsnThrAlaGluSerAsnAspLysserGlnAlaGluAsnTrp 2939
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RESULT 4
PCT-US95-16216-2
Sequence 2, Application PC/TUS9516216
GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Ratner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochores Protein, and Methods of Use
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10136 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-16216-2

Alignment Scores:
Pred. No.: 5,466-83 Length: 10136
Score: 1153.00 Matches: 736
Percent Similarity: 37.84% Conservative: 581
Best Local Similarity: 21.15% Mismatches: 1163
Query Match: 7.81% Indels: 1001
Gaps: 144

US-09-724-584-1 (1-2954) x PCT-US95-16216-2 (1-10136)

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Db 465 TTCCAGGAGAGCACTCAATTCAGGCAAA----- 494
QY 101 LeuGlyIleIleProGlnAlaIleGlnGluValPheLySleIleGlnGluIleProAsn 120
Db 495 -----AAACAATAGAAAAAAGCTGAGACGAACTTAAAGG 530
QY 121 ArgGluPheLeuLeuArgValSerTyrMetGluIleTyrAsnGluThrValLyAspLeu 140

Db 531 TGTAAATCTGAGCTTGAAAGAACCAAGAGCTGGCAGTCTGCAATGCTCTCTGAT 590
QY 141 LeuCyAspAspArgArgLy-----LysPheLeuGluIleArgGluAspPheAsn 157
Db 591 CCATCAATATACCAACAAAAATTTTCAACTCCATCAACCAACCAAGTCAATATATAGT 650
QY 158 ArgAsnValIlyValAlaAspLeuThrGluGluLeuValMetValProGlnHleValIle 177
Db 651 GGTTCAGATAT-----GAAGATCTTAAGAAAAATATATAAGAGCTTGA----- 698
QY 178 GlnTrpIleLySlyGlyGluLyAsnArgHisTyrGlyGluThrLysMetAsnAspHis 197
Db 699 -----GAACGAAAAAGATTAGAGGAGGAGGTTAAAGCTTCAGAGCT 740
QY 198 SerSerArgSerHisThrIlePheArgMetIleValGluSerArgAsp-----ArgAsn 215
Db 741 AAAAAAGCAAGCCAGACTCTTCCACAGCCACCAATGATATCAGGACATTCGCCGCT 800
QY 216 AspProThrAsnSerGlu-----AsnCysAspGlyAlaValMetValSerHisLeuAsnLeu 234
Db 801 CAGGCTTCATCATCTGTCTCTCATGGCAGACAGAAAGCCCAAGTCACTTTCA--- 857
QY 235 ValAspLeuAlaGlySerGluArgAlaSerGlnThrGlyAlaGluIlyValArgLeuLyS 254
Db 858 -----TCTAATTCCAAGAACT----- 875
QY 255 GluGlyCysAsnIleAsnArgSerLeuPheIleLeuGlyGlnValIleLySlySer 274
Db 876 -----CCAAATGAGAGAGATTCTCT 896
QY 275 AspGlyGlnAlaGlyIlyPheIleAsnTyrArgAspSerLySleuThr 290
Db 897 GCATCTTACTTTTCTGTGGAACTAGAGTGACTCCAGTCAATGATTCGAATAGG 956
QY 291 ---ArgIleLeuGlnAsnSerLeuGlyLyAsnAlaLySerValIleIleCyThrIle 309
Db 957 AAAAGAGAGCTAATACAGCTTCTTGGCAATTCAGC----- 995
QY 310 ThrProValSerPheAspGluThrLeuSerThrLeuGlnPheAlaSerThrAlaLyS 329
Db 996 AGTCTCATCTTTTGGAT-----CAATTAAGCGCAATCAAGAG 1037
QY 330 ValArgAsnThrProHisValAsnGluValLeuAspAspGluAlaLeuLeuLyArgTyr 349
Db 1038 CTAGAGAAAC-----AAGATTAAATGAGTTG-----GAAGTACCGCTGCAAGACAT 1082
QY 350 ArgLySlyIle-----LeuAspLeuLySlyGlnLeuGlu--- 361
Db 1083 GAAAAAGAAATGAAAGCGCAAGTGAATTAAGTTCAAGAACTCCAACTCCAACTGAGAGAA 1142
QY 362 ---AsnLeuGluSerSerSerGluThrLysAlaGlnAlaMetAlaSerGluGluHisThr 380
Db 1143 GCAAAAGTGGAATTAATGAAAAAGAAAGTTTGAACAAATGTGGAGTGAACTAGAG 1202
QY 381 GlnLeuLeuAlaGluIleLySlyGlnLeu-----HisLySlyGluArgLySlyGly 397
Db 1203 AGAACAACAGCAAAATACGACCGGCTCAACCAAGTATATGCAATGAGCAAAAACTG 1262
QY 398 TrpHisLeuThrAsnIleValAlaIleSerSerGlnGluSerGlnGln----- 413
Db 1263 AAAAAATTGACGGAATTTGAGTTGTCAAGCAAAATGCAAAAGTCCAGATCTTCT 1322
QY 414 ---AspGlnArgValIlyAsArgLySlyArgValIlyThrAlaPro---GlyLySleGln 431
Db 1323 CTGGAACAGAAAAATTAGAAAAAGAAAGAGATTTCAGAGAGAGCTCCGCTCAACAG 1382
QY 432 AsnSerLeuHisIleSerGlyValSerAspPheAspMetLeuSerArgLeu---ProGlyAs 451
Db 1383 CGTTCTTCCAAACACTGAGCAAGAGTCAATCCAGATTAAGGCGCACTCAACGAGG 1442
QY 451 nPheSerLySlyAlaLySlyPheSerAspMetProSerPheProGluIleAspAspSerVa 471
Db 1443 TTACAGCAAG-----CCAAGAAAT 1460

QY. 471 LCysThrGluPheSerAspPheAspAlaLeuSerMetMetAspSerAsnGlyLeuAs 491
 Db 1461 ATGCAACAAGCTCTGACGCTGAATGATTAACATCACTCACTAAGCAACGCTAGAA 1520
 QY 491 PALAGTTPAenLeuAlaSerLysValThrHisArgGluLysThrSerLeuHisGlnSe 511
 Db 1521 AACAAATTTGGAAAGATTAAAGCAAAAGTTGTGC-AAGCTGAACAGCGCTTCCAGCCGAG 1579
 QY 511 rMetIleAspPheGlyGlnIleSerAspSerValGlnPheHisAspSerSerLysGluAs 531
 Db 1580 TCAGATCAAGAGAAATGAGACTGAGAGAGACATGCGAG-----GAATGAGAGAGAGAAA 1633
 QY 531 nGlnLeuGlnTyrLeuProLysAspSerGlyAspMetAlaGluCysArgLysAlaSerPh 551
 Db 1634 CAACCTCCTTAAGAGTCACTGTGAGCAAAAGCCAGAGAAAGTCTGCACCTGAGAGGACA 1693
 QY 551 eGluLysGluIleThrSerLeuGlnGlnLeuGlnSerLysGluGluGluLysLysGlu 571
 Db 1694 ACTCAAGAACATCAAAACAGTGTTAATCAGACCCAGAAATTTTGCAGAAAGAAATGAAAGC 1753
 QY 571 uLeuValGlnSerPheGluLeuLysIleAlaGluLeuGluGluGlnLeuSerValLysAl 591
 Db 1754 GAAGATACCTCTCAGGAAACCATGTTAAGAGATCTTCAAGAAATA----- 1802
 QY 591 aLysAsnLeuGluMetValThrAsnSerArgGlnHisSerIle----- 605
 Db 1803 -----AATCAGCAAGAAACCTCTTGACTTGTAGAAAACCTGAA 1840
 QY 606 -----AsnAlaGluValGlnThrAspValGluLysGluValAlaArgLysGlu 621
 Db 1841 GCTTGCTGCTGCTGATCTGAAAAGCAGAGATTTCTTCAAGACCTTTTGAAGAAAAG 1900
 QY 621 uMetSerValLeuGlyAspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSerSe 641
 Db 1901 A-----GAACATCACATGAAACAATTATGATTAGTTAAGCAAGACACA 1945
 QY 641 rValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGlnHisArgLysMetLe 661
 Db 1946 GAAAGAGTCCAAAGCCTTGCTGAGTGC-----TT 1975
 QY 661 uGluGlnLysIleValAspLeuGluGluPheIleGlnAsnLeuAsnLys----- 677
 Db 1976 AAGAGTTAAAGAAAGAAATATGAAATGAAAGAAAGAAACCTCTTTCTTTGTTG 2035
 QY 678 -LysSerGluAsnAspLys-----GlnLysSerSerGluGlnAspPheMetGluSe 694
 Db 2036 GAAAGAGTGAAGAAAGAACTTTAACTCAGATGCAATCAGAAAGAAAGAACTTGACAGG 2095
 QY 694 r-----IleGlnLeuCys----- 698
 Db 2096 TAAAAATTAATCACTTGAAACCTTGCTGAAAGACACAGCAATATAAAAGTCATGAATACA 2155
 QY 699 -----GluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGlnLeuAlaLeuMe 715
 Db 2156 CGAGAGAGTAGAGACGCTGAGATGACAGAGAAACCTTAAGTGTGAGATCAAGAAACCT 2215
 QY 715 rArgAspAsnPheAspAsnIleIleLeuGlnAsnGlnThrLeuLysArgGluIleAlaAs 735
 Db 2216 TCACAACGCTTAGACAGTAAGTCAAGTGAAGAGACCCAGAAACTGATTATATGGA 2275
 QY 735 pLeuGluArgSer----- 739
 Db 2276 GCTACAGCAGAAAGCTGAGTCTCAGATCAGAAACATCAGAAAGAAATGAAATATGTG 2335
 QY 740 -LeuLysGluAsnGlnGluThrAsnGluPheGluIleLeuGluLysGluThrGlnLysGlu 759
 Db 2336 TTGGAAGACTCTCAAGCTTACCTGCGCAACTTGAAGATCTA-----GA 2377
 QY 759 uHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLysLeuValGluAsnAlaGlu 779
 Db 2378 ACACAAGCTTCAAGTACTGTCA-----AATGAATAATGCAAGAAAGACCG 2422

QY 779 uMetTyrAsnGlnAsnLeuGluGluAspLeuGluThrLysThrLysLeuLeuLysGluGlu 799
 Db 2423 GCTGTAC---CAAGACTTGACATGCCGAATATAGAGCTTCAGAGATCTGTCTAAATCCA 2479
 QY 799 nGluIleGlnLeu----- 803
 Db 2480 AAGATCTCTCTGTGAGCAATATGAAGATCATCAGAGAAAGTCTTTGGCTTTGATCAGCA 2539
 QY 803 ----- 803
 Db 2540 GCCTCGATGCATCATCTCTTGCAAAATATATGAGAAACAAGAGACATGCTTCACA 2599
 QY 804 -----AlaGluLeuArgLysArgAlaAspAsn-----LeuGlnLys 815
 Db 2600 GAGGAGTAGATGTCTTTAGAAAGCAGACCAAGTCCGAAAAATTCCTGCCATCTTACAAA 2659
 QY 815 rLysValAlaArgAsnPheAspLeuSerValSerMet-----GlyAspSerGlu 830
 Db 2660 TAGAGTTGATTCACTGTAATTTTCAATTAGAGTCCAAAACAGATGAATCAGACCTGCA 2719
 QY 830 uLysLeuCysGluGluGluIlePheGlnLeuLysGlnSerLeuSerAspAlaGluAlaValTh 850
 Db 2720 AAAGCAGCTGTAAGAGTTGCTGCAATCAAGAGAGAAATAGAA-----GAAATCTCAT 2773
 QY 850 rArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeuGluLeuLysGluLys 870
 Db 2774 GAAGCAGAACAGATGCATCAAGTTTGTGCTGAACAAACATCAGCCGATTAGTAAGTT 2833
 QY 870 eMetGluAspThrSerAsnTryptAsn-----Glu 880
 Db 2834 ACAGAGAGACATCTTGCTGCACAGATGTTGCTGAAACCTTAAGTCCCTTGAGAA 2893
 QY 880 nLysGluLysAlaAlaSerLeuPheGluLysGlnLeuGluThrGluLysSerAsnTyrLys 900
 Db 2894 CAAGGAAAAAGAGCTGCAACTTTTAATGATAGTAGTAAGAACTGAGCAGAGCATTTCA 2953
 QY 900 eLysMetGlu-----AlaAspLeuGlnLysGluLeuGln----- 911
 Db 2954 AGAATTAATAAAGAGCAACCATCTACTGAAAGACTCTTAAGAGACTTCAAACTTTATATC 3013
 QY 912 -----SerAl 913
 Db 3014 CGAAACCTTAAGCTTGAGAGAAAGAAATAGATTCATCTTTTAAATAAAAGGGA 3073
 QY 913 aPheAsnGluIleAsnTyrLeuAsnGlyLeuLeu-----AlaGlyLys 927
 Db 3074 AATTGAAGAGCTGACCCAAAGAGAAATGGAGCTTTAAGAAATTAATGATCATCTTAATCA 3133
 QY 927 eValProArgAspLeuLeuSerArgVal-----GluLeuGlu 939
 Db 3134 AGAGAAAGATGAACCTTAATCCAGAAAGAGTGGAGATTGCAAACTATATAGATGAAGGGA 3193
 QY 939 uLysLysValSerGluPheSerLysGlnLeuGlu----- 950
 Db 3194 GAAAGACATTCAGAGTTATCTGATCAGTACAGCAAGAAACTTATTACTTCAAAAG 3253
 QY 951 -----LysAlaLeuGluGlu 955
 Db 3254 ATGTGAAGAAACCGAAATGCATATGAGATCTTAGTCAAAATATCAAAAGCAGCAGCA 3313
 QY 955 uLysAsnAla-----LeuGlnAsnGluValThrCysLeuSerGluTyrLysPhe 971
 Db 3314 AAAGAAATCTTAATTAAGATGCTTGCTTAATGAATGACACTAGTCTTTGTGAAATATAG- 3371
 QY 971 eLeuProAsnGluValGluCysLeuLysAsnGlnIleSerLysValaSerGluGluIleMe 991
 Db 3372 -----AAAAATGAGTTGAAACAGCTTAAGAGACATTTCCAAAGAACCAAGATTTCTT 3427
 QY 991 rLeu---LeuLysGlnGluGluLysSerAlaSerIleIleSerLysGlnGluIleAl 1010
 Db 3428 AAACAATTTACATTTGCTGAAGAAAGAAATCAGAAATCTGATGCTTAAGTGGAGACAGT 3487
 QY 1010 eMetGln-----GluGlnSerGlu----- 1016

[illegible]

QY 2828 1elVehi:ileuuserProserLyValGlyLeuHisLys-----LysArgAlaLeuS 2846
 Db 9370 --CGAAGGTACTGAGTTTGGACCGAGGAGCTTCAGAAAGTTGTAAGAAAGGTTTC 9427
 QY 2846 eEPProAsnArg-----SerGluMetProThrGlnHisV 2857
 Db 9428 TGACATCCCGACAGAAAGACTAGCCCATATATCTCGCAAGAACACACCATGCA-- 9483
 QY 2857 aIIeSerProGlyLysThrGlyLeuHisLysAsn-----LeuThrG 2871
 Db 9484 --CTCGACCGACCCCGCTGGCTGCACAGAAAGTTAGGCTATCCCACTGAGTCTCGG 9541
 QY 2871 1userThrLeuPheAsnLeuSerSerProCysLysGlnGlnLysValGlnLysAsnL 2891
 Db 9542 CAAGAAAAATC-----TTGCAGAGTCTCTCCAAACCAACAGCTGTGGCA-----G 9586
 QY 2891 euAsnSerProLysGlyLysLeuPheAsp-----ValLysSerL 2904
 Db 9587 CAGATCAAAAGATCAAAAGTTGCTCAGCGAGCCCAAGATTCAGGACCATCTCCG 9646
 QY 2904 ySerMetProTyrcysProSerGln-----PhePheAsnSerLysLeuGlyA 2921
 Db 9647 AGAACCCACACGAATCCGTCCTCCAGTCAATATCTCTCGAGAGAGTCCAGCTGAGAG 9706
 QY 2921 sPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsnTrp 2939
 Db 9707 CCCAGAGAGGCGCTGAGGGTCAAGCGAGCCGAGCTTGTCCAGCCCAAAAGTGG 9762
 RESULT 5
 US-08-328-254-5
 Sequence 5, Application US/08328254
 Patent No. 5710022
 GENERAL INFORMATION:
 APPLICANT: Zhu, Xueliang
 APPLICANT: Lee, Wen-Hwa
 TITLE OF INVENTION: A No. 5710022zel Nuclear Mitotic Phosphoprotein
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/328,254
 FILING DATE: 24-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/141,239
 FILING DATE: 22-OCT-1993
 ATTORNEY/AGENT INFORMATION:
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 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-CJ 1191
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 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8789 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS

LOCATION: 544..7990
 US-08-328-254-5
 Alignment Scores:
 Pred. No.: 1,286-75
 Score: 1061.00
 Percent Similarity: 39.11%
 Best Local Similarity: 21.96%
 Query Match: 7,18*
 DB: 1 Gaps: 118
 US-09-724-584-1 (1-2954) x US-08-328-254-5 (1-8789)
 QY 529 LysGluAsnGluLeuGlnTyrcysProLysAspSerGlyAspMetAlaGluCysArgLys 548
 Db 460 AAAAGAAAGAAATATGAAGAAATG--AAAGAAAGAAAGAACTGTTTCTTGTGAAA 516
 QY 549 AlaserPheGluLysGluLysThrSerLeuGln-----GlnGlnLeuGlnSer--- 564
 Db 517 AGTAAAGAAAGAAAGAAAGTTTAACATGATGAAATCAGAAAGAAAGAAAGCTTGAGAGTAA 576
 QY 565 -----LysGluGluGluLysGlu 571
 Db 577 ATTAATCACTTGAAACTGTCTGAAAGACAGCAAAATAAAGTCAATATACAAACAG 636
 QY 572 LeuValGlnSerPheGluLeuLysLysLeuValGluLeuGlnGluGlnLeuSerValLysAla 591
 Db 637 AGAGTAAGAACCGCTGGAGATGAC-----AGAGAAAGCTTAAGTGTCCAGATC 684
 QY 592 LysAsnLeuGluMetValThrAsnSerArgGluHisSerLysAsnAlaGluValGlnThr 611
 Db 685 AGAAACCTTCAACAGCTTGTAGACGTAAG-----TCAGTGAGAGTGAAGACCCAGAA 738
 QY 612 AspValGluLysGluValValArgLysGluMetSerValLysGlyAspSerGlyTyrc 630
 Db 739 CTAGCTTATGAGAGCTACACAGAAA-----GCTGAGTTCTCAGATCAGAAACATCAG 792
 QY 631 --AsnAlaserAsnSerAspLeuGlnAspSerSerValAspGlyLysArgLysSer 649
 Db 793 AAGCAATAGAAATATGTTGTGAAGACTTCTCAGCTTACTGGGCAA----- 840
 QY 650 SerHisAspGluCysLysGluHisArg--LysMetLeuGluGlnLysLysValAspLeu 668
 Db 841 -----GTTGAAGATCTGAACACACAGCTTCACTTCTCAATGAATATATGACAAA 894
 QY 669 GluGluPheLysGluAsnLeuAsnLysLysSerGluAsn-----AspLysGlnLysSer 686
 Db 895 GACCGGTGTACCAAGACTTCATGCGCAATATGAGACCTCAGGAGATCTGCTAAATCC 954
 QY 687 SerGluGlnAspPheMetGluSerLysGlnLeuCysGluAlaLysMetAlaGluLysAla 706
 Db 955 AAAGATGCTTCTGCTGTACAAATGAAGATCATCAGCAAGCTTTTGT----- 1002
 QY 707 AsnAlaLeuGluGluLysAlaLeuMetArgAspAsnPheAspAsnLysLysLeuGlu--- 725
 Db 1003 ---GCTTTGATCAGACGCTGCATGATCATCTCTTGCMAATATATGAGAAACAA 1059
 QY 725 ----- 725
 Db 1060 GGAAGCATGCTTCAGAGAGAGTGAATGCTTTAGAAAGACCAAAAGTCCGAAAT 1119
 QY 726 AsnGluThrLeuLysArgGluLysLysLeuAspLeuGluAspSerLeuLysGluAsnGlnLys 745
 Db 1120 TCTGCATCTTAAGAAATAGAGTGAATTCATTTATTAAGAGTCTCAAAACAG 1179
 QY 746 ThrAsnGluPheGluLysLysGluLysThrGlnLysGluLysGluAlaGlnLeuLys 765
 Db 1180 ATGAAC-----TCAGACCTGCAAAAGCAGTGTGA--GAGTTGGT 1218
 QY 766 HisGluLysSerLeuLysLeuValGluAsnAlaGluMetTyrcysAsnGlnAsnLeu 785
 Db 1219 CAATCAAAAGAAATATGAAGAAATCTCATGAAGCAGAAACAGATCATCAAAAGTTT 1278

QY	786	GlUGlUaSplEugluThrIySthrIySLeuLeuLySgInGluIleGInLeuAlaGlu	805
Db	1279	GTG-----GCTGAACCAAGTCAGCCGCAATTAGTAATTCACAGAAAGACACTTCTGCTCAC	1332
QY	806	LeuIArgIySArgIaAspAsn-----LeuGInLySValArgAsnPhEaspLeu	822
Db	1333	CAGAATGTTGTTGCTGAACCTTAATGCTGCTTGAGAACAGAGAAAAAGAGCTGCACCTT	1392
QY	823	SerValSerMetGlyAspSerGluLySLeuCySgInGluIlePhEgInLeuLySInSer	842
Db	1393	TTAAATGATTAAGGTAAACAACTGAGCG-----GCGAGATTCAAGAAATTTAAAAAGAGCG	1446
QY	843	LeuSerAspAlaGluIleValThrIArgAspAlaGInLySgInLyCySerPhELeuArgSer	862
Db	1447	-----AACCATCTACTTGAAAGCTCTCTTAAGAGACTCAACCTTTA---TCC	1491
QY	863	GluAsnLeuGInLeuLySgInLySMetGluAspThrSerAsnTTPTyArgInGInLySgIn	882
Db	1492	GAACCCCTTAAGCTTGAGAGAAAGAAATGAAGTCCATCATCTTCTTAATATAAAGGGA	1551
QY	883	LySAlaIaSerLeuPhEgInLySgInLeuGInUthrgIySserAsnTTLyLeuMet	902
Db	1552	-----ATTGAAGGCTGACCCCAAGAGAAATGGGACTCTTAAGAAATT	1593
QY	903	GluAlaAspLeuGInLySgIn-----LeuGInSerAlaPhEAsnGluIleAsn	918
Db	1594	AATGATCCTTTAAATCAAGACAGAAAGATGAACCTTAATCCAGAAAGTGAAGTTTGCAAC	1653
QY	919	TyLeuAsnGlyLeuLeuAlaGlyIySValProIArgAspLeuLeuSerArgValGluLeu	938
Db	1654	TTATATAGAT-----GAAAGG	1668
QY	939	GluLySLySValSerGluPhEserLySgInLeuGIn-----	950
Db	1669	GAGAAAGGATTTTCAGAGTTATCTGATCAGTACAGACAGAAAGAAACTATTTTACTACAA	1728
QY	951	-----	954
Db	1729	AGATGTGAAGAAACCGAAATGCATATGAGAGATCTTACTCAAAAATCAAAAGCAGCACAG	1788
QY	955	GluLySAsnAla-----LeuGInAsnGluValThrCyLeuSerGluTyLyS	970
Db	1789	GAAAAGATTTCTAAATTAGAATGCTGCTGTAATGAAAGCACTAGCTTTGTGAAAATAGG	1848
QY	971	PhELeuProAsnGluValGluCySLeuLySAsnGInIleSerLySAlaSerGInGluIle	990
Db	1849	-----AAAAATGAATTTGAAACAGCTTAAGCAACATTTGGAAAGAAACCAAGAAATTC	1902
QY	991	MetLeu-----LeuLySgInGluGlyGInHisSerIaSerIleIleSerLySgInGluIle	1009
Db	1993	TTAACAAATTTAGCATTTGCTGGAAGAAAGAAATCAGATTCGATGCTGAGGTTGGAGACA	1962
QY	1010	IleMetGIn-----GluGInSerGlu-----	1016
Db	1963	GTGCAGCAAGCTGTGAGTCTGAGATGACAGATTAACAAACATTTAGAGCGAGGCT	2022
QY	1017	-----GInIleLeuGInLeuThrAspGluValThrIsthrgInSerLyS	1031
Db	2023	GGTGTTTAAAGCAAGAAATATATACCTTTAAGGAAAGACAAACAAATGCMAAAGGAA	2082
QY	1032	Val-----GInGInThrGluGluGInIyThrLeuGInMetLySlySMeChIAsp	1047
Db	2083	GTTATAGACTTATTACAAAGAAATGAACAGCTGTGAAGTAATGAAGATTAACATGGA	2142
QY	1048	AspLeuPhEgInLyS/TyrlIaArgAsnLySerGluAlaGluAspLeuLeuArg	1065
Db	2143	TGTCAAATATCTAGAAATCAGAACCAATTAAGAAACTCTGTGAAGAAAGAGAGCTGAGAGA	2202
QY	1066	GluMetGInLeuLeuLySgInLySMetGIn-----	1075
Db	2203	AATCAATGTAATTTTAAACCTCAGATGAGATCTTGAAGATTAAAGAAATTTCTCTAGATAGT	2262
QY	1076	-----SerValGluValLySleuIaAspThrLySgInLeuGIn	1089

Db	2263	TATATGCCGAGTTGGTCGCAATTAGAAAGCTATGCTAAAGAAATAGAAATTTAAACCTTCAG	2322
Qy	1090	GIuThr1IleArgAspIysGIuGlnLeuLeuHiGIuIysIysTyrPhepHeGlnAlaMet	110
Db	2323	GAAGAGTAGAAGGAGAAAGAGAGTCCCTGCACACATGAA-----TTA	236
Qy	1110	GIuThr1IlePheProIleThrProLeuSerAspSerLeuProProSerIysLeuValGlu	112
Db	2362	CAGACAAATT-----AGAGGAGATCTTGAAACACAGCAATTTGCAAGC	240
Qy	1130	GIYAsnSerGlnAspProIleGluIleAsnAspTyr-----	114
Db	2404	ATGCAGTCACAAAAAAATTAGTGGCTTTAAAGACTTGGAATAGATGCGGAAGAAAGTAT	246
Qy	1142	-----HisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCys	115
Db	2464	ATTTCAGGGCCTCATGATGATGTTGTCACAAAGCTCAAAACGAAATGACACACCTTCAGTCTCT	252
Qy	1158	LeuGluThrGIuArgAsnSerLeuIysGIuGlnValIleAspLeuAsnThrGlnLeuGln	117
Db	2524	CTCGAAACCAACATGAAACAAAGCTGATGAG-----CTGAGAAATATGTGAA	257
Qy	1178	SeuLeuGlnAlaGlnSerIleGlu-----LysSerAspLeu	118
Db	2572	ATACTCAGCGCTGAAAGATGATGAACCTGTAAGCTGAGCTGATGATGATTTCAAGGTCAGAAATGT	263
Qy	1190	GIuIysProIleGlnAspLeuGIuGlnGIuIysValIysLeuLeuLeuGluMetGluLeu	120
Db	2632	ATACACGCAACTAGAAATAATGCCAGAAAGAGTAGGAACCTATAATAGATTAATAATA	269
Qy	1210	LeuIysGly-----	121
Db	2692	TTAAATGATGAGAGTGGTCTTCCATGGTGAATTAGTGAAGACATACGAGAGTGAA	275
Qy	1212	-----	121
Db	2752	TTTGTGGAAACAACCAATGAAACAGACCCCTGTGCTTGGCTCCATTGGACAGAGTAAT	2811
Qy	1213	-----HisLeuThrAspSerGlnLeuSerIleGluIysLeuGlnLeuAsnLeu	122
Db	2812	TCCTACGACACTTGACA-----TTGTGACGAAAGAAATTCAATGACACTTGGC	286
Qy	1230	GIuVal1ThrGluIysLeuGln1ThrLeuGlnGluGluMetIysAsnIleThr1IleGluArg	124
Db	2863	GAATTGCAAGAAATTTCTTACTTTTCAAACTGAAACAAATTTTCATGATCAGAC	2922
Qy	1250	AsnGluLeuGln1ThrAsnPheGlnAspLeuIysValIleGln1AspSerLeuIysGlnAsp	126
Db	2923	TGTCAGATGAGCTCTTAATATGTCAGAGCTGCAGACCTATGTTGACTCTTAAAG-----	297
Qy	1270	LeuSerGlnAsn1IleGluGlnSer1IleGluThrGlnAspGluLeuArgAlaGlnGlu	128
Db	2977	---GCCGAAAAATTGGTCTTGTC-----ACGAAATCTGAGAAACTTTCAAGGT	302
Qy	1290	GIuLeuArgGluGlnIysGlnLeuValAspSerPheArgGlnGlnLeuAspCysSer	130
Db	3022	GACTTGGCGAAGAGATCAGCTG-----GCCTTGACGAGGGGGCTGTTCATCCCTG	307
Qy	1310	ValGlyIleSerSerProAsnHisAspAlaVal1IleAsnGlnIuIysValSerLeuGly	132
Db	3076	TCATCTCTTGTCGTCGACAGCTCTAGTCTTAGC-----AGTTTGGGA	312
Qy	1330	GIuValAsnSerLeuGlnSerGluMetLeuArgGluIuArgAspGluLeuGln1ThrSer	134
Db	3121	GAC---TCCTCTTTTACAGACTCTTTTGA-----CAACACGGA	315
Qy	1350	CysIysAlaLeuValSerGluLeuGlu---LeuLeuArgAlaHisValIysSerValGlu	136
Db	3160	GATATGCTCTTTTGAAGTAATTTGAAGAGGGGCTGTTCAGAAACCACTGACGTGATGAT	321
Qy	1369	GIyIuAsnLeuGlu1IleThrIysLeuAsnGlyLeuGluIysGlu1IleGluIys	138

Db	3220	-----GAAGTATT-----	-TGCACACTCTGCAGAGGAGAAATTCACCGG	3261
Oy	1369	SerGluGluSer-----	-GluValLeuLysSerMetLeuGluAsn	1401
Db	3262	AAAGAAACCCCTTCGCGCCCAAGCGAAGGATGTTGAAGAGCTTGAACTCCCTCTGTGAGGTG		3321
Oy	1402	LeuLysGluAspAsnAsnLysLeuLysLeuLysGluGlnAlaGluGluTyrSerSerLysGluAsn	1421	
Db	3322	TACCGGACGCTCCCTCGAGAGAGCTTAAAGAAATGAGAAAGTCAGAGGATTTATGAAAAAT	3381	
Oy	1422	GlnPheSerLeuGluGluValPheSerGlySerGlnLysLeuValAspGluLysLeuVal	1441	
Db	3382	AAG-----	-----GAATTCACAGG	3396
Oy	1442	LeuLysAlaGlnLeuLysAlaAlaGluGluTyrGluGlnLysLysAspArgAspTyrPhe	1461	
Db	3397	CTCGACGACGTTATTTAAGTTCTGGAAGGCAAGACGCTTACCTGCTTAGAAGACAGATTTGG	3456	
Oy	1462	GluLeuValGlnThrAlaAsnThrAsnLeuValGluGlyLysLeuGluThrProLeuGln	1481	
Db	3457	TCA-----	-----GAA	3462
Oy	1482	AlaAspHisGluGluAspSerLysAspArgArgSerGluGluMetGluLysValLeu	1501	
Db	3463	AATGAACAGTGGCAACACAGACGTGACAAAGCTGACTCTGGAGATGGAGTCCAAATGGCG	3522	
Oy	1502	GlyGluLysLeuGluArgAsnGlnTyrSerLeuGlu-----	ArgLeuGlnGlu	1517
Db	3523	GCAGAAAAGAAACACAGCGGAACACACTGCTTACCTGACGGAAATGACAGCACTCCAGCTA	3582	
Oy	1518	GluLysLeuGluLeuSerAsnLysLeuGlnLysLeuGlnLysGluMetGluThrSerVal	1537	
Db	3583	CAAGGTCTGACCTTAAGTTCTCGG-----	TCT	3609
Oy	1538	LeuLeuLysAspAspLeuGlnGlnLysLeuGluSerLeuLeuSerGluAsnLysLeu	1557	
Db	3610	TTCGCTGGCATCGACACAGAAAGATGCTTAATGAGC-----	CGA	3648
Oy	1558	LysGluAsnLysLeuAspThrThrLeuLysHisHisSerAspThrGlnAlaGlnLeuGlnLys	1577	
Db	3649	AATGAGAGCTGTGACATCTCAAAGAACATCTTCAAACTTACAGAAAGAACCAAG	3708	
Oy	1578	-----	-ThrGlnGlnLeuGlnLeu-	1584
Db	3709	CATGATGTTCAATCAGATTGTTGATTAAGATGCTCGACGACCTCAATCTGACATTGAG	3768	
Oy	1585	-----	-AlaLysAsnLeuAlaLysLeuLysSerPheAsnCysProLysThrGlnGluLys	1602
Db	3769	AAAAATTAACCTGAGACTGTGCACTTGAAACCCACAGAGAGAGCTCTGGGGAACAGTCCCA	3828	
Oy	1603	GluThr-----	SerAlaAspCysValHis	1610
Db	3829	GATACCAATTATGAGCTCCACGGGAGAGATTAACCCACAGGAGCTTCAAGATGCATTCT	3888	
Oy	1611	ProLeu-----	GluGln	1614
Db	3889	GAATTGTGCTATTTCTGCTCCTTAATGCTTTGGACCTATGATTCCTCGGGAAACAGAA	3948	
Oy	1615	LysIleLeuLeuLeuThrGlnGluLeuHisGlnLysThrAsnGlnGlnLysLeuLeu	1634	
Db	3949	GATATCCATAATCTTCAACCTCGGGGTAAAGACATCAAAATGGAATTTGAGATTACTT	4008	
Oy	1635	HisGluLysAsnGlnLeuGlnAlaGlnValGluLeuLysCysGluValGlnHisLeu	1654	
Db	4009	CATGTGATAGGACCGTGCAGAG-----	AAAGTTGAAAGTTTG	4047
Oy	1655	MetLysSerMetLysLeuSerLysSerLeuGluSerLeuGlnHisGluLysHisAsp	1674	
Db	4048	CTAATATGAATGAAGAAATTAAGACTCAAAATC-----	CATTTA	4086
Oy	1675	ThrGluGlnGlnLeuLeuAla-----	-LeuLysGlnGlnMetGln	1687
Db	4087	CAGGAGGTACAACTTAATGACCAAAATGACATGATGAAATTTGAAAAAATGTTGGTG	4146	

QY	1668	valValIthrlngIngluLyvsgIuleuInglInthrlsEgIuHlsleuThrlAlgluVal	1707
Db	4147	GAACTTAAAGAAAGAAACTCAGATTTAAGTAAAGTAAATTTCTTGTGATGC	4206
QY	1708	AephlsleuLyvsgIuAenHleuLeu-----GlyLeuAenPhelyvAenGIuAlglIn	1725
Db	4207	CAGGAGTTACTCCAGAGTAgAAACTTCTGAAGCCCTCAATTCTGATTTAGAAATGCAT	4266
QY	1726	--GlnLystrHrLyvsgIuGInCysleuLeuAngluAnLyS-----	1739
Db	4267	GCAGATAATATCATCCGAGAAATATGGAATATATGCGCAAGGAAATGACAGCTCG	4326
QY	1740	-----GluLeuGluGInserGInHlsArgleuGInCysGlu-----	1751
Db	4337	AAGGAGATTTCTTGATGTGGAAATAGCTGAGTAgATGCAGATCGAGAAAGCTAGC	4386
QY	1752	-----IleGluGluMetLyvserLeuLyvAepLyGluSer	1764
Db	4387	ATTGAGCATGAAGCCCTTACTGTAGAGCTGACTTAAAGGTATGTTCAACAGAAAGCTA	4446
QY	1765	AlaleuGluThrlLeuLyvsgIuserGInLyvAlle--AenLeuAenGInImec	1783
Db	4447	TGTTTAGAAAAAGACATGAAATTAAGCAGAAAGTTATTGTCTCCCTTGAAGAAAGCTC	4506
QY	1784	GluMetvAlmeLeuGluMetGluGluLeuLyvAenSerGInArghrValleAlglu	1803
Db	4507	TCAGTGGTCACAGTGAAGAGAAACACAGCTTGCTGAGAAATTAGATCTATGTCAAAAAA	4566
QY	1804	Arg-----ArgGInLeuGInAepAepLeuArgGluSerValGluMetSerIleGlu	1820
Db	4567	ACCAAGGACATCGATCAGATTGTCTGAAAAATGAAGAGAAACACAA--GAGCTTGAG	4623
QY	1821	Thr-----GlnAepAepLeuArgLyvAla	1828
Db	4624	TCTCATCAAGTGAAGTGTCTTCATTCGATTCAGGTGCACAGACGACGAGGAAAG	4683
QY	1829	GIngluAlaleuGInglIngluLyvAepLyvAlglInleuThrlSerGInleSerVal	1848
Db	4684	ACGGAACCTTCAGACTTGTGTCTCGATGTGAGTGAGCTGTAAAAAGACAAATCAT	4743
QY	1849	LeuGIngluLyvIleSerLeuLeuGluAenGInMeLeuTyvAenValAlaThrlValLyS	1868
Db	4744	CTCCAGGAAAACTGCAGAGATTGTGAAAAAGACACACAGCAGCTCTTTGACAAATGT	4803
QY	1869	GluThrlLeuSerGluAArgAepAepLeuAenGInSerLyvGInHlsleuPheserGluIle	1888
Db	4804	GAGCTGAAAAACCAAAATTGCACAACTAAATTAAGAAAGAAATTTGTTGCAGAAATCT	4863
QY	1889	GluThrlLeuSerLeuSerLeuLyvGluLyvGluHe-----Ala	1901
Db	4864	GAAAGCCTGCAGGCCACAGCTGAGTAAATTCAGATTATGAAGACGAAATGTCTCCAGGCC	4923
QY	1902	LeuGIngluAlaGluLyvAepLyvAlaAepAlaAlaArgLystrHlsAepIleThrglu	1921
Db	4924	TTGGAGGCGGCACGTGTGAGAAAGAGTGTGCTGATTGAGCTGAGCTCAACACAGAG	4983
QY	1922	LyvIleSerAnlle-----Glu	1927
Db	4984	GAAATGCATCACTGAGAGAGAGAGCAGATCAGAGAACTGAGAGTTCGATTGAGCGCATGAA	5043
QY	1928	GluGInleuLeuGIngluAlaThrlAenLeuLyvGluThrlLeuTyvGluArgGluSerLeu	1947
Db	5044	AAGAAGCAGCTGCACATCGCAGAGAACTGAAAGAACCCGACGGGGAATGATTCCTT	5103
QY	1948	IleGInCysLyvGluGInleuAlaleuAenThrluHlsleuArgGluThrlLeuLyvSer	1967
Db	5104	-----AAGATAAAGTTGAAGAACCTTGAAGAAAGGAATTTGCAGATCTCAGAAAGAAAC	5154
QY	1968	LyvAepLeuAlaleuGlyLyvMetGluGIngluArgAepGluAlaAenLyvAlle	1987
Db	5155	CAGAGGCTAGTGATT-----CTTGAGTCGAGAAATTCAAAGCA-----	5193

QY 1988 AAlaLeuThrGluLysMetSerSerLeuGluGluGlnIleAsnGluAsnValThrThrLeu 2007
 Db 5194 -----GAAGTAGAGACTCTAAACAAACAAATAGAAAGATGGCCAGAAAGCTG 5241
 QY 2008 LysGluGluGlu-----GlyGluLysGluThrPheThrLeuGlu 2020
 Db 5242 AAAAGTTTGAATTAGACCTTGTACGTTAAGTCTGAAAGAAATGTGACAAACAA 5301
 QY 2021 ArgProSerLysGlnInserSerSerGlnMetGluGluLeuArgGluSerLeuLysThr 2040
 Db 5302 ATACAGAAACAAACAGCTAGTGTCTAGAACTAGAACAACTACTCTCTTCAATTTAAAGT 5361
 QY 2041 LysAspLeuGlnLeuGluGluGlnIleGluLysGluLysSerGlnAlaThr----- 2056
 Db 5362 CTGTTAGAAAGAAAGAGCAGACAGATACAGATCAAGAAATCTAAACCTGCAGCTG 5421
 QY 2057 -----AsnGluLysAsnLeuThrAlaLysLysSerSerLeu-----Glu 2070
 Db 5422 GAGATGCTTCAGAAATCAGTTAAAGAGCTAAATGAGCCAGTACGCTGTGTGTGTGAC 5481
 QY 2071 GlnGluLysLeuGln-----AsnAlaSerLysLeuAsnGluAlaValSerGluArgGluAsn 2089
 Db 5482 CAGAGAAATATAGAGCCACAGACAGACTAGACCCCAATAGAGAAAGACATCAG 5541
 QY 2090 LeuArgHisSerLysGlnInserLeuValSerGluLeuGlu-----GlnLeu 2104
 Db 5542 CTGAGAAATATAGCATTGAAAGAGCTGAGAGCCGCTGAGAGTGAATGAAAGAGAGCTC 5601
 QY 2105 SerLeuThrLeuLysSerArgHisAlaPheAlaGlnSerLysArgGluLysArgGlu 2124
 Db 5602 TGTGCTTACAAACCTGAAG-----GAAAGTGAGCATCATGCAAGTTTAA 5646
 QY 2125 AlaValAsnLysIleAlaSerLeuAlaGluGluLysIleLeuThrLysGluMetAsp 2144
 Db 5647 CTTAAGGATAGAGTGGAGAACCTTGAAGAGAGCTAGAGTACCAAGCAACCAAGAG 5706
 QY 2145 -----GluPheArgAspSerLys-----GluSerLeuGlnGluInser 2157
 Db 5707 CATGACGCTCTTACAGCAGACAGAAATTCMAAGAGAGAGTACAGACCTTAAACCAAAATA 5766
 QY 2158 SerHisLeuSerGluGluLeuGluCysThrTrpLysThrGluLeuGlnMetLeuLysGlnGln 2177
 Db 5767 GAGGAGATGACCCAAAGCTTGAGAGGCTCTGGAATTAGATGTGTTACTTAAGGTCAGAA 5826
 QY 2178 LysGluAspIleAsnAsnLysLeuAlaGluLysValLysGluValAspGluLeuLeuGln 2197
 Db 5827 AAAAGAAATCTGCAAAATGAATTTACAAAGAGAGCAAGCAATATCTGAATTA----- 5880
 QY 2198 HisLeuSerSerLeuLysGluGlnLeuAspGlnIleGlnMetGluLeuArgAsnGluLys 2217
 Db 5881 -----GAAATAATAATAATTCATCA 5898
 QY 2218 LeuArgAsnTrpGluLeuGluCysGluLysMetAspIleMetGluLysGlnLysSerValLeu 2237
 Db 5899 TTTGAAAT-----ATTG 5913
 QY 2238 ArgLeuMetGlnAsnGluProGlnGlnGlnIleuAspAspValAlaGluArgMetAspIle 2257
 Db 5914 CAGAGAAAGAGCAAGAAAGTACAGATGAAAGAAATCAAGCACTGCCATGAGATG 5973
 QY 2258 LeuGluSerArgAsnGlnGluIleGlnGluLeuMetGluLysIleSerAlaValLysSer 2277
 Db 5974 CTTCAAAAC-----CAATTAAGAGCTCAATGAGAGAGTGGCAGCCCTGCATATAT 6024
 QY 2278 GlnGlnHisThrLeuLeuSerSerLeuSerSerGluLeuGlnLysGluThrGlnLysHis 2297
 Db 6025 GACCAA-----GAGGCTGT 6039
 QY 2298 LysHisCysMetLeuAsnIleLysGluSerLeuSerSerThrLeuSerArgSerPheGly 2317
 Db 6040 AAG-----GCCAAAGAGCAGAAATCTTAAGTGTCAAGTAGAG 6075
 QY 2318 SerLeuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPhe 2337

Db 6076 TGTCTTGAACCTTGAGAAAGCTCAGTTGCTTACAAAGCCCTTGTAGCCCAAAATATATAT 6135
 QY 2338 LysValIleAlaTrpArgThrAlaIleValLysGluAspHisSerLeuIleLysAspTrpGlu 2357
 Db 6136 ATGTGTTTGCAATCTTCACTG-----AATGGCTTATTCAGAACTAGAA 6180
 QY 2358 LysAspLeuAlaIleGluGlnLysArgHisAspGlu-----LeuArgLeuGlnLeu 2374
 Db 6181 GATGCAAGCAAGAACTGAGAGAAAGATGAGAAATCAGTACAGTGAATAATCAATT 6240
 QY 2375 GlnCysLeuGluGlnHisGlyArgGlyTrpSerAspSerAlaSerGluGluLeuLysPhe 2394
 Db 6241 CAAGCAAGAGCAGCTTGTCTTAACTGTGCCAGGTGGAAGAGACCACTGAG 6300
 QY 2395 -----CysGluLysGluPheLeuAsnGlnLeuLeuPheLysLysAlaSerIle 2410
 Db 6301 AAGAGCAAACTTGAAATCTGAGAAATCTGACAGTGAATTTGAGCAGAAATCCAACTG 6360
 QY 2411 IleGlnSerValGlnAspAspPheSerGluValGlnValPheLeuAsnGlnValGlySer 2430
 Db 6361 CTACATCCAAAAATGCTCTTTCAGAGACACATTAAGTGTGTCAGAGTTCTTAAG 6420
 QY 2431 ThrLeuGlnGluGluLeuGlu-----HisLysLysGlyPheMetGlnTrpLeuGluPhe 2449
 Db 6421 AATCTAGAAATGAGCTTGAATTTGACAAAAATGTGACAAATGTCTTGTGAAAGTA 6480
 QY 2450 Gly-----AspLeuHisValAspAlaLysLys 2458
 Db 6481 AACAAATGACTGCAAGAAATCTGAGTGCAGAGAGAAATGCAATGATGGCACAGAA 6540
 QY 2459 -----LeuSerGluGlyMetGlnGlnLysAsnArgGlnIleAlaSerThrIleGln 2475
 Db 6541 ACAGCAGAGCTGCAAGAAAGAACTCAGTGAAGAGAAATAAGCTGAGAGAGTTGAG 6600
 QY 2476 LeuLeuThrLysArgLeuLysAlaValAlaGlnSerLysIleGlnArgGlnIleThrVal 2495
 Db 6601 TTACTGTTGAAAGAAATTAAGC-----ACCAAAATGCA----- 6636
 QY 2496 TyrLeuAsnGlnPheGluAlaLysLeuGlnGluLysLysGlnGlnAsnLysGluLeuMet 2515
 Db 6637 -----TTGAAGAGCTCCACACTAGAAATTAAGTGAAG 6672
 QY 2516 ArgArgMetGluHisHisGlyProSerAlaSerValMetGluGluGlnAsnAlaArgLeu 2535
 Db 6673 AAG-----AGCTTATGTTGATGATGACCAAAAGCAGGTGAAAG 6711
 QY 2536 LeuGlyIleLeuLysThrValGlnAspGluSerLysLysLeuGlnInserArgIleLysMet 2555
 Db 6712 GAAAGG-----AAAGTGAAGAGAAATAGCTGAATATCAGCTACGG----- 6753
 QY 2556 LeuGluAsnGluLeuAsnLeuValLysAspAspAlaMetHisLysGlyLysLys----- 2573
 Db 6754 -----CTTATGAAGCTGAAAGAAACAC 6777
 QY 2574 ValAlaIleLeuGlnAspLysLeuLeuSerArgAsnAlaGluAlaGluLeuAsnAlaMet 2593
 Db 6778 CAGGCTTTGCTTTGAGC-----ACAAACAAACAGTATGAGTGAAGTGAATCCAGACATAC 6831
 QY 2594 GlnValLysLeuThrLysLysGlnAspAsnLeuGlnAlaIleMetLysGluIleGluAsn 2613
 Db 6832 CGAGCAAAATGACTCTTAAGAAAGAAATGTCTCAGCTTACAGAAAGCTGAGATGACCTT 6891
 QY 2614 LeuGlnLysMetValAlaLysGlyAlaValProTrpLysGluGluLysLeuAspAsn----- 2631
 Db 6892 TTAAGTCTAGT-----AAGAAAGCTCAATATATCATTTG 6927
 QY 2632 -----LeuLysThrLysValValLysIleGlnMetGluLysIleLysTrp 2646
 Db 6928 AAAGCTACTACAGATTTTGAAAGAAATGGAAGAAACCAAGATGCAACATTAATAATAT 6987
 QY 2647 -----SerLysAlaThrAspGlnGluIleAlaLysTrpLeuLys 2658

QY	~	906	LeuGlnIuYsGlu-----LeuGlnSerAlaPheAsnGluIleAsnIyr	913
Db	2197	CTGGATGGAAGAAAGACATAAAACTAAAGCTTCAGCAGCATGTTGAACAACTGGAAAT	2256	
QY	920	LeuAsnGlyLeuLeuAlaGlyIysValProArgAspLeuLeuSerArgValGluGlu	939	
Db	2257	CATTTCACCAAAATG-----CAGAGCTTTTCTCATCGAAAAGATT---	2299	
QY	940	LybIysValSerGluPheSerIysGlnLeuGluYsaIaLeuGlnIuYsAsnAlaLeu	959	
Db	2299	-----GATTGGACCAAAACAGAGAAAGAGCTTCTCACAGTTGATGATGCTCT	2348	
QY	960	GluAsnGluVal---ThrcYsLeuSerGluYrIuYsPheLeuProAsnGluValGluYs	978	
Db	2347	GAAGAAAGCTTCAAGAGACTCAACTAAAAATGACTTTTGTAAAGAGAGTACATGAC	2406	
QY	979	LeuIysAsnGlnIleSerIysLeuAsnGlnGluIleMetLeuLeuYsGlnIu-----	996	
Db	2407	CTGCGAGTACGTCCTTCATTCCTGCTCACAAGAGCTTCTTCAGTGAATTTGGAATATG	2466	
QY	997	-----GlyGluHisSerAlaSerIleIleSerIysGlnIuIleMet	1011	
Db	2467	TCATTCAAAAGCAATCAGAGCAAAAGAAATTCACAAACTTCCGAAAGACACATGATGTA	2526	
QY	1012	GlnGluGlnSerGluGlnIleLeuGlnIleuThrArgGluValThrlHisIthGlnSerIys	1033	
Db	2527	CAGCTTCAATTAATGATATCTCAGGTTAGAAAACGAAAGCTGCTTGAAGACAAACCTGC	2586	
QY	1032	ValGlnGlnThrGluGluGlnIuYrIleuGluMetIysIysMetHisAspAspLeuPheGlu	1053	
Db	2587	CTACAGAGTTCCTATGACCACTTACAGAAATTAAGAAATTGAGATTGACCAACTTCA	2646	
QY	1052	LybTyrlIleArgAsn---LysSerGluAlaGluAspLeuLeuArgGluMetGluAsnIleu	1070	
Db	2647	AGAAACCTCCAAACCTTCACAAACAAATAAGAAATCTGAATCTGATGATTAATTGG	2706	
QY	1071	LysGlyThrMetGluSerValGluValIys-----IleAla	1082	
Db	2707	ATGGAAGCTTCTTGAGCGCAAAACAAACGCAATTAACAAATTATCTTCAGTTTGAAGA	2766	
QY	1083	AspThrIysHisGluLeuGluGluThrIleArgAspIysGlnIleuLeuHisGluIys	1102	
Db	2767	GATTAAGAAACACGTTTAATGAAGAACTTTAAAGCTTCTTGAGCGCTGATCGTCAGAGAA	2826	
QY	1103	---LybTyrlPhePheGlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSer	1121	
Db	2827	CAGAAAGAGACGGCCCAAGCTGTGACGAGACGCAAGGCAAAAGTACAGAAACTGAAACAGAC	2886	
QY	1122	LeuProPheSerIysLeuValGluIuYsSerGlnAspProIleGluIleAsnAspIyr	1141	
Db	2887	TTG-----	2888	
QY	1142	HisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGlu	1161	
Db	2890	-----CTTGCTACTGAAAAA-----GATGACGTTCCCTGGAAAAAGCT	2922	
QY	1162	ArgAsnSerLeuYsGlnGlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAla	1181	
Db	2929	AGAGATTCTGATTAACAAAGTTGTACTGACCTCATGAACCAAGATCCAGAGACTGAATGAC	2988	
QY	1182	GlnSerIleGluYsSerAsp---LeuGlnIysProIysGlnAspLeuGluGluYsIu	1200	
Db	2989	TCCGCTGTGTACAAAACAGAAACTATACACACCCGAAACAAAGAACTGAAGACATAAT	3048	
QY	1201	ValIys-----LeuLeuLeuGluMetGluLeuLeuYsGlyHisIleuThrAspSer	1217	
Db	3049	TGCAATATCAACTCTGCTTGCTGTGACAGAGAA-----GAGAG	3087	
QY	1218	GlnLeuSerIleGluYsLeuGlnIleuGlnAsnIleuGluValThrGlnIuYsLeuGlnThr	1233	
Db	3088	AGAGGTGATCAAAAGACGAGATGTGATATTCTGATCTGAAGAAACCTTAAG---	3144	

OY	1238	LeuGIInGIuMeLyuAenLIeThrLIeGIuArgAnGIuLeuGIInThrAenPheGIu	1257
Db	3145	-----CTGAGAAATCTTCTGAG	3162
OY	1258	AsPLeuYsAlaGIuHIsAsPserLeuYsGIInAsPLeuSerGIuAenLIeGIuIn---	1276
Db	3163	GACATTA-----GAGAGGGATATCTCTGGAGAGACCTGGCTCATGGCACATGAGCACTG	3216
OY	1277	-----SerTLeGIuThrGIInAsPLeuGIuAraGIaLaGIInGIuIn	1290
Db	3217	AACATGCTCACAGAGGCGCTCAAAAAAACATCGGGCGTGGCTGACGTGGCCACAGAAAGA	3276
OY	1291	LeuArgGIuGIInuYsGIInLeuValAsPserPheArgGIInGIInLeuAsPcySerVal	1310
Db	3277	CTGACCAAGAGGAAGCCCTGATTCACAGAACTTAGACAAGCTTA-----	3321
OY	1311	GIYLeSerSerProAenHIsAsPAlaValAlaAsnGIInuYsValSerLeuGIYGIu	1330
Db	3322	-----AACCAAAAGAA-----	3333
OY	1331	ValAsnSerLeuGIInSerGIuMeLeuArgGIYGIuArgAsPLeuGIInThrSerCyA	1350
Db	3334	-----GAGGAAGTGAACACAGAAAGAAATGAATTAATCTCAAAATG	3375
OY	1351	LYsAlaLeuValSerGIuLeuGIInLeuLeuArgIaHIsValLYsSerValGIuGIYGIu	1370
Db	3376	AGGCAACTA-----GAACATGTGATGATCTTGGCTGTGAG	3411
OY	1371	Asn-----LeuGIuIleThrLYsLeuAen	1379
Db	3412	GATCCCAAGAGTCTTAAGACACCACTTCATTAACACATTTGGCAAACTCTGGAA	3471
OY	1380	GIYLeuGIuYsGIuIleLeuGIYLYsSerGIuGIuSerGIuValLeuLYsSerMeLeu	1399
Db	3472	ACACAGAGAACAGAGATA-----GAAATGGAAGAGCGCTTAAGACTCTTTGG	3519
OY	1400	GIuAsnLeuLYsGIuAsPAsnLYsLeuLYsGIu-----GIInaGIuGIuTYSer	1417
Db	3520	GAAACACCTTGTAAACAAAGCTTAAAGAAAGACAGAAATCAAAATGCTGAATCTTCAGA	3579
OY	1418	SerLYsGIuAenGIInPheSerLeuGIuGIuValPheSerGIYsSerGIuLYsLeuValAsP	1437
Db	3580	ATGAAGGAGCACTTGGCGTGAATGAAAACTTAAGCGCTCGAAATGACAGCTTAATGAG	3639
OY	1438	GIuIleGIuValLeuLYsAlaGIInLeuLYsAlaIaGIuArgLeuGIuIleLYsAsP	1457
Db	3640	AAAAAAGCGCTCCCGCAAGGCTCACTGATGATTTAAAGACAAAGAAACAGATCAT	3699
OY	1458	ArgAsPTRYpHeGIuLeuValGIInThrAlaAsn-----	1468
Db	3700	CAGATCATCCAGATTAATCAACACAGTGAAGATTAACAGAAAGAAATATCAAGAAAGA	3759
OY	1469	-----ThraenLeuValGIuGIYLYsLeuGIuThrProLeuGIInaAsPnHIsGIu	1485
Db	3760	CTTCAGAAAAGTAAATATGTTGAAGAAATGCTGAA-----ATGAAGACAGACTTGAA	3813
OY	1486	GIuAsPserLIeAsPArgSerGIuGIuMeGIuIleLYsValLeuGIYGIuLYsLeu	1505
Db	3814	GAAGTCCAAAGTGGCCCTTTACAAACAAAGATGAAATGCCCTTAGAATGACATGAAAGTC	3873
OY	1506	GIuArgAsnGIYTRYLeuLeuGIuArgLeuGIInGIuLYsLeuGIuLeuSerAsnLYs	1525
Db	3874	GAAAGAACCCCAACTTTGGAGTCTTAAGACATTCACAGAAAGAAAGCAACTGACATCAAG	3933
OY	1526	LeuGIuIleLeuGIInuYsGIuMeGIuThrSerAlaLeuLeuLYsAsPLeuGIIn	1545
Db	3934	CTGGAAGAAATGTATGAAGAAAGAGAAACATCCACAGAGATGAAATCTTAAGAGAG	3993
OY	1546	LYsLeuGIuSerLeuLeuSerGIuAsn-----IleIleLeuYsGIuAenLIeAsPThr	1563
Db	3994	CAGGTGAGAGTCTTCTTGGAGGAAATGGAAGATGTAGATGCCAAAAATTTG-----	4047
OY	1564	ThrLeuLYsHIsAsPAsPThrGIInaGIInLeuGIInuYsThrGIInGIuLeuGIIn	1583

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Db      4048 -----CATGAGAAATTGCTGATGCTGAGTCAAGAAAGAAATGTCAGG 4095
QY      1584 LeuAlaLysAsnLeuAlaIleAlaSerAspAspCysProIleThrGlnGluVal 1603
Db      4096 CTTGCTGAGAGACAGAAAAAGTTCGCGCGGAAATGATTTTAAAGAAAGAAAGA 4155
QY      1604 ThrSerAla 1606
Db      4156 AGTGAATCT 4164

RESULT 7
US-09-723-262-1
Sequence 1, Application US/09723262
Patent No. 6379912
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
TITLE OF INVENTION: No. 6379912e1 motor proteins and methods for
TITLE OF INVENTION: their use
FILE REFERENCE: 1017
CURRENT APPLICATION NUMBER: US/09/723,262
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US 09/572,191
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4757
TYPE: DNA
ORGANISM: Human
US-09-723-262-1

Alignment Scores:
Pred. No.: 3,34e-75 Length: 4757
Score: 1051.00 Matches: 417
Percent Similarity: 42.34% Conservative: 304
Best Local Similarity: 24.49% Mismatches: 548
Query Match: 7.12% Indels: 434
DB: 4 Gaps: 60

US-09-724-584-1 (1-2954) x US-09-723-262-1 (1-4757)
QY      2 SerGlnGlyAspAlaValLysValCysValArgValArgProIleGlnArgGlu--- 20
Db      64 AATGAAGGATGATGCTCAAGTCTTTCGCAATTCGCTCCGCAAGAAAGATCTGGG 123
QY      21 -----GlnGlyAspGlnAlaAsnLeuGlnTrpLysAlaGlyAsnAsnThrIleSerGln 38
Db      124 TCAGCTGATGAGAGACAG---AACTTATGCTTATCTGCTGCTGCTCCACGAGTCTCCGG 180
QY      39 ValAspGlyThr-----LysSerPheAsnPheAspArgValPheAsnSerHisGlu 55
Db      181 CTGCACTCCCAACCTGAGCCCAAGACCTTCACGTTGATCATGTTGCAGATGTGATACC 240
QY      56 SerThrSerGlnIleTyrlGlnIleValAlaValProIleIleArgSerAlaLeuGlnGly 75
Db      241 ACTCGAATCTGTATTCGCAACTGTGCTAAAGCAATTCGTGACATGACGCGT 300
QY      76 TyrAsnGlyThrIlePheAlaTyrlGlnThrSerSerGlyLysThrThrTyrlThrMet 95
Db      301 TATATGATGATCACTTTGCTATGACACAGACTGCTCAGGAAACATTTACTATGATG 360
QY      96 Gly-----ThrProAsnSerLeuGlyLysIleIleProGlnAlaIle 108
Db      361 GCACCATCTGAATCTGATATATTTTCTCATACCTGAGAGAGATATCCACGAGATT 420
QY      109 GlnGluValPheLysIleIleGlnIle-----ProAsnArgGlnPhe 123
Db      421 GAATATTTGTTTCTTATATGATGCTGAAAAAGAGCTGAGCTGGAAGAGTTTC 480
QY      124 LeuLeuArgValSerTyrMetGlnIleTyrlAsnGlnIleThrValLysAspLeuLeu 143

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Db      481 CTTTGAATGTTCTTTATGAAATCTAACACGAGCATATATATGATCTACTG----- 534
QY      144 AspArgGlyLysProLeuGlnIleArgIleAspPheAsnArgValTyrValAla 163
Db      535 GACTCTGATCGGCTGGACCTGACTTAAAGGAGCATATCAAGAACGAGACTTTGTTGTT 594
QY      164 AspLeuThrGlnGluLeuValMetValProGlnHisValIleGlnTrpIleLysLysGly 183
Db      595 GGTGGGAGGAGCAGAGTGTAACTCACTGAGTGAAGCTTACAGTGTGTTGCTGAGAGA 654
QY      184 GlnLysAsnArgHisTyrlGlyLysThrLysMetAsnAspHisSerSerArgSerHisThr 203
Db      655 TGGAGAAATACACGTGTGCATCAACCAATGAAACAGAGATCTCTTACGCTTCATCC 714
QY      204 IlePheArgMetIleValGlnSerArgAspArg---AsnAspProThrAsnSerGlnAsn 222
Db      715 GTCTTTACATTTACATATGATGATGAGAAAAAGTAAATGAGATTGTAAT----- 765
QY      223 CysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAlaGlySerGlnArg 242
Db      766 -----ATACGAGCTCCCTACTCAACCTGGTGGATTGACAGATCTGAAAG 813
QY      243 AlaSerGlnThrGlyAlaGlnGlyValArgLeuLysGlnGlyCysAsnIleAsnArgSer 262
Db      814 CAAAAAGATACCATGACAGAGGATGAGATTGAAAGACAGCATTAATCATGATCA 873
QY      263 LeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAlaGly-----Gly 280
Db      874 TTGAGCTGCTGGGCGCAAGTATTAACAGACATTTGTCACGTGGGTAATGAAAAACAGGA 933
QY      281 PheIleAsnTyrlArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGlyLysn 300
Db      934 CATGTTCTACAGAGACTCAAACTTACTTACTTACAGGATTCCTTGAGAGATAT 993
QY      301 AlaLysThrValIleIleCysThrIleThrProValSer-----PheAspGlnThrLeu 318
Db      994 GCCAAAGAGCCATTAATGCAATATGTCATCTGATCTGATCCAGCTGTTTGGGAAACCTTA 1053
QY      319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValAsnGlu 338
Db      1054 TCACACTTAATCTTGTCCAAAGAGCCAGCTGATTAACAAAGCAGCTGTAATGAA 1113
QY      339 ValLeuAspAspGlnAlaLeuLeuLysArgTyrlArgLysGlnIleLeuAspLeuLysLys 358
Db      1114 -----GACACCCAGAGAAATGTGAGCCAGCTCCAACTGAAAGAGAGCTCAAGAA 1167
QY      359 GlnLeuGlnAsnLeuGlnLysSerSerSerGlnThrLysAlaGlnAlaMetAlaLysGlnGlu 378
Db      1168 CAACCTGGGAGCTTGCTTCGACAGACACACACACCAAGACCTTCGACCAAGAGACAA 1227
QY      379 HisThrGlnLeuLeuAlaGlnIleLysGlnLeuHisLysGlnArgGlnAspArgIleTrp 398
Db      1228 AAGAAGACTAATCTATATGAGATATTCAG-----GAAGCAATGTTATTC 1272
QY      399 HisLeuThrAsnIleValAlaLysSerGlnGlnLysSerGlnGlnAspGlnArgValLys 418
Db      1273 TTT-----AAGAAATCTAACAACGAAAAAGAG----- 1299
QY      419 ArgLysArgArgValThrTrpAlaProGlyLysIleGlnAsnSerLeuHisAlaSerGly 438
Db      1299 ----- 1299
QY      439 ValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysAlaLysPhe 458
Db      1300 ---TCTCTGATAGAAAAAGTTAACCAATTGAAGACCTCAACCCCAAAAAAGAAATTT 1356
QY      459 SerAspMetProSerPheProGlnIleAspAspSerValCysThrGlnPheSerAspPhe 478
Db      1356 ----- 1356
QY      479 AspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGlnTrpAsnLeuAlaSer 498

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Db 1357 -----ATTCAATCTAATAATGATTGTAATTCGGA---GAGCAT 1395
 QY LysValThrHisArgGluYsThrSerLeuHisGlnSerMetLeuAspHeGluGlnIle 518
 Db 1396 CAATAATATACGCTTGAAAAAG-----CTCCAC----- 1422
 QY SerAspSerValGlnPheHisAspSerSerLysGlnAsnGlnLeuGlnIleuProLys 538
 Db 1423 -----AAGCAATCCCGGAGAGCTTTCTGCTGAG 1452
 QY AspSerGlyAspMetAlaGluCysArgLysAlaSerPheGlnLysGlnIleThrSerLeu 558
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 QY LeuGlnLysGln-----LeuGlnSerAlaPheAsnGlnLysLeuAsnTrp 919
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OY 1201 ValIys-----LeuLeuGlnMetGluLeuLeuYsGlyHisIleuThraspSer 1217
DB 3049 TCGAAATATACACTCTCTTGGTTGACAGAGAA-----GAGAGC 3087
OY 1218 GlnLeuSerIleGluYsLeuGlnLeuGlnAenLeuGlnValThrGluYsLeuGlnThr 1237
DB 3088 AGAGTGTGATCAGAAAGCAGAGATGCTGATTCGATCGAAAGAAACCTTAGG--- 3144
OY 1238 LeuGlnGluMetYsAsnIleThrIleGlnArgAsnIleuGlnThrAspMetGlu 1257
DB 3145 -----CTGAGAAATCTTCTGAG 3162
OY 1258 AspLeuYsAlaGluHisAspSerLeuYsGlnAspLeuSerGlnAenIleGlnGln--- 1276
DB 3163 GACATA-----GAGAGGATATGCTCTGTGAGAGACCTGCTCATGCCACTGAGCAGCTG 3216
OY 1277 -----SerIleGluThrGlnAspGluLeuArgAlaAlaGlnIuGlu 1290
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OY 1291 LeuArgGlnIuYsGlnLeuValAspSerPheArgGlnIuGlnLeuAspCysSerVal 1310
DB 3277 CTGACCAAGAAAGAACCTTATTCAGAACTTACAGACAAAGCTA----- 3321
OY 1311 GlyIleSerSerProAsnHisAspAlaValAlaAsnGlnIuYsValSerLeuGluYs 1330
DB 3322 -----AACCAAAAGAA----- 3333
OY 1331 ValAsnSerLeuGlnSerGlnMetLeuArgGlyGluArgAspGluLeuGlnThrSerCys 1350
DB 3334 -----GAGGAAGTAGAAACAGAAAGAAATGAAATATACTCAAAATG 3375
OY 1351 LysAlaLeuValSerGluLeuGlnLeuArgAlaHisValYsSerValGluGluYs 1370
DB 3376 AGGCAACTA-----GAACATGTGATGATTCGTGCTGTG 3411
OY 1371 Asn-----LeuGlnIleThrYsYsLeuAsn 1379
DB 3412 GATGCCCAAGAGCTTACAGACCACTCACTTCAAAACATTTGGCAAAACCTCGGAA 3471
OY 1380 GlyLeuGlnYsGluIleLeuGlyYsSerGlnGluSerGluValLeuYsSerMetLeu 1399
DB 3472 ACACAGAAACAGAGTA-----GAGATGAGAAAGAGCTCTAAGACTCTCTTGTG 3519
OY 1400 GluAsnLeuYsGluAspAsnAsnYsLeuYsGlu-----GlnAlaGlnIuYrSer 1417
DB 3520 GAACACCTGTGTAACAAAGCTTAATGAAACAGAGAGAGCTCAAAATGCTGAATCCTCAGA 3579
OY 1418 SerLeuGlnAsnGlnPheSerLeuGlnIuValPheSerGlySerGlnYsLeuValAsp 1437
DB 3580 ATGAAAGACACAGTGGTGAATGGAAACCTACCGCTGGAAGAGTCACAGTTAATAGAG 3639
OY 1438 GlnIleGlnValLeuYsAlaGlnLeuYsAlaAlaGlnIuArgLeuGlnIleYsAsp 1457
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OY 1458 ArgAspIyrPheGlnLeuValGlnThrAlaAsn----- 1468
DB 3700 CAGAAATCATCCAGATATCAACAGCTGAAGATGAACAGAAAGAAATGATCAAGAAAGA 3759
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DB 3760 CTTCGAAAAAGTAAATATGTTGAGAAATGCTGAAA-----ATGAAAGCAGACTGAGA 3813
OY 1486 GluAspSerIleAspArgSerGlnIuMetGluIleYsValLeuGlnIuYsLeu 1505
DB 3814 GAAAGTCAAAAGTCCCTTTACAAAGAGATGAGATCCCTAGAAATGATGATGAGATC 3873
OY 1506 GluArgAsnGlnIyrLeuLeuGlnIuArgLeuGlnIuGlnIuYsLeuGlnLeuSerAsnYs 1525

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DB 3874 GAAAGAACCCAAACCTTGGAGTCTTAAGCATTCACAGAAAAGAAACAACTGATCAAG 3933
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DB 3934 CTGGAAGAAATGATATGAAAGAGAGAGACATCCACAGAGATGGAATGTTAAAGAAAG 3993
OY 1546 LysLeuGlnSerLeuLeuSerGluAsn-----IleIleLeuYsGluAsnIleAspThr 1563
DB 3994 CAGGTGAGATGCTTGTCTGAGGAGAAATGAAAAGTTGTAGTCACCAAAATTTG----- 4047
OY 1564 ThrLeuYsHisSerAspThrGlnAlaGlnLeuGlnYsThrGlnGlnIuGln 1583
DB 4048 -----CATCAGAAAGTTGATGATGAGTACGTAAGTCAAAAGAAAGAAATGTCAGG 4095
OY 1584 LeuAlaYsAsnLeuAlaIleAlaIleSerAspAsnYsProIleThrGlnIuYsGlu 1603
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OY 1604 ThrSerAla 1606
DB 4156 AGTGAATCT 4164

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RESULT 8
US-09-723-219-1
/ Sequence 1, Application US/09723219
/ Patent No. 6391613
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Sakowicz, Roman
/ APPLICANT: Wood, Kenneth
/ TITLE OF INVENTION: No. 6391613el motor proteins and methods for
/ FILE REFERENCE: 1017
/ CURRENT APPLICATION NUMBER: US/09/723,219
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: US 09/572,191
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4757
/ TYPE: DNA
/ ORGANISM: Human
US-09-723-219-1

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Alignment Scores:
Pred. No.: 3,34e-75 Length: 4757
Score: 1051.00 Matches: 417
Percent Similarity: 42.34% Conservative: 304
Best Local Similarity: 24.49% Mismatches: 548
Query Match: 7.12% Indels: 434
DB: 4 Gaps: 60
US-09-724-584-1 (1-2954) x US-09-723-219-1 (1-4757)
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OY 21 -----GlnGlyAspGlnAlaAsnLeuGlnIuThrIleAspIleAspThrIleSerGln 38
DB 124 TAGAGTATGAGAGACAG---AATTAAGCTTATCTGTCTGTCTCTCCACAGAGTCTCGG 180
OY 39 ValAspGlyThr-----LysSerPheAsnPheAspArgValPheAsnSerHisGlu 55
DB 181 CTGCACTCAACCTCGACCCCAAGACCTTCAAGTTTATCATGTTGCAAGATGAGATACC 240
OY 56 SerThrSerGlnIleYrGlnGlnIleAlaValProIleIleArgSerAlaLeuGlnIy 75
DB 241 ACTCAGGAATCTGATTCGCAACTGTGCTAAAGCAATTTGGAGAGTCTTCGATGAGCGGT 300
OY 76 TyrAsnGlyThrIlePheAlaIyrGlyIuThrSerSerGlyYsThrIyrThrMetMet 95

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Db 361 GGACCATCTGAATCTGATTAATTTTCTCAACTGAGAGAGATATCCCAAGAAATTTT 420
Qy 109 GInGUValPheIleIleIleGInGUle-----ProAsnArgIlePhe 123
Db 421 GAATATTTGTTTCTTAATGATGCTGAAAAAGAAAGCTGAGCTGGAAGAGTTTC 480
Qy 124 LeuLeuAsnValSerTyrMetGluIleTyrAsnGluThrValIleAspLeuLeuCyAsp 143
Db 481 CTTTGTAGTGTTCTCTTATTAATCTTAACAGAGACAGATATATGATGATCTG----- 534
Qy 144 AspArgIleGlyLeuPheLeuGluIleArgGluAspPheAsnArgAsnValIleValAla 163
Db 535 GACTCTGCATCGGCTGAGCTGTACTTAAGGAGACATATCAAGAAAGGAGCTTTGTTGT 594
Qy 164 AspLeuThrGInGUleValMetValProGInGUleValIleGInThrIleIleGly 183
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Db 655 TGGAGGATATAGCCTGTGSCATCAATCAATCAATCAAGAGATTCGTAGCTCATGCC 714
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Qy 359 GInGUleGluAsnLeuGluSerSerSerGluThrIleValAlaGlnAlaMetAlaLeuGlu 378
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Qy 379 HisThrGInGUleValGluIleLeuGlnLeuHisIleGlyArgGluAspArgIleTrp 398
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Qy 399 HisLeuThrAsnIleValAlaIleAspSerGInGUleGluAspGlnArgValIle 418
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Db 1356 ----- 1356
Qy 479 AspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGluThrAsnLeuAlaSer 498
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Qy 499 LysValIleThrHisArgGluIleThrSerIleuHisGlnSerMetIleAspPheGlyGlnIle 518
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Qy 519 SerAspSerValGlnPheHisAspSerSerIleGluAsnGlnLeuGlnTyrLeuProLys 538
Db 1423 -----AAGAAATCCCGGAGAGCTTTCTGCTGAG 1452
Qy 539 AspSerGlyAspMetAlaGluCysArgIleValAspPheGluIleThrSerLeu 558
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Db 1614 ----- 1614
Qy 639 AspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHisArg 658
Db 1614 ----- 1614
Qy 659 LysMetLeuGlnGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLysLys 678
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Qy 679 SerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeuGly 698
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QY 798 GluGlnGluIleGlnIleuAlaGluLeuArgLys---ArgAlaAspSerLeuGln----- 814
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QY 815 -----LysLysValAlaAsnPhe-----AspLeuSerValSer 825
DB 1978 ACTACACCAACCAAGGCTTACCAACTTCATTCGCCAGCACTACCAAAATTMACCCCTGAA 2037
QY 826 MetGlyAspSerGluLysLeuGluGluIlePheGlnLeuLysGlnSerLeuSerAsp 845
DB 2038 ATGGGAAGCTTGGCTGCTCTA-----TACACTGAGAATCTACATATTAGAT 2085
QY 846 AlaGluIleValIleThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeu 865
DB 2086 AATGATATATTAATGAGCCAGTTCCTCTGAG----- 2118
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QY 886 SerLeuPheGluLysGlnLeuGluIleThrGluLysSerAsnTyrLysLysMetGluAlaAsp 905
DB 2137 GAGCCATTCTCGAAGAGCTTAGAACAGTCAGCAAGAACAAATGAGTCTCTTCAAGCCAA 2196
QY 906 LeuGlnLysGlu-----LeuGlnSerAlaPheAsnGluIleAsnTyr 919
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QY 920 LeuAsnGlyLeuLeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGlu 939
DB 2257 CATTCACCCAATG-----CAGAGCTTTTCTCATCAAGAAAGAAAT--- 2298
QY 940 LysLysValSerLeuPheSerLysGlnLeuGluLysAlaLeuGlnGluLysAsnAlaLeu 959
DB 2299 -----GATTGACCAAAACAGCAGAAAGAGCTTCTGCACAGTGAATGTCCT 2346
QY 960 GluAsnGluVal---ThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCys 978
DB 2347 GAAAGACAGCTTCAGAGACTCAACCTAAATAATGACTTTTGAAGAAAGAGCTACATGAC 2406
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DB 2407 CTGCGAGTAGTCTCTCATCTCTGCTGCAAGAGAGCTTCTTCAAGTAATGGAATATAGT 2466
QY 997 -----GlyGlnHisSerAlaSerIleIleSerLysGlnGluIleIleMet 1011
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DB 2887 TTG----- 2889
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RESULT 10
US-09-592-054-7
; Sequence 7, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684el motor proteins and methode for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592,054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Human
US-09-592-054-7

Alignment Scores:
Pred. No.:      2,25e-66      Length:      4127
Score:          941.00      Matches:      357
Percent Similarity: 42.37%      Conservative: 243
Best Local Similarity: 25.21%      Mismatches:  449
Query Match:      6.37%      Indels:      368
DB:              4          Gaps:      53

US-09-724-584-1 (1-2954) x US-09-592-054-7 (1-4127)
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Db 3171 CCTAAGCCAAACCTTCTCGTGTAAAGAAAGTTTCTGAGCAAAAGCATGACATCGAG 3230
QY 1258 AspLeuLyb-----AlaGlnHisAspSerLeuLybGlnAspLeuSerGlnAsnIleGlu 1275
Db 3231 GATCTTAAATATATTGTCAGAGCATCTGTGAATGACATGAGATGATGATGTATGTC 3290
QY 1276 GlnSerIleGluTrpGlnAspGlu-----LeuArgAlaAlaGln 1288
Db 3291 CACAGTATGAGGGGAGATGATGAGAAATGGAAGCCAAATTAATGTCAGGTCTCCAG 3350
QY 1289 GlnGluLeuArg-----GlnGlnLybGlnLeuValAspSer 1300
Db 3351 AAGAACATCCAAAGGCTTCTCGCAAGGCTGTGTGGAAACACAGACTGT-----GCG 3404
QY 1301 PheArgGlnGlnLeuLeuAspCysSerValGlyIleSer---SerProAsnHisAspAla 1319
Db 3405 TGCAGAGAGCAAAAGTCACAGACTGTGTGTGACTGTACTGTGACCCCAAAAGTGTGCG 3464
QY 1320 ValAlaAsnGlnGluLybValSerLeuGlnGlyValAsnSerLeuGln 1335
Db 3465 AACCCCGACAGAGCGAAGATAGCTTGGGCACTGTGTAACAGACCCAG 3512

RESULT 11
US-09-722-139-1
; Sequence 1, Application us/09722139
; Patent No. 6355471
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6355471el motor proteins and methods for
; FILE REFERENCE: 1055
; CURRENT APPLICATION NUMBER: US/09/722,139
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4176
; TYPE: DNA
; ORGANISM: Human
US-09-722-139-1

Alignment Scores:
Pred. No.: 2,676-64 Length: 4176
Score: 915.50 Matches: 416
Percent Similarity: 40.59% Conservative: 246
Best Local Similarity: 25.51% Mismatches: 536
Query Match: 6,204 Indels: 433
DB: 4 Gaps: 71

US-09-724-584-1 (1-2954) x US-09-722-139-1 (1-4176)
QY 6 AlaValLybValCysValArgValArgProLeuIleGlnArgGluGlnGlyAspGlnAla 25
Db 7 TCGGTCAAGGTGGCCGTGAGGTCCGCCATGATGCCAGGAAAGAGACTGTGAGGCC 66
QY 26 Asn-----LeuGlnTrpLybAlaGlyAsnAsnTrpIleSerGlnVal-----39
Db 67 AAGTTCATTATTCAGATGAGAAAGCAAAACACAAATCTTAAGATACAGANA 126
QY 40 -----AspGlyTrpLybSerPheAsnPheAspArgValPhe 51

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OY 699 GluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAsp 718
 Db 2062 -----CAGAAATCGAGCTGCAGAAAGAGA 2088
 OY 719 PheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuArg 738
 Db 2089 -----CAGAAAGAGACCTTCTCCGCTCCAGAAAGAACTCCAGACA 2133
 OY 739 -----SerLeuLysGluAsnGluThrAsnGluPheGluIleLeuGluLys----- 754
 Db 2134 CTCAAGAAGACTCAACACAGAGAGAGCTGAGAGTTTCAGATTTTCAGAACTGGAC 2193
 OY 755 GluThrGluLysGluHisGluAlaGluLeuIleHisGluIleGlySerLeuLysLeu 774
 Db 2194 CAGCTCCAAAGAAAAAGATGAACAGATGCC--AAGCTTGAACCTGAAAAAAGAGA 2250
 OY 775 ValGluAsnAlaGlu-----MetTyrAsnGluAsnLeuGluAspLeuGlu 790
 Db 2251 CTAGAGGACGAGAGAGAGAGAGCTCATGCTCCGCGCCCATCTGGAAAGACAGCTCCGA 2310
 OY 791 ThrLys-----ThrLysLeuLeuLysGluGluIleGluLeuAlaGluLeuArg 807
 Db 2311 GAGAAAGCAGAGATGATCCAGCTCCTGCGCGCTGGAGAGTACAGTGGGTGAACAGAGAG 2370
 OY 808 LysArgAlaAspAsnLeuGluLysValArgAsnPheAspLeuSerValSerMetGly 827
 Db 2371 AAGAGG----- 2376
 OY 828 AspSerGluLysLeuCyGluGluIlePheGluLeuLysGlnSerLeuSer----- 844
 Db 2377 GACCTGAGAGCATTCGGGAATCCTCTCCGCGGAGAAAGAGCTCCGCGGAGGGAGT 2436
 OY 845 ---AspAlaGluAlaValThrArgAspAlaGlnLysGluCySerPheLeuArgSerGlu 863
 Db 2437 GAAAGTGGCAGAGAGATTGAAAAAGCTCACTGCTTCTTCGAATTCAGAGAAAGCAGAG 2496
 OY 864 AsnLeuGluLeuLysGluLysMetGluAspThrSerAsnTyrTyrAsnGluLysGlu 883
 Db 2497 CTTTGCAAGCTAGTGAACCTTGAGAGAACCTGCTTCAGCAGAAAGAGCTCTGAAAAA 2556
 OY 884 AlaAlaSerLeuPheGluLysGluLeuGluThrGluLysSerAsnTyrLysMetGlu 903
 Db 2557 GAACTCCAGAAAGACAGAGACATCTTAGAGCTTTAAATGTGAACATGACAAAGATCT 2616
 OY 904 AlaAspLeuGluLysGluLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGlyLeu 923
 Db 2617 AGATTGTTGAAAAACATGATGAGTGCACAGAT----- 2652
 OY 924 LeuAlaGluLysValProArgAspLeuLeuSerArgValGluLeuGluLysValSer 943
 Db 2653 ---GTCACGGAAGTCCCTCAAGATTTGAGAAATTAAGCCAGTGTACAGGCTGGAA 2709
 OY 944 GluPheSerLysGluLeuGluLysAlaLeuGluGluLysAsnAlaLeuGluAsnGluVal 963
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 Db 2752 CCAACTGCTTGGAAGAAAGACAGACATTTGAATTTCTGACAGAGGCCCTCTCAGC 2811
 OY 979 LeuLysAsn-----GlnLysSerLysAlaSerGluGluIleMetLeuLeuLysGln 995
 Db 2812 TTAGACAAACACTTTTATCAAGTAGAAAAAGAAATGAGAA----- 2853
 OY 996 GluGluGluHisSerAlaSerIleSerLysGlnGluIleIleMetGlnGluGlnSer 1015
 Db 2854 -----AAAGAGAACAGCTTGACACAGTACAGGCC 2883
 OY 1016 Glu-----GlnIleLeuGlnLeuThrAspGluValThr-----His 1027
 Db 2884 AATGCAAAACAGAGCTCAAAAGCTCCAAACCCACTTTGAATTCACAGCCACATTTGCAGCT 2943

OY 1028 ThrGlnSerLysValGlnGlnThrGluGluGlnTyrLeuGluMetLysLysMetHisAsp 1047
 Db 2944 CAGAGCAAAAAGTACAGAAAAAGAAAGACAGATTTTGAGTCC----- 2988
 OY 1048 AspLeuPheGluLysTyrIleArgAsnLysSerGluAlaGluAspLeuLeuArgGluMet 1067
 Db 2989 -----AGAGAGAAAGACAGAGAGAGAGCGCTGACCGGCCCTG 3027
 OY 1068 GluAsnLeuLysGlyThrMetGluSerValGluValLysIleAlaAspThrLysHisGlu 1087
 Db 3028 GCCAGGCTGAGAGAGACAGATTCGCGCTGAG-----AGGACATCC 3069
 OY 1088 ---LeuGluGluThrIleArgAspLysGluLeuLeuHisGluLysLysTyrPhePhe 1106
 Db 3070 ACCCTGGCAGAGATTTGAAGACAGAGCAG----- 3102
 OY 1107 GlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProSerLys 1126
 Db 3103 -----AAA 3105
 OY 1127 LeuValGluGlyAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAla 1146
 Db 3106 CTTGCCAGCTGAAACAGTGC----- 3126
 OY 1147 LeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGluArgAsnSerLeuLys 1166
 Db 3127 ---AGCAGAGAGCTCAGGCTCAGAGCTTACCTGAGCTGAGCAGAAAGCCCTGAG 3183
 OY 1167 GluGlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGluLys 1186
 Db 3184 AAGAGCCAGAGAGAGATTGAAATGAAATCAGACAGCTGAAACAGAAAGATTATGAGTGC 3243
 OY 1187 SerAspLeuGlnLysProLysGlnAspLeuGluGluGluVal---LysLeuLeuLeu 1205
 Db 3244 GATGCTGTTCAAAAAGATCATCATGAGACCTCGAAGGAAAGTGGCTTCTTCACAGCTTG 3303
 OY 1206 GluMetGluLeuLysGlyHisLeuThr-----AspSerGlnLeuSer----- 1220
 Db 3304 CCAGTCAGTGTGAAAAATTCACACCTGGTTCCCTCATGATGTCAGAGATCAATGCTTAC 3363
 OY 1221 IleGluLysLeuGlnLeuGluAsnLeuGluValThrGluLysLeuGlnThrLeu----- 1238
 Db 3364 ATTGAAGA-----GAGTCCAAAGAGCCCTTCAGAGATTTGCATGCT 3405
 OY 1239 -----GlnGluGluMetLys 1243
 Db 3406 GTGATTAGTAAGGCTGACATACATCTGCAGACACAGATGAAGATTAAGAAAACTTCAC 3465
 OY 1244 AsnIleThrIleGluArgAsnGluLeuGlnThrAsnPheGluAspLeuLys----- 1260
 Db 3466 AATGGACCATTTCAACGTAACTAAATATGAGCTGTGTCTGACCTCTGTGTCTG 3525
 OY 1261 -----AlaGluHisAspSerLeuLysGlnAspLeuSer 1271
 Db 3526 ATGCCAGAGCTGATGCCGCTGCTGCGCTATATCATCTTGTCTCCAGAAAGATCTG--- 3582
 OY 1272 GluAsnIleGluGlnSerIleGluThrGlnAspGluLeu-----Arg 1285
 Db 3583 ---GTTCACTTCTCTTGAATTTGAAAAACAGAAATCCCTGATTAGTTTGCCAAAT 3636
 OY 1286 AlaAlaGlnGluGluLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnGlnLeu 1305
 Db 3637 GGAAGTACAGGTGATCCAAATTCACAGACTACCTTGTGACATGATTT-----TACTTT 3650
 OY 1306 LeuAspCySerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnLys 1325
 Db 3691 CTTGATGGAATAATAGAAATGCAATGCTCT----- 3720
 OY 1326 ValSerLeuGluGluValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGlu 1345
 Db 3721 ---TCCCTGGAGAAATTTCAGTTACTCTCTACACACAGTGAAGATCATGGGTGACTCT 3777
 OY 1346 LeuGlnThrSerCyLysValAlaLeuValSerGluLeuGluLeuLeuArgAlaHisValLys 1365

Db 3778 GGCCATGACCAAGTCCAGTCCGTAATC-----CTTCTGAACACCCACATTGCA 3825
 QY 1366 SerValGlu-----
 Db 3826 CTGGTGAAGGAAGACGTGTTTTTATCCAGCATTGATTCGAAACATACCTCTCCG 3885
 QY 1369 GtYGLuAsnLeuGluLeuThrLysLysLeuAsnGluLys-----Glu 1384
 Db 3886 GGTGACCAATTGATGATGATC---AAATGCATCTTTAAGTGAATTCAGCTGTGTTGT 3942
 QY 1385 IleLeuGtYLYSserGluSerGluValLeuLysSerMetLeuGluAsnLeuLysGlu 1404
 Db 3943 GTTCCAGAAAAGAAAATGTGTCAACAGTACACTCTTTTACAGAAACTCAAACT 4002
 QY 1405 AspAsnLeuLysLeuLysGluGluAlaGluGluLysSerLysGluAsn-----Gln 1422
 Db 4003 TCAGTGGTTCAGAAAATGATCCACCTGACACCTTCAGGAAGCCCAATGTCCAGTTG 4062
 QY 1423 PheSerLeuGluGluValPheSerGtYLYSserGluLysLeuValAspGluIleGluValLeu 1442
 Db 4063 TTCACCAACCCCATGTTGATCTTCAAGGAGTCCAGAAATGTCCACT---GAGGTCTGG 4116
 QY 1443 LysAlaGluLeuLysAlaAlaGluGluLysGlu 1453
 Db 4117 AAATTACTTTCATTCTCAAGATGAGGCTCTT 4149
 RESULT 12
 US-09-721-832-1
 / Sequence 1, Application US/09721832
 / Patent No. 6399346
 / GENERAL INFORMATION:
 / APPLICANT: Berard, Christophe
 / APPLICANT: Freedman, Richard
 / TITLE OF INVENTION: No. 6399346e1 motor proteins and methods for
 / FILE REFERENCE: 1055
 / CURRENT APPLICATION NUMBER: US/09721,832
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1
 / LENGTH: 4176
 / TYPE: DNA
 / ORGANISM: Human
 / US-09-721-832-1

Alignment Scores:
 Pred. No.: 2.67e-64 Length: 4176
 Score: 915.50 Matches: 416
 Percent Similarity: 40.59% Conservative: 246
 Best Local Similarity: 25.51% Mismatches: 536
 Query Match: 6.20% Indels: 433
 Gaps: 71

US-09-724-584-1 (1-2954) X US-09-721-832-1 (1-4176)

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 Db 7 TCGGTCAAGCTGCGGCTGAGGTTCGGCCATGATCGCAGGAAAAGCACTGGAGGCC 66
 QY 26 Asn-----LeuGlnTrpLysAlaGlyAsnAsnThrLysSerGlnVal----- 39
 Db 67 AAGTTCATTATTCAGATGAGAAAAGCAAAACGACATTCACAACTTAAAGATACCGAA 126
 QY 40 -----AspGtYLYSserPheAsnPheAspArgValPhe 51
 Db 127 GGAGCACTGGGACTCAGGAAGAAAGCAAGCAAGCTTTCACCTTAATGACTTTCTTT 186
 QY 52 AsnSerHisGluSerThrSer-----GlnIleYrGlnGluLeu 64
 Db 187 TATTCGTGCTATACAAAAGCCAGATTACGTTTCACAGAAATGGTTTCAAAACCTC 246

QY 65 AlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGlyThrIlePheAlaTyrGly 84
 Db 247 GGCACAGATGTCGGAAGTCTGCATTGTAAGGTTATTAAGCTTGCTCTTGCATATGCG 306
 QY 85 GlnThrSerSerGtYLYSThrThrMetMetGtYLYSProAsnSerLeuGtYLYSLeu 104
 Db 307 CAACTGATCTGGAAGATCATACATATGATGAGGAAAATTCGAGATTCTGGCTTATA 366
 QY 105 ProGlnAlaIleGlnGluValPheLysIleIleGlnGluLeu-----ProAsnArg 121
 Db 367 CTTGGATGTGTGAAGAGCTTTCAGTCGGAATTAATGAACACCAATGGATGGAAGCT 426
 QY 122 GluPheLeuLeuArgValSerThrMetGluIleTyrAsnGluThrValLysAspLeuLeu 141
 Db 427 TCTTTTCGAATCGAAGTCACTACTATGAAATTTATACGAACGTCGAGAGATCTACTT 486
 QY 142 CysAspAspArgValLysLysPro-----LeuGluIleArgGluAspPheAsn 157
 Db 487 -----CGCGGAAGTCACTTAAACCTTCATTGAGAGTCCGTGACATCCCAAA 537
 QY 158 ArgAsnValTyrValAlaAspLeuThrGluGluLeuValMetValProGluHisValIle 177
 Db 538 GAAGCCCTTATGTTGAGATTATCCAAACATTTAGTACAGAAATATGATGACGTAAGA 597
 QY 178 GlnTrpIleLysGtYLYSgltYLYSAsnArgHisTyrGtYLYSThrLysMetAsnAspHis 197
 Db 598 GAACCTTATGATGCGGGCAATATCAACCGGACCGGACGAGCTGGATGAAACGACCTC 657
 QY 198 SerSerArgSerHisThrIlePhe-----ArgMetIleValGluSerArgAspArgAsn 215
 Db 658 AGTGCAGCTGTCACTGACATCTTCACACATCAAGTTCACTCAGGCTAAATTTGATTGCA 717
 QY 216 AspProThrAsnSerGluAsnGtYLYSAspGlyAlaValMetValSerHisLeuAsnLeuVal 235
 Db 718 ATGCCA-----TGTGAA-----ACGTCAGATGATCACCATTGCT 753
 QY 236 AspLeuAlaGtYLYSserGluArgAlaSerGlnThrGtYLYSAlaGluGlyValArgLeuLysGlu 255
 Db 754 GATCTTCCGGAAGAGAGGCTGACATGCCACCGGAGCACCGGGGTTAGCTTAAAGGAA 813
 QY 256 GlyCysAsnIleAsnArgSerLeuPheIleLeuGtYLYSAlaValIleLysLysLeuSerAsp 275
 Db 814 GCGGAAATATTTAAAGATCCTTGTGACTGTGGGAAAGCTATTCTGCTTACCTGAT 873
 QY 276 GlyGlnAlaGlyGly-----PheIleAsnTyrArg 285
 Db 874 TTATCTCAGATGCTGCAATACCTTGCAAAGAAAGCAAGATTTCGTGCTTACAG 933
 QY 286 AspSerLysLeuThrArgGtYLYSLeuGlnAsnSerLeuGtYLYSAsnAlaLysThrValIle 305
 Db 934 GATTCGTGCTTGACTTGTGTTTAAAGATGAGCTTGGAGGAAACTCTAAACTATCATG 993
 QY 306 IleCysThrIleThrPro-----ValSerPheAspGluThrLeuSerThrLeuGlnPhe 323
 Db 994 ATTGCCACATTTACCTGCTGATGTCATATGAGAAACCTTAAAGTACTTTCGCTAT 1053
 QY 324 AlaSerThrAlaLysHisValArgAsnThrProHisValAsnGluValLeuAspAspGlu 343
 Db 1054 GCAAAATGAGCCAAAACATCATCAACAGCTTACCATTAATGAGAGTCAACAGCTCAA 1113
 QY 344 AlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLys----- 357
 Db 1114 -----CTTATCCGTGAGCTGAGCTGAAATACCGAGCTGAAAACGCTGCTTCAAGGG 1170
 QY 358 LysGlnLeuGluAsnLeuGluSerSerSerGtYLYSAlaGlnAlaMetAlaLysGlu 377
 Db 1171 AATGATGATGCTGCTTGAATCCCA-----GCTTAAAGTATGAG 1215
 QY 378 GluHisThrGlnLeu-----LeuAlaGluIleLysGlnLeuHisLysGluArgLysArg 396
 Db 1216 GAAAACCTTCAGCAATGAGCAAGAGTTCAAGAAATTCACCAAGAAATGACAAATTAAG 1275
 QY 397 IleTrpHisLeuThrAsnIleValAlaLysSerSerGlnLysGlnAspGlnArg 416

[illegible]

Db	2089	-----CAAGAAAGAGAGACTTTCTCCGCGCTCAAGAAAGAACTCCAAACA	2133
OY	739	-----SerLeuLysGluAenGlnGluThrAenGluPheGluIleLeuGluLys-----	754
Db	2134	CTCAAGAACTCAACCAACACAGAGAGCTGAGAACTTCAGATATTTCAAGAACTGGAC	2193
OY	755	GluThrGlnLysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysIleLysLeu	774
Db	2194	CAGCTCCAAAAGGAAAAAGATGAACAGATATGCC--AAGCTTGAACCTGAAAAAAGAGA	2255
OY	775	ValGluAenAlaGlu-----MetTyrAenGlnAenLeuGluLysAenLeuGlu	790
Db	2251	CTAAGAGAGACGAGACAAAGAGACAGCTACTGCTCGTGGCCCATCTGGAAGAGACAGTCCGA	2310
OY	791	ThrLys-----ThrLysLeuLeuLysGluGlnGluIleGlnLeuAlaGluLeuArg	807
Db	2311	GAGAAAGCAGAGATGATGATCAGCTCTCGTGGCGGTGGAGAGTACAGTGGGTGGAAGAGAG	2370
OY	808	LysArgAlaAenAenLeuGlnLysLysValArgAenPheAenLeuSerValSerMetCys	827
Db	2371	AAGAGG-----	2376
OY	828	AspSerGluLysLeuCysGluGluIlePheGlnLeuLysGlnSerLeuSer-----	844
Db	2377	GACCTGGAGGCGATTCGGGAAATCCCTCTCGGGGTGAAGAGGCTCGTCCGAGAGGGAT	2435
OY	845	--AspAlaGluAlaValThrArgAenAlaGlnLysGluCysSerPheLeuArgSerGlu	863
Db	2437	GAAATGGCGAGAGATTGAGAAAAGGCTCAACTGGGTTTCTTGAATTCAACAGAAAGCAG	2496
OY	864	AenLeuGluLeuLysGluLysMetGluAenPheSerAenTyrTyrAenGlnLysGluLys	883
Db	2497	CTTGTCAAGCTAAGTGAACCTTGAGAGAGGACCTGGTTCAGCAGAAAGACATCTCGTAAAAA	2556
OY	884	AlaAlaSerLeuPheGlnLysGlnLeuGlnThrGluLysSerAenTyrLysLysMetCys	903
Db	2557	GAACTCCAGAGAACAGACAGAGATCTCTAGAGCTTTAAATGATGAACATGACAAAGAACTT	2616
OY	904	AlaAenLeuGlnLysGluLeuGlnSerAlaPheAenGluIleAenTyrLeuAenGluLys	923
Db	2617	AGATTGTTGGAAAAACAATGATGAGAGATGTCACAAAT-----	2653
OY	924	LeuAlaGluLysValProArgAenPheLeuLeuSerArgValGluLeuGluLysLysValSer	943
Db	2653	---GTCAACGGAAGTGCCTCAAGATTTCGAGAAAATAAAGCCAGTGGAGTACAGCTGCCAA	2709
OY	944	GluPheSerLysGlnLeuGlnLysLysAlaLeuGlnGluLysAenAlaLeuGlnAenGluVal	963
Db	2710	TATTAAGAACCCCAAGCTTACAG-----TACCTCTGTCACAAATCACTTGG	2751
OY	964	ThrCysLeuSerGlu-----TyrLysPheLeuProAenGluValaGluCys	978
Db	2752	CCAACCTCTGTTGGAAAGAAAAGCAGACAGCATTTGAATCTTGCACAGAGCCCTCTACG	2811
OY	979	LeuLysAen-----GlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGln	995
Db	2812	TTAGACAACACTCTTTATCAAGTGAAGAAAGAAATGAGACA-----	2853
OY	996	GluGluGluHisSerAlaSerAlaSerLysGlnGluIleIleMetGlnGlnGlnSer	1015
Db	2854	-----AAAAAGAACAGCTTTGCAACATACAGAGCC	2883
OY	1016	Glu-----GlnIleLeuGlnLeuThrAenArgValaThr-----His	1027
Db	2884	AATGCAAAACAGCTGCAAAAGCTCCAAAGCCATTTGAATTCACATGCCAACATTTGCAGCT	2943
OY	1028	ThrGlnSerLysValGlnGlnThrGluGlnGlnTyrLeuGlnMetLysLysMetHisAenP	1047
Db	2944	CAGCAGGAAAAAGTCAGGAAAAAGAAAGAGATTTTGGAGTCC-----	2988
OY	1048	AspLeuPheGluLysTyrIleArgAenLysSerGluAlaGluAenPheLeuAlaArgGluMet	1067
Db	2989	-----AGGAGAAAGCAGAGAGAGAGAGCGCTGGAGAGCGGCGCTTG	3027

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QY 1068 GluAsnLeuIleGlyThrMetGluSerValGluValLysIleAlaAspThrLysHisGlu 1087
DB 3028 GCCAGCGCTGGAGAGAGACATTCCTGGCTGCAG-----AGGCACATCC 3069
QY 1088 ---LeuGluGluThrIleArgAspLysGluLeuHisGlyLysLysPhe 1106
DB 3070 ACCCTGGGACGAGATTGAAAGACAGAGCAG----- 3102
QY 1107 GluAlaMetGluThrIlePheProIleThrProLeuSerAspSerLeuProSerLys 1126
DB 3103 -----AAA 3105
QY 1127 LeuValGluGluAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAla 1146
DB 3106 CTTGCCAGCTCGAACAGCTGC----- 3126
QY 1147 LeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGluArgAsnSerLeuLys 1166
DB 3127 ---AGCAGAGAGACATCGAGGCTCGAGGCTAGCCTGAGAGGCTGAGAGAGCCCTGGAG 3183
QY 1167 GluGluValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGluLys 1186
DB 3184 AAGGACGAGAGAGGTTAGAAATGAAATCCAGACGCTGAACAGAAATTTTGAGGTC 3243
QY 1187 SerAspLeuGlnLysProLysGlnAspLeuGluGluVal---LysLeuLeuLeu 1205
DB 3244 GATGCTGTTCAAAAGATCATCATGAGACCCCTGAGAGGAGGCTTCTTCACGCTTG 3303
QY 1206 GluMetGluLeuLeuLysGlyHisLeuThr-----AspSerGlnLeuSer 1220
DB 3304 CCAGCTGAGCTGTAATAATCACCTCGTTCCCTCATGATGCCAGAGATCAATGCTTAC 3363
QY 1221 IleGluLysLeuGlnLeuGluAsnLeuGluValThrGluLysLeuGlnThrLeu 1238
DB 3364 ATTTAAAGAA-----GAAGTCAAAAGAGCCTTCAGATTTCATCGT 3405
QY 1239 -----GlnGluLysLeuLys 1243
DB 3406 GTGATTAGTAGAGGCTGCATACATCTGCAGACACATGAAAGATTAATGAAACTTCAC 3465
QY 1244 AsnIleThrIleGluThrArgAsnGluLeuGlnThrAsnPheGluAspLeuLys----- 1260
DB 3466 AATGGACCCATTCAGCTAACTAAATAATGAGCTGTGTCGAGCCTCGTGCTGCTCG 3525
QY 1261 -----AlaGlnHisAspSerLeuLysGlnAspLeuSer 1271
DB 3526 ATGCCAGAGCCTGATCCGCTGCTGCTGCTAATCATCTTCCTCAGCAAGATCTG--- 3582
QY 1272 GluAsnIleGluGlnSerIleGluThrGlnAspGluLeu-----Arg 1285
DB 3583 ---GTTCAAGCTTCTCTGATTGGAACAGAAATCCGATTGATTGTTGCCAAT 3636
QY 1286 AlaAlaGlnGluGlnLeuArgGlnLysGlnLeuValAspSerPheArgGlnLeu 1305
DB 3637 GGAAGTTCAGGTGATCCAAATTCAGACTCTTGTTGACATGATT---TACTTT 3690
QY 1306 LeuAspCysSerValGlyLysSerProAsnHisAspAlaValAlaAsnGlnLys 1325
DB 3691 CTTTCATGGAATATGGAAGTCAATGCTCT----- 3720
QY 1326 ValSerLeuGlyGluValAsnSerLeuGlnMetLeuArgGlyGluArgAspGlu 1345
DB 3721 ---TCCCTGGCAGAAATTCACTTACTGCTTACACACAGTGAAGATGAGGAGCTCT 3777
QY 1346 LeuGlnThrSerCysLysAlaLeuValSerGluLeuGluLeuAlaGlnHisValLys 1365
DB 3778 GGCCATGACCAAGTCCAGCTCGCTAGTC-----CTTTCGAACCCACCATTTGCA 3825
QY 1366 SerValGlu----- 1368
DB 3826 CTGGGAAGGAAGCTGTGTTTTTATTCACGACATTCGATCTCGAACAATACCTCCTCG 3885

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QY 1369 GlyGluAsnLeuGluIleThrLysLysLeuAsnGlyLeuGluLys-----Glu 1384
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QY 1385 IleLeuGlyLysSerGluGluSerGluValLeuLysSerMetLeuGluAsnLeuLysGlu 1404
DB 3943 GTTCCAGAAAGAAATAATGTGTCAACAGTAGAATGCTTCTTACAGAACTCAAACT 4002
QY 1405 AspAsnAsnLysLeuLysGluGlnAlaGluIleLysSerLysGluAsn-----Gln 1422
DB 4003 TCAGTGGGTTCAGAAATAGTCCACTGACACCTTCAGAGGCCCAATGTCAGTTG 4062
QY 1423 PheSerLeuGluGluValPheSerGlySerGlnLysLeuValAspGluIleGluValLeu 1442
DB 4063 TTCACCAACCCCATTTGATCTTCAAGGACGTCAGATGCGACCT-----GAGCTGG 4116
QY 1443 LysAlaGlnLeuLysAlaAlaGluGluArgLeu 1453
DB 4117 AAATTTACTTTCATATTCATGATGAGGCTCTT 4149

RESULT 13
US-09-721-689-1
/ Sequence 1, Application US/09721689
/ Patent No. 6440685
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Freedman, Richard
/ TITLE OF INVENTION: No. 6440685e1 motor proteins and methods for
/ TITLE OF INVENTION: their use
/ FILE REFERENCE: 1055
/ CURRENT APPLICATION NUMBER: US/09/721,689
/ CURRENT FILING DATE: 2000-11-24
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4176
/ TYPE: DNA
/ ORGANISM: Human
US-09-721-689-1

Alignment Scores:
Pred. No.: 2,67e-64 Length: 4176
Score: 915.50 Matches: 416
Percent Similarity: 40.59% Conservative: 246
Best Local Similarity: 25.51% Mismatches: 536
Query Match: 6.20% Indels: 433
DB: 4 Gaps: 71

US-09-724-584-1 (1-2954) x US-09-721-689-1 (1-4176)
QY 6 AlaValLysValCysValArgValArgProLeuIleGlnArgGluGlnGlyAspGlnAla 25
DB 7 TCGGTCAAGGTGCGCGTGAAGGCTCGCGCCATGAAATCCAGAGAAAGACTTGAGAGCC 66
QY 26 Asn-----LeuGlnTrpLysAlaGlyAsnAsnThrIleSerGlnVal----- 39
DB 67 AAGTTCATTATTCAATGAGAGAAAGCAAAACGAAACCAACCAAACTTAAGATACAGAA 126
QY 40 -----AspGlyThrLysSerPheAsnPheAspArgValPhe 51
DB 127 GGAGCACTGGGAGCTCAGAAAGAAAGCAAGACCTTCACTTATGACTTTTCTTTT 186
QY 52 AsnSerHisGluSerThrSer-----GlnIleTyrGlnLysIle 64
DB 187 TATTTGCTGTATACAAAAGCCAGATTACGTTTCACAGAAATGCTTCAAAAACCTC 246
QY 65 AlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGlyThrIlePheAlaTyrGly 84
DB 247 GGCAAGATGTCGGAAGTCTGCATTGAAAGTTATATGCTGTGTGTTGATATGGG 306
QY 85 GlnThrSerSerGlyLysThrTyrThrMetMetGlyThrProAsnSerLeuGlyIleIle 104
DB 307 CAATCTGATCTGGAAGATCATACATATGATGAGAAATTCGAGATTCGTGCTTAATA 366

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Db	2194	CAGCTCCAAAGAGAAAAGATGACAGTATGCC---	AACTTGAACCTGGAAAAAAGAGA	2250
Qy	775	ValGluAsnAlaGlu-----MetTyrAsnGlnAsnLeuGluAspLeuGlu		790
Db	2251	CTAGAGAGACAGAGAGAGAGAGAGCTCAATGCTCGTGCCCATCTTGAAGACAGACTCCGA		2310
Qy	791	ThrLys-----ThrLysLeuLysGluGlnGluGlnLeuAlaGluLeuArg		807
Db	2311	GAGAGCCAGAGATGATTCAGCTCTCTGGCGCGGTGGAGAGTACATGGTGTGAAGAGAG		2370
Qy	808	LysArgAlaAspAsnLeuGlnLysLysValArgAsnPheAspLeuSerValSerMetGly		827
Db	2371	AAAGAG-----		2376
Qy	828	AspSerGluLysLeuGlySerGluGlnLysPheGlnLeuLysGlnSerLeuSer-----		844
Db	2377	GACCTGGAAAGCATTCGGGAATCCCTCTCGCGAGTGAAGAGAGGCTGTGCGGAGGGGAT		2436
Qy	845	---AspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGlu		863
Db	2437	GAAATGGCGAGAGATTGAAGAAAGGCTCAACGCGCTTCTCGAATTCAAGAGAAGCAG		2496
Qy	864	AsnLeuGlnLysLeuGlnLysMetGlnAspThrSerAsnTyrTyrAsnGlnLysGlnLys		883
Db	2497	CTTGTCAGCTAGTGAACCTGGAGAGAGACCTGTTGCAGCAAGAAAGCATCTCGAATAAAA		2556
Qy	884	AlaAlaSerLeuPheGluLysGlnLeuGlnThrGluLysSerAsnTyrLysLysMetGlu		903
Db	2557	GAACTCCAAAGAAAGACAGAGAGTCTTAAGTGTTTAAATGTGAACATGACAAAGAAATCT		2616
Qy	904	AlaAspLeuGlnLysGlnLeuGlnSerAlaPheAsnGlnLysAsnTyrLeuAsnGlyLeu		923
Db	2617	AGATTGTGCAAAAACATGATGAGAGTGCACACAT-----		2652
Qy	924	LeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGlnLysLysValSer		943
Db	2653	---GTCACGGAAGTGCCTCAAGATTTCGAGAAAAATAAGCCAGTGAAGTACAGGCTGCA		2709
Qy	944	GluPheSerLysGlnLeuGlnLysAlaLeuGlnLysAsnAlaLeuGlnAsnGluVal		963
Db	2710	TATAAAGAACCCACAGCTACAG-----TACTCTGCGAATCACTTG		2751
Qy	964	ThrCysLeuSerGlu-----TyrLysPheLeuProAsnGluValGluCys		978
Db	2752	CCAATCTGTTGGAAAGAAAGCAGAGACATTGAATAATCTTGACAGAGGCCCTCTCAGC		2811
Qy	979	LeuLysAsn-----GlnLeuSerLysAlaSerGluGlnLysMetLeuLysGln		995
Db	2812	TTAGACACACACTTTATCAGTGAAGAAAGAAATGAGAAG-----		2853
Qy	996	GluGlyGlnLysSerAlaSerIleLeuSerLysGlnGlnLysIleMetGlnGlnGlnSer		1015
Db	2854	-----AAAGAAAGAACAGCTTGACAGATCCAGAGGCC		2883
Qy	1016	Glu-----GlnIleLeuGlnLeuThrAspGluValThr-----His		1027
Db	2884	AATCAAAACACGCTGCAAAAGCTCCAAAGCACCCTTGAATTCACTGGCAACATTGCAAGT		2943
Qy	1028	ThrGlnSerLysValGlnGlnThrGluGlnGlnTyrLeuGlnMetLysLysMetHisAsp		1047
Db	2944	CAGAGAGAAAAGTGAAGAAAAGAAAAGAGAGATTTTGAGATCC-----		2988
Qy	1048	AspLeuPheGlnLysTyrIleArgAsnLysSerGlnAlaGlnAspLeuArgGlnMet		1067
Db	2989	-----AGAGAGAGCAGCAGAGAGAGCGCTGAGCGGCGCTCG		3027
Qy	1068	GluAsnLeuLysGlyThrMetGlnSerValGluValLysIleAlaAspThrLysHisGln		1087
Db	3028	GCCAGCGTGAAGAGACATTCTGCGCTCGAG-----AGCGACTCC		3069
Qy	1088	---LeuGlnGlnThrIleArgAspLysGlnGlnLeuLeuHisGlnLysLysTyrPhePhe		1106

Db	3070	ACCCTGGCAGCGAGATTGAAGACAGAGCGAG-----	3107
QY	1107	GlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProProSerLys	11226
Db	3103	-----	AAA 3105
QY	1127	LeuValGlnGlyAsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAla	11446
Db	3106	CTTGCCAGCTCTGAACAGTGGC-----	3126C
QY	1147	LeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrGluArgAsnSerLeuLys	11666
Db	3127	---AGCAGAGACAGCAGCGGCTCCAGCGTACCCTCGAGCGCTGACAGACAGAACCCCTGGAG	31858
QY	1167	GluGlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGluLys	11866
Db	3184	AAGGACCCAGAGAGGTGTGAATATGAAATATCCAGCGCTGGAAACAGAAAGATTTATGAGCGCT	32446
QY	1187	SerAspLeuGlnLysProLysGlnAspLeuGlnGluGluVal---LysLeuLeuLeu	12056
Db	3244	GATGGCTTCAAAAAGATCATCATATGAGACCCCTGGAGGAGAGAGTGTCTTCCACAGCTTG	33036
QY	1206	GluMetGluLeuLeuLysGlyHisLeuThr-----AspSerGlnLeuSer-----	12202
Db	3304	CCAGTCAGTGCAGTGAATAATTCACACCTGGTCCCTCCATGATGCCAGATCAATGCTTCA	33656
QY	1221	IleGluLysLeuGlnLeuGlnAsnLeuGlnValIleThrGluLysLeuGlnThrLeu-----	12338
Db	3364	ATTGAGAA-----GAGTCCMAAGACGCTTCAAGATTTGATGATCGT	34056
QY	1239	-----GlnGluGluMetLys	12433
Db	3406	GTTATTAGTGAAGGCTGCAGTACATCTGCAGACACGATGAAGAGATTAATAGAGAACTTCAC	34655
QY	1244	AsnIleThrIleGluArgAsnGlnLeuGlnThrAsnPheGluAspLeuLys-----	12606
Db	3466	AATGGCACCATTCACAGTAAATATAGCTGTGTCTGTGACCTTCGTGTGTCTGTG	35255
QY	1261	-----AlaGluHisAspSerLeuLysGlnAspLeuSer	12717
Db	3526	ATGCCAGAGCCGTAATGCCGCTGCCTGAGCTATCATCCTCTTGCTCCAGCAAGATCTG--	35826
QY	1272	GluAsnIleGlnGlnSerIleGluThrGlnAspGluLeu-----Arg	12855
Db	3583	-----GTTACGCTTCTCTTGATTTGGAAACAGAAATCTCCGTATTAAGTTTGGCCAAAT	36366
QY	1286	AlaAlaGlnGlnGluLeuArgGlnGlnLysGlnLeuValAspSerPheArgGlnGlnLeu	13056
Db	3637	GGAGTTCAGGTGCATCCCAATTCACAGATCACTTGTGTGACATGATT-----TACTTT	36596
QY	1306	LeuAspCysSerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnGluLys	13255
Db	3691	CTTCATGGAATATGAGAAATCAATAGTCCCT-----	37206
QY	1326	ValSerLeuGlnGluValAsnSerLeuGlnSerLeuMetLeuArgGluArgAspGlu	13456
Db	3721	---TCCCTGGCAGAGTTCACGTTACTGCTCTTACCAACAGGAAAGTCATGGGTACTCT	37776
QY	1346	LeuGlnThrSerCysLysAlaLeuValSerGlnLeuGlnLeuLeuArgAlaHisValLys	13656
Db	3778	GGCCATGACCCAGTCCCACTGCTAGTCT-----CTTCTGAACACCCACATTTGCA	38256
QY	1366	SerValGlu-----	1368
Db	3826	CTGGTGAAGGAGACGCTGTTTTTTATCCACGATTCGATCTCGAAACATACCTCTCCG	38856
QY	1369	GlyGlnAsnLeuGlnIleThrLysLysLeuAsnGlyLeuGlnLys-----Glu	13846
Db	3886	GGTCCACAAATTGATGTGATC-----AAATGCCATGCTTTAGTGAATTCAGGTGTGTTCT	39426
QY	1385	IleLeuGlnLysSerGlnGluSerGluValLeuLysSerMetLeuGlnAsnLeuLysGlu	14046
Db	3943	GTTCCAGAAAAAGAAAAATGTGTCAACAGTGAACATGACTCTTCTTACAGAAATCCAAACCT	40026

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QY 1405 AspaAaenLyLeuLySgluGlnaGluGluTyrsSerSerLySgluAsn-----Gln 1422
DB 4003 TCAGTGGGTTCCAGAAATATGTCACCTGAGCACCTTCAGAGAACCCCAATGCTCAGTTG 4062
QY 1423 PheSerLeuGluGluValPheSerSerGlySerGlnLyLeuValAspGluIleGluValLeu 1442
DB 4063 TTCACACACCCCATGTGATCTTCAAGCAGCATCAGAAATGTGCAACT-----GAGGTCTGG 4116
QY 1443 LySAlaGlnLeuLyAlaAlaGluGluValGlu 1453
DB 4117 AAACCTTACTTTCATTCATTCAGATGAGGCTCTT 4149

RESULT 14
US-09-592-054-1
/ Sequence 1, Application US/09592054
/ Patent No. 6440684
/ GENERAL INFORMATION:
/ APPLICANT: Beraud, Christophe
/ APPLICANT: Finer, Jeffrey
/ APPLICANT: Sakowicz, Roman
/ APPLICANT: Wood, Kenneth
/ TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
/ FILE REFERENCE: 1016
/ CURRENT FILING DATE: 2000-07-20
/ CURRENT APPLICATION NUMBER: US/09/592,054
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4308
/ TYPE: DNA
/ ORGANISM: Human
US-09-592-054-1

Alignment Scores:
Pred. No.: 8,57e-64 Length: 4308
Score: 909.50 Matches: 358
Percent Similarity: 42.44% Conservative: 275
Best Local Similarity: 24.29% Mismatches: 503
Query Match: 6.16% Indels: 369
DB: 4 Gaps: 61

US-09-724-584-1 (1-2954) x US-09-592-054-1 (1-4308)
QY 3 GlnGlyAspAlaValAlaValCySerValArgValArgProLeuIleGlnArgGlu----- 20
DB 76 AAGGGAATTCCTGTAAGAGTGGCGCTGCTTGCCTGCTGCTGCCCAAGAGATTAGC 135
QY 21 GlnGlyAspGlnAlaAsnLeuGlnTrpLySAlaGlnGlyAsnAsnThrIleSerGlnValAsp 40
DB 136 GAGGCTCCGACATGCTGCTTCCCTTCGTCGCCGAGAGAGCTCAGATG-----GTGGTT 189
QY 41 GlyThr---LysSerPheAsnAspArgValPheAsnSerHisGluSerHisSerGln 59
DB 190 GGTAAAGATTAATCTTCACTCACTAGATTTGTATTGATCCCTCTAGCTGAACAGAGAA 249
QY 60 ILeTyrglnGlnIleAlaValProIleIleArgSerAlaLeuGlnIleTyrsAsnGlyThr 79
DB 250 GCTCTCAATACAGCAGTACGCCCACTCATTAAGAGTATTAAAGATATATAGCAACG 309
QY 80 ILePheAlaTyrglnIleThrsSerGlyLySThrTyThrMetMetGly----- 96
DB 310 GTCCGTGCTTATGGGACAGCTGCTCTGAAAAACCTATTCAATGAGGAGTGCATATACT 369
QY 97 -----ThrProAsnSerLeuGlyIleIleProGlnAlaIleGlnGluValPhe 112
DB 370 GCAGAGCAAGAGATGAACCAACAGTGGGTTATTCCTAGGCTATATCAACTGCTCTTC 429
QY 113 LysIleIleGlnGluIleProAsnArgGluPheLeuLeuArgValSerTyThrMetGluIle 132
DB 430 AAAGAAATTTGATTAATAAGAGTGAATTTGATTTACTCTGAAGTGTCTTACTTAGAGATT 489

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QY 133 TyrAsnGluThrValIleAspLeuLeuCySerAspArgValArgLeuProLeuGluIle 152
DB 490 TACATGAAGAAATTTTGGATCTTCTATGTCATCTCGAGAAACCTCAATAGAGATT 549
QY 153 ArgGluAspPheAsnArgAsnValTyrgValAlaAspLeuThrGluGluValMetVal 172
DB 550 TACAATGAAGAAATTTTGGATCTTCTATGTCATCTCGAGAAACCTCAATAGAGATT 609
QY 173 ProGluIleValIleGlnIleTrpIleLySValGlyIleValAsnArgHisIleTyrgIleVal 192
DB 610 GCCTTGATCTGCTTCTGCTTGGACAGGGAACAACCTGAGACCTGAGCTGCCAG 669
QY 193 LysMetAsnAspHisSerSerArgSerHisIleTrpIlePheArgMetIleValGluSerArg 212
DB 670 GGTATGAACCTCCAGTCCGTCGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 729
QY 213 AspArgAsnAspProThrAsnSerGluAsnCySerGlyAlaValMetValSerHisIleu 232
DB 730 AAGAAAGATGACAAAGATAGCAGC-----TTTCGCTCCAAAGCTG 768
QY 233 AsnLeuValAspLeuAlaGlySerGluArgAlaSerGlnThrGlyAlaGluGlyValArg 252
DB 769 CATCTTGATGACCTGCTGATCAGAAAGACAGAAAGAACCAAGCTGAGAGGATGCT 828
QY 253 LeuLySgluGlyCyAsnIleAsnArgSerIlePheIleLeuGlyGlnValIleLyS 272
DB 829 CTAAAGAGGATTAATTAATTTACCGAGGCTCTGATGCTGGAATTAATCAAGTCT 888
QY 273 LeuSerAspGlyGlnAlaGlyGlyPheIleAsnTyrgArgSerSerLySLeuThrArgIle 292
DB 889 CTTGAGATGACAAAGAGTGGCTTGGCCCTCAGAGATTCAGATGACTGCACTG 948
QY 293 LeuGlnAsnSerLeuGlyGlyAsnAlaLySThrValIleIleCyThrIleThrProVal 312
DB 949 CTTCAAGATTCCTCTGAGAGTATAGCCATCTTATGATGATGCTGCTGCTGCTGCT 1008
QY 313 -----SerPheAspGluThrLeuSerThrLeuGlnIlePheAlaSerThrAlaLySHisVal 330
DB 1009 GACTCCATCTTAGAGAAACATTTAATACCTTCCCTGCTGCTGACAGCAAGAAATATC 1068
QY 331 ArgAsnThrProHisValAsnGluValIleuAspArgGluAlaLeuLeuLySArgTyrgArg 350
DB 1069 AAGAACAAACCTATGTTAAT-----ATTGATCCCAAGAC----- 1104
QY 351 LySgluIleLeuAspLeuLySgluLeuGluValAsnLeuGluSerSerSerGluThrLyS 370
DB 1105 GCTGAACCTTAATCATCTTAAGCAACAGGTACAAACGCTA----- 1143
QY 371 AlaGlnAlaMetAlaLySgluGluIleHisThrGlnLeuLeuAlaGluIleLySgluIleHis 390
DB 1144 -----CAAGCTTGTG----- 1155
QY 391 LySgluArgGluAspArgIleTrpHisIleThrHisIleValAlaIleSerSerGlnGlu 410
DB 1155 ----- 1155
QY 411 SerGlnIleAspGlnArgValIleArgLySArgArgValThrTrpAlaProGlyLyS 430
DB 1155 ----- 1155
QY 431 GlnAsnSerLeuHisIleSerGlyValSerAspPheAspMetLeuSerArgLeuProGly 450
DB 1156 -----CTACAGGCCCATGGA-----GTTACCTGCTGGA 1185
QY 451 AsnPheSerLySValAlaLySPheserAspMetProSerPheProGluIleAspAspSer 470
DB 1186 TCTATTAAGTGGAA-----CATCA----- 1206
QY 471 ValCyThrGluPheSerAspPheAspAspAlaLeuSerMetMetAspSerArgGlyIle 490
DB 1207 -----GAGAACTCAATCCCTGATGAGAGAAAT----- 1236
QY 491 AspAlaGluTrpAsnLeuAlaSerLySValIleHisIleArgGluLySLeuThrSer-----Leu 508

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Db	1237	-----CACTCCCTGGTGTAGAGCAAGTGAATAAATTAAAGTGTGTGTG	1278
Qy	509	HisGlnSerMetIleAspPheGlnIleSerAspSerValGlnPheHisSerSer	528
Db	1279	AGCCAGGACGTGTGCAGACGCCGAGATGTTGGAGAGATCATTTGGACAGCAAGCG	1338
Qy	529	LysGluAsnGlnLeuGlnIlePheProLysAspSerGlyAspMetAlaGluCysArgLys	548
Db	1339	AATGAA-----AAAATGAACCCCAACTGGAAGACTCAGGCGAG	1377
Qy	549	AlaSerPheGlnLysGlnIleThrSerLeuGlnGlnIleGlnSerLysGln	566
Db	1378	CATCGGCGCTGCAGAACTGATCTTCAAAAGCTAGCGACTTTGGAGAGCAAGCAATTG	1437
Qy	567	GluGlnLysLysGlnLeuValGlnSerPheGlnLeuLysIleAlaGlnLeuGlnGln	586
Db	1438	AAAGAAATGTAGATTAATTGTGTAACCTGCAGCAATTGATTCACCAATTGCGGATGAA	1497
Qy	587	LeuSerValLysAlaLysAsnLeuMetValThrAsnSerArgLysHisSerIleAsn	606
Db	1498	-----ACTGTTGCTTCATGCTGCAGCCATTGATCTGCGGTGAG	1539
Qy	607	AlaGluValGlnThrAspValGlnLysGlnValAlaArgLysGlnMetSerValLeuGly	626
Db	1540	CAGAAAGCCCACTAGAAACCACTCCAGG	1569
Qy	627	AspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSerValAspGlyLysArg	646
Db	1570	-----ACGAGCAGGCTCTTCTGACGCTTTTACACTGACGATGCTCTCCGT	1614
Qy	647	LeuSerSerSerHisAspGlnCysIleGlnHisArgLysMetLeuGlnLysIleVal	666
Db	1615	CAGGCCAGATGCTTAAGAGCTGTTGAGTTGAATAAAGCGCTTGACCTGAGAA	1668
Qy	667	AspLeuGlnGlnPheIleGlnAsnLeuAsnLysLys-----SerGlnAsnLysGln	684
Db	1669	-----GAGGCCCTGGCTGAGAAAGTACTGAGATGACCGCAACTG	1710
Qy	685	LysSerSerGlnGlnAspPheMetGlnSerIleGlnLeuGlnAlaIleMetAlaGln	704
Db	1711	CAGCTTATTCAGTACCAATTCACAGATTAACATA-----	1743
Qy	705	LysAlaAsnAlaLeuGlnGlnLeuAlaLeuMetArgAspAsnPheAspAsnIleLeu	724
Db	1744	AAAGAGCCAGAAATTAGAGTCAATCATCTGCAAAAGGAAAG-----GAAATATGGTCTT	1800
Qy	725	GluAsnGlnThrLeuLysArgGlnIleAlaAspLeuGlnArgSerLeuLysGln	744
Db	1801	GAACTTCAGACGAAAGAGATGCCAACCAAGTGAAGTGAAGCGCCGCCGCAAA	1860
Qy	745	GlnThrAsnGlnPheGlnIleLeuGlnLysGlnThrGlnLysGlnAlaGlnLeu	764
Db	1861	CGTCTCCAGAGCTGGAGGCTCAAAATTCGTGATCTGAGAGAGAA-----	1905
Qy	765	IleHisGlnIleGlySerLeuLysLysLeuValGlnAsnAlaGlnMetTyrAsnGlnAsn	784
Db	1906	CTGATATGAGCTGCAAACTTCTGAAATTAAGGAATCCACAGACGCTACTCTCCAA	1965
Qy	785	LeuGlnGlnAspLeuGlnThrLysThrLysLeuLeuLysGlnGlnGlnIleGlnLeuAla	804
Db	1966	CTGAGACAGAGAGATA-----CGATGATGATAAAACACGCGGTACAGTTA	2010
Qy	805	GlnLeuArgLysArgAlaAspAsnLeuGlnLysValArgAsnPheAspLeuSerVal	824
Db	2011	-----ATGCGTCAATGAAGAAGTGTGTAG-----AGTTTACAGCTGG	2052
Qy	825	SerMetCysAspSerGlnLysLysCysGlnGlnIlePheGlnLeuLysGlnSerLeuSer	844
Db	2053	-----AAGCAGAAAGAGACAAAGAAAGTAATACAGTTAAAGAA-----	2091
Qy	845	AspAlaGlnAlaValThrArgAspAlaGlnLysGlnCysSerPheLeuArgSerGlnAsn	864
Db	2092	-----CGAGACCGTAAGAGGCA-----TATGACGTG	2118
Qy	865	LeuGlnLeuLysGlnLysMetGluAspThrSerAsnThrTyrAsnGlnLysGlnLysAla	884
Db	2119	CTGAAACTTGAAGAAATCTCCAGAAACAATCATGCTCTCAGACGTAAACGAGAGAG	2178
Qy	885	AlaSerLeuPheGlnLysGlnLeuGlnThrGlnLysSerAsnTyrLysMetGluAla	904
Db	2179	GCACACCTGCCAAACAGCGCTCCAAAGATGCTCTCCAGAAACACGAGAGCTT---GCA	2235
Qy	905	AspLeuGlnLysGlnLeuGlnSerIleAspAsnGlnIleAsnTyrLeuAsnGlyLeu	923
Db	2236	GATACGGGAAAGACTCAGAGC-----CGTGAATGAA	2271
Qy	924	LeuAlaGlyLysValProArgAspLeuSerArgValGlnLeuGlnLysVal	942
Db	2272	GGCACCTGACCTGAGTGAAGAATTGGCTGGAAACGAATTTAGAGTTATGTCAGTACT	2331
Qy	943	SerGlnPheSerLysGlnLeuLysAlaLeuGlnGlnLysAsnAlaLeuGlnAsnGln	962
Db	2332	GAGAAAGCCAAAGCCATGTGAATGACTCTTCAAGATGAAAGATCTGCGCTCAAGAT	2391
Qy	963	ValThrCysLeuSerGlnTyrLysPheLeuProAsnGlnValGlnCysLeuLysAsnGln	982
Db	2392	GTCGCTCACTCAAGAA-----	2409
Qy	983	IleSerLysAlaSerGlnGlnLysMetLeuLeuLysGlnGlnGlnHisSerAlaSer	1002
Db	2410	-----AAAAGAAATCTGGCGAGATCCACTCTCT	2439
Qy	1003	IleIleSerLysGlnGlnIleIleMetGlnGlnSerGlnGlnIleLeuGlnLeuThr	1022
Db	2440	AAACTCCGAGGCGTACATCTCCCTTACTGAAAGTCCGTGCAATTTCCGAGTCAGAA	2499
Qy	1023	AspGluValThrHisThrGlnSerLysValGlnGlnThrGlnGlnGlnIleThrLeuGlnMet	1042
Db	2500	GATTCTATTACA-----AAGCAGATGAAGAGCTGAGACTGAATGAATTCAGAGTGT	2556
Qy	1043	LysLysMetHisAspAspLeuPheGlnLysTyrIleArgAsnLysSerGlnAlaGlnArg	1062
Db	2557	CAGATTTGCT-----GACTTACAGACGAGAGTCTGTG-----GATCCAGAAAGTGAAGAC	2604
Qy	1063	LeuLeuArgLys-----MetGln	1068
Db	2605	AGACCAAAACAAACCGTGGAGAAATATTGCCACACTTCTGAAAGCCAAAGTGTCCCTGAAA	2664
Qy	1069	AsnLeuLysGlnThrMetGlnSerValGlnValLysIleAlaAspThrLysHisGlnLeu	1088
Db	2665	TATTGATTTGAGAGCTGCTCTCTCCAAATACAGCTACAGCAAACTTGAAAGCAGCTGT	2724
Qy	1089	GlnGln-----ThrIleArgAspLysGlnLeuLeuLeuHisGlnLysLysTyrThe	1105
Db	2725	AAACAGAGCAAGACACTGTCTGACATGACAGAAAGATCTTTTGAGAGAAAGAAATCAT	2784
Qy	1106	PheGlnAlaMetGlnThrIlePheProIleThrProLeuSerAspSerLeuProSer	1125
Db	2785	TTTCCGAGATAGACAGAGTTA-----CAAGCT	2814

[illegible]

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
:
: COMPUTER: AST Ascentia 900N
: OPERATING SYSTEM: DOS 6.22
: SOFTWARE: Word Perfect 6.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/713,815A
: FILING DATE: 13-SEP-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Alan J. Howarth
: REGISTRATION NUMBER: 36,553
: REFERENCE/DOCKET NUMBER: T3214/U-2202
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (801)566-6633
: TELEFAX: (801)566-0750
: INFORMATION FOR SEO ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3572 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
:
: US-08-713-815A-2
:
: Alignment Scores:
: Pred. No.: 1,65e-60 Length: 3572
: Score: 867.50 Matches: 310
: Percent Similarity: 44.00% Conservative: 192
: Best Local Similarity: 27.17% Mismatches: 365
: Query Match: 5.87% Indels: 275
: DB: 2 Gaps: 40
:
: US-09-724-584-1 (1-2954) x US-08-713-815A-2 (1-3572)
:
: Oy 5 AspAlaValIyValCyseValArgValArgPProIeuIIegInArgGluGInGlyAspGln 24
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 351 GACAGCATCAAAAGTGTCTGCCGATTCGCCAGCTGAACGACAGCGAAGAGACAGCCGCC 410
:
: Oy 25 AlaAsnIeuGInTrpIyValIaGlyAsnAn-----ThriIeserGInValAspGly 41
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 411 TCCAAAGTCGTGTCAAGTTTCCCAACCAATCGAGAGAGAACTGCATTCATCCATCCGGCC 470
:
: Oy 42 ThrIySerPheAsnPheAspArgValPheAsnSerHisGluSerThrSerGInIleTyr 61
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 471 ---AAGGTGATTTGTTTCACAAAGGCTTCAAAACCGAATGCATCCCAAGAAAGGCTTAC 527
:
: Oy 62 GInGluIIAlaIValProIleIleArgSerAlaIeuGInGlyTyrAraGInYThrIlePhe 81
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 528 AATGAGCGCGCCAAATGCATTTGTACGAGATGCTCTGCGCGGGGTACAAATGAAACGATATTC 587
:
: Oy 82 AlaTyrGlyGInThrSerSerGlyIySthTyrThrMet-----MetGlyThrPro 98
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 588 GCATATGTCTAAGCGTCTCCCGGAAACCGCATACGATGAGAGGCGGTGATCGGGACTCC 647
:
: Oy 99 AsnSerIeuGlyIleIleProGInAlaIleGInGluValPheIySIIeIIeGInGluIle 118
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 648 GTAAAAACAGGGATACATACACGATTCCTCAACGACATTTCAATCAATCTACGCGATG 707
:
: Oy 119 Pro---AsnArgGluIhPheIeuIeuArgValSerTyrMetGluIleTyrAraGInUthVal 137
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 708 GAGGTGAACCTGGAGATTTCATCATCAAGGCTCTCTAATACGAGATCTTCAATGAAACGATT 767
:
: Oy 138 IyAspArgIeuIeuCyseAspAspArgIyArgIyAspProIeuGInIleArgGluIleAspPheAsn 157
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 768 CGAGATCTGTG-----GACGTCCTCCAAAGGTGAACCTTGAATGTCACAGAGATMAAAC 821
:
: Oy 158 ArgAsnValTyrValAlaAspIeuThrGInGluIeuValMetValProGInHisValIle 177
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 822 CGGGTCCCGTAACGTCAAAGGCGCTACGGAACGGTTTCGTCGTGCGCGGAGAGATGTTTC 881
:
: Oy 178 GInTrpIleIyValyGlyGluIyAsnArgHisTyrGlyGInUthTyrIyMetIleAspHis 197
:   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
: Db 882 GAGGTATGAGAGAGGCAAAATCCATATGTCACATTCGCTGTGACAAACATGAAGACAT 941

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QY 188 SerSerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnAspPro 217
DB |||||
DB 942 TCTTGGCGATCCACACTGATATTCTTATCATGTGAAG----- 980
QY 218 ThrAsnSerGluAsnGlyAspGlyAlaValMetValSer---HisLeuAsnLeuValAsp 236
DB |||||
DB 981 -----CAGAGAAACCTGGAGAACCCAGAAACATATCCGGCAAACTTCACTGATGAT 1034
QY 237 LeuAlaGlySerGluArgAlaSerGlnThrGlyAlaGluGlyValArgLeuLysGluGly 256
DB |||||
DB 1035 TTGGCCGGTTCGAGAAAGTTTCCAGACTGGAGGGAGGAGAACCTTTGATGAAGCC 1094
QY 257 CysAsnIleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGly 276
DB |||||
DB 1095 AAGAACATCAACAGTCCGCTCGCCCTGGGCAACGTAATTTCTGCCCTGGCGGAGCGA 1154
QY 277 GlnAlaGlyGlyPheIleAsnTyrArgAspSerLysLeuThrArgIleLeuGlnAsnSer 296
DB |||||
DB 1155 AACAAA---AGCACATCCCTACCGTGAATTCAGGCTAAAGCGCATCTCGCAGGAGTGG 1211
QY 297 LeuGlyGlyAsnAlaLysThrValIleIleCysThrIleThrProValSerPheAsp--- 315
DB |||||
DB 1212 CTGGAGGCGAACGACGACCAACCATCGTCATCTGCTCTCCAGCCATTTCACAGAA 1271
QY 316 ---GlnThrLeuSerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrPro 334
DB |||||
DB 1272 TCTGAACGAAAGTCAAGCTGAGACTTGGTGTGTAAGCCCAAGACAGTAAGAACGTGGTC 1331
QY 335 HisValAsnGluValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGluIleLeu 354
DB |||||
DB 1332 TGGCTTAACGAGGAGCTTACTGCCGAGGAATGGAAGGACGCTATGAAGAGG--- 1385
QY 355 AspLeuLysSerGlnLeuGluAsnLeuLysSerSerSerGlnThrLysAlaGlnAlaMet 374
DB |||||
DB 1385 ----- 1385
QY 375 AlaLysGluGlnHisThrGlnLeuAlaGluIleLysGlnLeuHisLysGlu----- 392
DB |||||
DB 1386 ---AAGAAAAGAACCCCGCACTTAAGGGTAAAGGTGAAGTGAAGATCGAGCTTGCG 1442
QY 393 -----ArgGluAspArgIleTyrHisLeuThrAsnIle 403
DB |||||
DB 1443 CGCTGAGAGCGGGGTAAACTGTTAAGCGGAGAGCAACAATC---AACATGAGGATCTC 1499
QY 404 ValValAlaSerSerGlnLysGlnIleAsp-GlnArgValLysArgLysArgVal 423
DB |||||
DB 1500 ATGAGAGCAAGCAGCGCCAACTGGAAAGTGAAGGACAGACAGCGCGCGCGAGGCC 1559
QY 423 ThrTyrAlaProGlyLysIleGlnAsnSerLeuHisAlaSerGlyValSerAspPheAs 443
DB |||||
DB 1560 GCTTTGGCGCCGACGCA----- 1578
QY 443 PheLeuSerArgLeuProGlyAsnPheSerLysLysAlaLysPheSerAspMetProSe 463
DB |||||
DB 1579 -----CGGCTCTC-GCCAAATATGTCCTCATCGTGGCCGTGAAGCGAGCGCAG 1627
QY 463 rPheProGluIleAspAspSerValCysThrGluPheSerAspPheAspAlaLeuSe 483
DB |||||
DB 1628 GCTGGCTACAGAGTGGAGCGTCTTACCAAGACGTGACACAAAGATGAG----- 1679
QY 483 rMetLeuAspSerAsnGlyIleAspAlaGluTyrAsnLeuAlaSerLysValThrHisAr 503
DB |||||
DB 1679 ----- 1679
QY 503 GlnLysThrSerLeuHisGlnSerMetIleAspPheGlyGlnIleSerAspSerValG 523
DB |||||
DB 1680 -----GAGATCATATCGACAGACCA 1699
QY 523 nPheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuProLysAspSerGlyAspMe 543
DB |||||
DB 1700 GTACCGCGAGCAGCTCAAGAGCAGGTGATGAG-----CAGAGGAACTCAT 1747
QY 543 TalGluCysArgLys-----AlaSerPheGluLysGluIleThrSerLeuGlnGlu 561
DB |||||
DB 1748 CGCTAAGCTCGCGCGAGTATGAGACTTTGACGCGGAGTGGCCGCAATCCACAGCA 1807
QY 561 nLeuGlnSerLysGluGluGluLysGluLeuValGlnSerPheGluLeuLysIleAl 581
DB |||||
DB 1808 GAACAGACTCGCCAGAGAAAGGTTAAAGAGGTGCTCCAAAGCTTCGAA----- 1856
QY 581 aGluLeuGluGluGlnLeuSerValLysAlaLysAsnLeuGluMetValThrAsnSerAr 601
DB |||||
DB 1857 -GAGCTGACTGTAAACTACGACCAAGAAATCCAGAGATCAT----- 1898
QY 601 GlnHisSerIleAsnAlaGluValGlnThrAspAlaGluLysGluValValArgLysG 621
DB |||||
DB 1899 -----AACAAAGAACAGATATGATGCTTCAACAGAGGAGCTGACAGCA 1945
QY 621 uMetSerValLeuGluLysAspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAsp 639
DB |||||
DB 1946 GCAGTCTGTG-----TTCAACGCCGCTCCACAGACTACAGCAGCTCA 1990
QY 640 -----SerSerValAspGlyLysArgLeuSerSerHisAspGluCysIleGluHis 657
DB |||||
DB 1991 TCACATCTCTCACACCAAGAAAGCCATCAG----- 2024
QY 657 sArgLysMetLeuGluGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLys 677
DB |||||
DB 2025 ---GAATGCTTAACCAACCTACTGCGCGACTTGGCGGAAAGTGGCGGACCATGGCCC 2080
QY 677 sLysSerGluAsnAspLysGlnLysSerSerSerGluGlnAspPheMetGluSerIleGln 697
DB |||||
DB 2081 CGCGAGTCCAGCATCCAGCTTAAGATGAGT----- 2111
QY 697 uCysGluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGlu----- 711
DB |||||
DB 2112 ---GCTTGGCTTGCACACGATGCCAGCAAGTGAAGGAAATTCACATGCGCGC 2164
QY 712 -----LeuAlaLeuMetArgAspAsnPheAsnIleIleLeuGluAsnGluThrIle 729
DB |||||
DB 2165 TTTGTTTATCAGCAAGATGAAGACGAGGCAAGAACATTGCCACGATGCTCCAAAT 2224
QY 729 uLysArgGluIleAlaAspLeuGluLysSerLeuLysGlu---AsnGlnGluThrAsnG 748
DB |||||
DB 2225 GGAACACACAGAGCTGACTCCCAACAGAAAGATCTCCGATATGAGAAAGATCTGGCCA 2284
QY 748 uPheGluIleLeuGluLysGluIleThrGlnLysGlnHisGluAlaGlnLeuIleHisGlu 768
DB |||||
DB 2285 GTACCGGCTACTC-----ATTTCGACGACGAGGACGATG----- 2321
QY 768 eGlySerLeuLysLysLeuValGluAsnAlaGluMetTyrAsnGlnAsnLeuGluLys 788
DB |||||
DB 2322 -AAGTGGCTGCAGAGATGATGCGGAGGACAGCAAGAACAGCGCACGCTGACGAGAAC 2380
QY 788 PLeuGluThr-----LysThrLysLeuLysGluGlnGluIleG 802
DB |||||
DB 2381 AATCGATTCGCTCGCGGAGAAATGCGCAAGCTCAAGCGCCGCGAGCAGCTTCCGCCGT 2440
QY 802 nLeuAlaGluLeuArgLysArgAlaAspAsnLeuGlnLysValArgAsnPheAspLe 822
DB |||||
DB 2441 TAAAGCCGAGGAAACACCGGGCTGAGAGACTGGCC----- 2477
QY 822 uSerValSerMetGlyAspSerGluLysLeuGluGluIlePheGlnLeuLysGlnSe 842
DB |||||
DB 2478 -----TTCATGTTCTGATTTCTAG-----ATGACAGCAGCTA----- 2507
QY 842 rLeuSerAspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSe 862
DB |||||
DB 2508 -----CGCGAAGCCCAACACCGG-----CAGCTGTCCAGCTCCGGGA 2545
QY 862 rGluAsnLeuGluLeuLysGluLysMetGluAspThrSerAsnTyrTyrAsnGlnLysG 882
DB |||||
DB 2546 CGAAATTTGCCCGCAAGCAGCAAGAAATGAGAGATGAAGAT--GTCCATCAAAAG-- 2600
QY 882 uLysAlaAlaSerLeuPheGluLysGlnLeuGluThrGluLysSerAsnTyrLysLysMe 902
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Db 2601 -----CTGCTCTTGGCGCCACCAACAGATGACGGCCGACCTACGAGAAAGTCCGCCAGGA 2653
QY 902 tGluAlaAspleuGlnYsgIuLeuGlnSerAlaPheAsnGluIleAsnTYrLeuAsnG1 922
Db 2654 GGATGCCGAGAAAGTCCAGCAGACTTCAG-----AACAT 2686
QY 922 yLeuLeuAlaGlyValProArgAspleuLeuSerArgValGluLeuGluYsLYsVa 942
Db 2687 CATCCTCACC----- 2696
QY 942 lSerGluPheSerLYsGlnLeuGluYsAlaLeuGluGluYsAsnAlaLeuGluAsnG1 962
Db 2697 -----AACGAGCCTCGGAGACAGCGCGCAAGACTCAAGCGCCTGGAGAC-- 2744
QY 962 uValThrCYsLeuSerGluTYrLYsPheLeuProAsnGluValGluCYsLeuLYsAsnG1 982
Db 2745 -----ACGCTGGCCCAAGAGTTCAGACCGCTACACAACCTGCGAATACTTTCCTTCAGGA 2800
QY 982 nIlSerLYsAlaSerGluGluIleMetLeuLeuLYsGlnGluGluLYsGluHlaserAlase 1002
Db 2801 TCTACAGCAACGAATCCGAAGAATGCTGTAAACGAGAGACCGAGAGACGCTGATC 2860
QY 1002 rIllelSerLYsGlnGluIleleMetGlnGlnSerGluGlnIleLeuGlnLeuth 1022
Db 2861 ACTGCCGAGAAACGAAGATTCTCTTGGAGAACAC-----CT 2902
QY 1022 rAspGluValThrHlSerThrGlnSerLYsValGlnGlnThrGluGluGlnTYrLeuGluMe 1042
Db 2903 CGACCAGCTGACC----- 2915
QY 1042 tLYsLYsMetHlAspAspLeuPheGluLYsTYrIleArgAsnLYsSerGluAlaGluAs 1062
Db 2916 -----AAGGTGCACAAAGCAATTG-----GTGCGGACCAAGCGCATCTGCGGTG 2959
QY 1062 pLeuLeuArgGluMetGlu---AsnLeuLYsGLYThrMetGluSerValGluValLYsI1 1081
Db 2960 CGAGCTGCCCAAGCTGGAGAAAGCTGTACGCTGTACATGGAGCGGGTGAAGCTCTGGA 3019
QY 1081 eAlaAspThrLYsHlSerGluLeuGluGluThrIleArgAspLYsGluGlnLeuLeuHlserG1 1101
Db 3020 GACAGCGCTCAAGAGGCGGAGAGGAGGCGCAATGCGGATCGCAAGCGCTACCAATACGA 3079
QY 1101 u 1101
Db 3080 G 3080
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Search completed: October 22, 2003, 21:22:47
Job time : 930 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 22, 2003, 21:01:12 ; Search time 1494 Seconds

(without alignments)
5302.570 Million cell updates/sec

Title: US-09-724-584-1

Perfect score: 14769
Sequence: 1 MSBDDAVKVCVRVPLIQR.....QAEKNWYAKKETAECKTS 2954

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1792395 seqs, 134090451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPRO.spool/US09724584/runat_22102003_161414_1215/app.query.fasta_1.3143
-DB=Published Applications NA -FORMAT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09724584@CGN_1_1_1053@runat_22102003_161414_1215
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAOP=6 -FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2:	/cgn2_6/ptodata/2/pubpna/PTCT_NEW_PUB.seq:
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/2/pubpna/PTCT_PUBCOMB.seq:
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12:	/cgn2_6/ptodata/2/pubpna/US09D_NEW_PUB.seq:
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14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
16:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
17:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3615.5	24.5	7992	11	US-09-893-519A-140 Sequence 140, App

2	3613.5	24.5	8493	13	US-10-071-766-51	Sequence 51, App1
3	3613.5	24.5	8503	14	US-10-037-270-130	Sequence 130, App
4	3611.5	24.5	8491	12	US-10-133-013-260	Sequence 260, App
5	1153	7.8	10300	10	US-09-960-253-145	Sequence 145, App
6	1152	7.8	10096	10	US-09-960-253-163	Sequence 163, App
7	1149	7.8	10081	14	US-10-084-817-361	Sequence 361, App
8	1147	7.8	10281	12	US-10-240-965-201	Sequence 201, App
9	1139	7.7	10190	10	US-09-864-864-292	Sequence 292, App
10	1139	7.7	10211	10	US-09-954-456-1153	Sequence 1153, App
11	1139	7.7	10211	10	US-09-967-768A-186	Sequence 186, App
12	1139	7.7	10211	11	US-09-918-624B-2	Sequence 2, App1
13	1050	7.1	4775	14	US-10-146-473-81	Sequence 81, App1
14	1032.5	7.0	7694	12	US-10-096-534-14	Sequence 34, App1
15	1032.5	7.0	8063	12	US-09-814-353-21776	Sequence 21776, App
16	1024.5	6.9	12313	14	US-10-171-311-7	Sequence 7, App1
17	1024.5	6.9	12438	14	US-10-171-311-3	Sequence 3, App1
18	1022.5	6.9	12337	14	US-10-171-311-5	Sequence 5, App1
19	1022.5	6.9	12462	14	US-10-171-311-1	Sequence 1, App1
20	998	6.8	11677	14	US-10-082-830-134	Sequence 134, App
21	946	6.4	3753	12	US-10-116-712-668	Sequence 668, App
22	941.5	6.4	4348	12	US-10-116-712-661	Sequence 661, App
23	941.5	6.4	4348	12	US-10-116-712-667	Sequence 667, App
24	900.5	6.1	6386	13	US-10-098-841-40	Sequence 40, App1
25	891.5	6.0	7497	10	US-09-960-253-175	Sequence 175, App
26	891.5	6.0	7792	13	US-10-044-090-359	Sequence 359, App
27	888.5	6.0	3366	10	US-09-938-842A-2651	Sequence 2651, App
28	872	5.9	6452	14	US-10-205-823-418	Sequence 418, App
29	848	5.7	6773	10	US-09-864-864-336	Sequence 336, App
30	836	5.7	14800	10	US-09-954-456-1601	Sequence 1601, App1
31	836	5.7	14800	12	US-10-269-909-61	Sequence 61, App1
32	829	5.6	7065	9	US-09-874-923-115	Sequence 115, App
33	829	5.6	7065	10	US-09-991-496-115	Sequence 115, App
34	828	5.6	580073	12	US-10-205-220-1	Sequence 1, App1
35	814	5.5	14833	12	US-10-240-965-113	Sequence 113, App
36	797	5.4	15231	10	US-09-917-800A-1505	Sequence 1505, App
37	795.5	5.4	5641	12	US-10-032-585-6646	Sequence 6646, App
38	795	5.4	10625	9	US-09-727-384-5	Sequence 5, App1
39	795	5.4	10625	14	US-10-023-219-3	Sequence 3, App1
40	786.5	5.3	6586	10	US-09-954-456-1115	Sequence 1115, App
41	786.5	5.3	6586	10	US-09-954-456-1790	Sequence 1790, App
42	786.5	5.3	6586	14	US-10-157-031-17	Sequence 37, App1
43	776	5.3	8948	9	US-09-735-705-119	Sequence 119, App
44	776	5.3	8948	10	US-09-850-716A-119	Sequence 119, App
45	776	5.3	8948	10	US-09-897-778-119	Sequence 119, App

ALIGNMENTS

RESULT 1
US-09-893-519A-140
Sequence 140, Application US/09893519A
Publication No. US20030027243A1
GENERAL INFORMATION:
APPLICANT: ANADYS PHARMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BURMAN, Ed T.
APPLICANT: BRADLEY, John
APPLICANT: DESILVA, Thamara
APPLICANT: HARRIS, Sandra
APPLICANT: KOMARNITSKY, Svetlana
APPLICANT: MENDILLO, Marc
APPLICANT: MOORE, Daniel
APPLICANT: MCCOY, Melissa
APPLICANT: SANDERSON, Karen
APPLICANT: HAO, Tariq
APPLICANT: ZHU, Shuhao
APPLICANT: LONG, Fan
APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTI-FUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/IG548-US2
CURRENT APPLICATION NUMBER: US/09/893, 519A
CURRENT FILING DATE: 2001-06-28

QY 598 ThrAsenSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluIysGluVal 617
 DB 1498 TTGAACCTCA----- 1506
 QY 618 ValArgLySGluMetSerValIleuGlyAspSerGlyTyrAsnAlaSerAsnSerAspIleu 637
 DB 1506 ----- 1506
 QY 638 GlnAspSerSerValAspGlyLysArgIleuSerSerSerHisAspGluCysIleGluHis 657
 DB 1506 ----- 1506
 QY 658 ArgIysMetLeuGluGlnLysIleValAspLeuGluGluPheIleGluAsnLeuAsnLys 677
 DB 1506 ----- 1506
 QY 678 LysSerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGluLeu 697
 DB 1506 ----- 1506
 QY 698 CysGluAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAsp 717
 DB 1507 -----CTGCTGCT 1515
 QY 718 AsnPheAspAsnIleIleLeuGluAsnGluThrIleLysArgGluIleAlaAspLeuGlu 737
 DB 1516 GACTATGATTAATCTGGTATTGACTATGATAACAACCTACGAAACGAAAGAAAGAAATGTGA 1575
 QY 738 ArgSerLeuLysGluAsnGluThrArgAsnGluPheGluIleLeuGluLysGluThrGln 757
 DB 1576 TTGAATATTAAAGAAAGAAATGATCTTGGATGATTTGAGCTCTGAAAGAAAGAAACTAA 1635
 QY 758 LysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLeuValGluAsn 777
 DB 1636 AAAGATCAAGATCAACATAATTCATGAAATTCGAACTTAAAGAAATTTAGTTAAGCAT 1695
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 DB 1696 CGAGAAAGATTAATCAAGATCTTGAGAAATGAACTCAGTTCAAAGGTGAGCTGTGA 1755
 QY 798 GlnGlnGluIleGlnLeuAlaGluLeuArgLysArgAlaAspAsnLeuGlnLysVal 817
 DB 1756 GAAAAGAAAGACGATTAAGAAAGCTACGAAATACATAGACTCTCAAAAGCTAAGAAAT 1815
 QY 818 ArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeuCysGluGluIlePhe 837
 DB 1816 ATAAAGATGACCTGTCTACTACTCATTTG-----GAAAGCATTGAAAGACCAAAA 1863
 QY 838 GlnLeuLysGlnSerLeuSerAspAlaGluAlaValThrArgAspAlaGlnLysGluCys 857
 DB 1864 CAAAGAAAGACGACTCTGTTGATGCTGAAACTGTAGCCCTTGATGCCAAGGAAATCA 1923
 QY 858 SerPheLeuArgSerGluAsnLeuGluLeuLysGlnLysMetGluAspThrSerAsnTrp 877
 DB 1924 GCCTTTCTTAAGAGTGAATAATCTGAGATTGAGAGGAAATAAGAAAGAACTTCAACTCA 1983
 QY 878 TyrAsnGlnLysGluLysAlaAlaIleSerLeuPheGluLysGlnLeuGluThrGluLysSer 897
 DB 1984 TACAAGCAAAATGAAATATGATTCAGTTATATCAAGGCAATTTGAGGCAAAA----- 2037
 QY 898 AsnTyrLysLysMetGluAlaAspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIle 917
 DB 2038 -----AAGAAATGCAAGTTGATCTGAGAAAGAAATTAACAATCTGCTTTTATAGATA 2091
 QY 918 AsnTyrLeuAsnGluLysLeuAlaGlyLysValProArgAspLeuLeuSerArgValGlu 937
 DB 2092 ACAAAACTCACTCCCTTATAGATGCAAAAGTTCCAAAGATTTCTCTGTATTTGGAA 2151
 QY 938 LeuGluLysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGluGluLysAsn 957
 DB 2152 TTGGAAGGAAGATTAATGATCTTCAGAAAGAACTAAATTAAGAAAGTTGAAAGAAATGA 2211
 QY 958 AlaLeuGluAsnGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGlu 977

DB 2212 GCTTTGGCGGAAGAAAGTATTGTTGCTTTCAGATTAAGAAATCTTTACCTTCGAACTAGA 2271
 QY 978 CysLeuLysAsnGlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGlnGlu 997
 DB 2272 AGGCTGAGAAAGAAATGCAAGACAAATCTGAGAGCTCCATATTAATCAATCAAGAAA 2331
 QY 998 GluHisSerAlaSerIleIleSerIysGlnIleIleMetGlnGluGlnSerGluGln 1017
 DB 2332 GATTAATTTGTTTCTGAAGTATGTTCAATAGAGAGCTAGATCAAGTTTACTTGAAGA 2391
 QY 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnGlnThrGluGlu 1037
 DB 2392 ATTGGGAAAGAAAGAAAGATGACCTACCACTACACAGTGAATTAAGAAAGCACTATCA 2451
 QY 1038 GlnTyrLeuGluMetLysLysMetHisAspAspLeuPheGluLysTyr----- 1053
 DB 2452 GAATTCCAAAATTTCAAAACCTTCATGTGACTTGCACTTGCAAAAGTATTAAGATGCTCCT 2511
 QY 1054 -----IleArgAsnLysSerGluAlaGluAspLeuLeuArgGluMetGluAsnLeu 1070
 DB 2512 GAGGAGATGAGAGAAATGAAATCAGGAAATGATTATCTCTTAAGAAAGCCCAAAATTT 2571
 QY 1071 LysGlyThrMetGluSerValGluValLysIleAlaAspThrLysHisGluLeuGluGlu 1090
 DB 2572 GATTGAGATTGGGTGGCTTTGAAGACGAGCTTTCTTCAAGACCAAGAACTTACAGAG 2631
 QY 1091 ThrIleArgAspLysGluGlnLeuLeuHisGluLysLysTyrPhePheGlnAlaMetGln 1110
 DB 2632 AAACAGCTGAGGTTCAGAAAGAACTAATATGATGAGAAACGCTGAGAAAGAAATTAAGA 2691
 QY 1111 ThrIlePheProIleThrProLeuSerAspSerLeuProProSerLysLeuValGluGly 1130
 DB 2692 AAT-----AGAGATTCCTCCCTGCAAACTGTAAGAAAGGAGAAACACTGATTACTGAG 2745
 QY 1131 AsnSerGluAspProIleGluIleAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
 DB 2746 AAACGCGACCAACTTTAGAA-----GAAGTAAAACTTTAATCAAGAAAGAAATGAT 2799
 QY 1151 ArgAsnAsnIleMetValCysLeuGluThrGluArgAsnSerLeuLysGluGluVal--- 1169
 DB 2800 CTAAGAAACATCCAAAGAAAGCTTGCAAAATTAAGAGGACCAAACTCAAAAGTATTCAC 2859
 QY 1170 -----IleAspLeuAsnThrGlnLeuGln---SerLeuGlnAlaGln 1182
 DB 2860 GATACGTTAACATGAAATATGATTAATCAAGAAACATTAAGCAAAATGCTTGTGAGCTCTG 2919
 QY 1183 SerIleGluLysSerAspLeuGlnLysProLysGlnAspLeuGluGluGluValLys 1202
 DB 2920 AAACAACTCAAGAAACATTAATTAACACTTAAATGAAATTTCTGAG--GAAGTTTCC 2976
 QY 1203 LeuLeuLeuGluMetGluLeuLeuLysGlnHisIleThrAsp-----SerGln 1218
 DB 2977 AGGAATTTGCATATGAGAGAAATATACAGAGAAACTAAAGTGAATTCAGAAAGATG 3036
 QY 1219 LeuSerIleGluLysLeuGlnLeuGluLysAsnLeuGluValThrGluLysLeuGlnThrLeu 1238
 DB 3037 GTTGCGATATGATTAAGAAAGCAG-----GATTTGGA--GCTAAAAATATCCCAACACTA 3087
 QY 1239 GlnGluGluMetLysAsnIleThrIle----- 1247
 DB 3088 ACTGCAGATGTTAAGGATTAAGATTAATTAAGCAACAAGAAAGATTTTCTTTAATA 3147
 QY 1248 --GluArgAsnGluLeuGlnThrAsnPheGluAspLeuLysValGlnHisAspSerLeu 1266
 DB 3148 CAGGAGAAATTAAGAACTCAACAATGTTAAGAGTGTATTATAGCAAGAAAGAAACAATTTG 3207
 QY 1267 LysGlnAspLeuSerGluAsnIleGluGlnSerIleGluThrGlnAspGluLeuArgAla 1286
 DB 3208 AAGACTGACCTTAAGAAAGAAATTAAGAAATGACCATTTGAAACCGAGAAAGATTAAGACTT 3267
 QY 1287 AlaGlnGluLysLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnGlnLeuLeu 1306

Db 3268 CTGGGATGTAACCTTAAAGCAACAAAGATAGTTCACACAGAAAAACATGCCATA 3327
QY 1307 ASPCySerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnIlyVal 1326
Db 3328 AAG--AAAGAGAGAGCTTTCTAGAGCCTGTGACGACTGGCAGAAAGTTGAAGAAAA 3384
QY 1327 SerLeuGlyValAlaSerLeuGlnSerGluMet-----LeuArgGly 1341
Db 3385 CTAAGGAAAAAGCCAGCAACCTCCAAAGAAAAACAGAACACATCTTAACTAACAAGAA 3444
QY 1342 GluArgAspGluLeuGlnThrSerCysLysAlaLeuValSerGluLeuGluLeuVal 1361
Db 3445 GAGATGAGTGAAGATGCAGAAAAAG-----ATTATGATAATGAGAAATTAAAG 3492
QY 1362 AlaHisValLysSer-----ValGluGlyLysLeuLeuGluLeu 1374
Db 3493 AATGAATTAAAGAACAAAGAAATTGACATTCGAAACATATGSAACAGAGGCGTTGACTGG 3552
QY 1375 ThrLysLysLeuAsnGlyLeuGlyValGluIleLeuGlyLysSerGluLeuVal 1394
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QY 1395 LeuLysSerMetLeuGluLeuLeuLysGluAspAsnAsnLysLeuLysGluGlnAlaGlu 1414
Db 3613 CTAAGGAATTACAGAAAGTCAATTGAAAACAGAGAGACACACTTGAGGATAT----- 3666
QY 1415 GluTyrSerSerLysGluAsnGlnPheSerLeuGluValPheSerLysSerGlnLys 1434
Db 3667 -----ATTAAGAAATTGAAAGCTACAGGCTACAA 3696
QY 1435 LeuValAspGluIleGluValLeuLysAlaGlnLeuLysAlaAlaGluLysLeuGlu 1454
Db 3697 ACCAAGAAAGAACTAAATAATGCTCATATTCACCTAAAGAACACCAAACTATATGAT 3756
QY 1455 IleLysAspArgSerPheTyrPheGlu--LeuValGlnThrAlaAsnThrAsnLeuValGlu 1473
Db 3757 GAACATAAGAAAGAGCGTATCTGAGAGACAGCTCAATATATATATCTCAGAGACTTAAGA 3816
QY 1474 GlyLysLeuGluThrProLeuGlnAlaAsp-----HisGluLysAsp----- 1487
Db 3817 ---AAATCCCATACAAATTACAGAAAGATCCAGTGCCTCATGAGAAACAGAGTTA 3873
QY 1488 -----SerLeaAspArgSerGluMet-----GluIleLysValLeu 1501
Db 3874 CTGGCTAATGTGAAAAAGTCACTGAGACTCAGGAAACATGATGAATGAATGATTA 3933
QY 1502 GlyLysLys--LeuGluArgAsnGlnIlyLeuLeuGluArgLeuGlnIlyLysLeu 1520
Db 3934 ACAGAAAGCTCCACAACCAAGAGCTCAACACACTGGCAAGATGAATGAATGAAGAGCTC 3993
QY 1521 GluLeuSerAsnLysLeuGluIleLeuGlnLysGluMetGluThrSerValLeuLys 1540
Db 3994 AGGTGGAATGAAAAATTTCAAGAAAGTCAAGAGATGAATCTCTAACCAGAGAAAGA 4053
QY 1541 AspAspLeuGlnGlnLysLeuSerLeuSerLeuSerGluAsnIleIleLeuLysGluAsn 1560
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Db 4114 ATTAGAGAAACTTTG-----GCTAAATCCAGAGAGCTCAAGC 4152
QY 1581 GluLeuGlnLeuAlaLysAsnLeuAlaIleAlaAspAspAsnCysProIleThrGln 1600
Db 4153 AAACAAAGAACAGCTCTTAATATGAAAGAAAAAGCAATGAATCAACCAAAATCCTGAGT 4212
QY 1601 GluLysGlu-----ThrSerAlaAspCysValHisProLeuGluGluLysLeu 1617
Db 4213 GAGATGAGCAATTAACAAACCAAGATTCAGACACTACTAGAGATGAATGAATGAATGCTC 4272
QY 1618 LeuLeuThrGluGluLeuHisGlnLysThrAsnGluGlnIlyLysLeuLeuHisGluLys 1637
Db 4273 GGATTTGTCACAAAGACTTCAGAAAGTCATGATGAATGAATGTAATCTGTAGAGAGAA 4332

QY 1638 AsnGluLeuGluGlnAlaGlnValAlaGluLeuLysCysGluValAlaGlnHisLeuMetLysSer 1657
Db 4333 GATGACCTTACAGAGGCTGCAGAAAGTTCTTCAATCTGAAAAGTACACAGCTC----- 4383
QY 1658 MetIleGluSerLysSerLeuGlnSerLeuGlnHisGluLysHisAspThrGluGln 1677
Db 4384 -----AAAGAAACATAAAAGAAATTTAGCTTAAACACCTGGAAACTGAAG 4431
QY 1678 GlnLeu-----LeuAlaLeuLysGlnGlnMetGlnValAlaThrGlnLys 1693
Db 4432 GAACCTTAAGTTGCTCATATTGTTGCTGAAGAAACAGAGAAACTTATTAATGACTTAAGA 4491
QY 1694 LysGluLeuGlnGlnThrHisGluHisLeuThrAlaGluValAspHisLeuLeuGluAsn 1713
Db 4492 GTGAATCTTTCAGAGAAAGAA-----ACTGAATAATCAACCATTCMAAGCAG 4539
QY 1714 IleGlu--LeuGlyLeuAsnPheLysAsnGluAlaGlnGlnLysThrThrLysGluGln 1732
Db 4540 TTAGAAAGCAATCAATGATTAATTAACAGAAACAGATCCAAAGAGATTATGAGAAAGAGAA 4599
QY 1733 CysLeuLeuAsnGluAsnLysGluLeuGluLeuSerGlnHisArgLeuGlnCysGluIle 1752
Db 4600 CAACTT-----AATATAAACAAATTAAGTGAAGTTCCGAAAACTGAAT--GAAGCTG 4650
QY 1753 GluGluLeuMetLysSerLeuLysAspLysGluSerAlaLeuGluThrLeuLysGluSer 1772
Db 4651 AAACAAATTCAGAGGATCCGAAAGCCAGAGATTCAGACCTACCAAGATAT----- 4701
QY 1773 GluGlnLysValIleAsnLeu-----AsnGlnGluMetGluMet 1785
Db 4702 GAAAGTAAGATGCTCGAGTTACCAACAGACTTCAGAAAGTCAAGAAATCAAAAT 4761
QY 1786 ValMetLeuGluMetGluGluLeuLysAsnSerGlnArgThrValIleAlaGluArgAsp 1805
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QY 1806 GlnLeuGlnAspAspLeuArgGluSerValGluMetSerIleGluThrGlnAspAspLeu 1825
Db 4822 CAACGAAAGAAACACATAAGAAATTTAGCTAAATTAAGAAAGATCTCAAGAA----- 4875
QY 1826 ArgLysAlaGlnGlnAlaLeuGlnGlnLysAspLysValGlnGluLeuThrSerGln 1845
Db 4876 AAAGAAATATCACTTTTAAGATGACAGCTGTCAATGAGACTCGAGAAATGTGTGAA 4935
QY 1846 IleSerValLeuGlnGlnLysIleSerLeu-----LeuGluAsn----- 1858
Db 4936 ATTAAGACATTGAAGAGCAATTTGAGAACCCAGAAAGTTAAACCTGGAAGAACTAGAAACG 4995
QY 1859 -----GlnMetLeuTyr--AsnValAlaThrValLysGluThrLeu 1871
Db 4996 GAGAAATTAAGTTGACTCAGATCTACATGAAAACCTTGAGAAATGAGATCTGTAACA 5055
QY 1872 SerGluArgAspAspLeuAsnGlnSerLysGlnHisLeuPheSerGluIleGluThrLeu 1891
Db 5056 AAAGAAAGAGATGACTTGAAGAGTGGAGAGAACTCTCAAGATGAGAGAGACAGCTC 5115
QY 1892 SerLeuSerLysGluLys--GluPheAlaLeuGluGlnAlaGluLysAspLys-- 1909
Db 5116 AAGGAAACCTTGAAGAACTATTAATCTAGAGACTTAAGAAACAGAGAGCTTAATAAT 5175
QY 1910 -----AlaAspAlaAlaArgLysThrIleAspIleThrGluLysIleSerAsn 1925
Db 5176 GTTCACATGCATGTAAGAGACACCAACCAATTTGAT-----AAACTAAGAGCG 5226
QY 1926 IleGluGluGlnLeuLeuGlnGlnAlaThrAsnLeuLysGluThrLeu--TyrGluArg 1944
Db 5227 ATTGTTTCAAGAAAAACAAATGAATTAATCAATATGAAAAAGACTTAAGAACTCAAT 5286
QY 1945 GluSerLeu-----IleGlnCysLysGluGlnLeuAlaLeuAsnThrGlnHis 1960
Db 5287 GATGCTTAAAGACACAGATCTGAAGAAATATCAAGAGAACTTAAGAAATGTGTCACATGCAT 5346

QY 1961 LeuArgGluThrLeuLeuSerLysSerPheLeuAlaLeuGluLysMetGluGlnGluArgAsp 1980
 DB 5347 CTGAAAGACGACAGAGAACTATTGACAACTCAGAGAAATTGTTCTGAGAAAGACAGAT 5406
 QY 1991 GUAUAAlaAsnLysValIleAlaLeuThrGluLysMetSerSerLeuGluGlnIle 2000
 DB 5407 AAACATCATCAATATCCAAAAAGATTAGAAAATTCAAAATTCAAATTCAAGAAAAGATT 5466
 QY 2001 AsnGluAsnValThrThrLeuLysGluGluGluGluGluGluGluThrPheTyrLeuGln 2020
 DB 5467 CAGAA-----CTTAGGCCTAAGAACTCAACCTATTACGTTAAAAAAGAT 5514
 QY 2021 ArgProSerLysGlnLysSerSerGlnMetGluGluLeuArgGluSerLeuLysThr 2040
 DB 5515 GTCATAGACACACAAAAAGTGTGAAATGGAGCACTTAAGAAAATAAATAAGAC 5574
 QY 2041 LysAspLeuGlnLeuGluGluAlaGluLysGluLysSerGluAlaThrAsnGluLys 2060
 DB 5575 CAAACCTTAACCTCTAGTAATTA-----GAAATAGAG 5607
 QY 2061 AsnLeuThrAlaLysIleSerSerLeuGluGluGluIleLeuGlnAsnAlaSerIleLeu 2080
 DB 5608 AATTTA-----AATTGGCTCAAGAACTTCATGAAAACCTTGAGAAAATG 5652
 QY 2081 AsnGluAlaValSerGluArgGluAsnLeuArgHisSerLysGlnLeuValSerGlu 2100
 DB 5653 AAATGTGTAATGAAAGAAAGATATCTTAAGAAAGATAGAGAGACACTCAAACTGAG 5712
 QY 2101 LeuGlnLeuSerLeuThrLeu-----LysSerArgAspHisAlaPheAlaGln 2117
 DB 5713 AGAGACCAACTCAAGAAAGCTGCAGAAACCAAAAGCTAGAGATCTGGAATATACACAG 5772
 QY 2118 -----SerLysArgGluLys-----AspGluAlaVal 2126
 DB 5773 GAACAAAACTGCTCGATGCTATCAAAAGAAACCAAAAGAACTGTGATTAATAG 5832
 QY 2127 AsnLysIleAlaSerLeuAlaGluGluIleLysIleLeuThrLysGluMetAspGluPhe 2146
 DB 5833 GAAATAATTTTCGAAAAGACAACTCAAAATTTCAACATTCAAAAGGATTTAATATAA 5889
 QY 2147 ArgAspSerLysGluSerLeuGlnGlnLysSerHisIleLeuSerGluGluLeuCysThr 2166
 DB 5890 -----TCAAAAGATGAATTAAGAAAAGATCCAAAGAACTTCAG----- 5928
 QY 2167 TyrLysThrGluLeuGlnMetLeuLysGlnIleLysGluAspIleAsnAsnLysLeuAla 2186
 DB 5929 ---AAAAAGAACTTCAACTGCTTAGA---GTGAAAGAAAGATGTCAATATGAGT---CAT 5979
 QY 2187 GluLysValLysGluValAspGluLeu----- 2195
 DB 5980 AAAAAAATTAAATGAATGAGACAGTTGAAGAAAGCAATTTGAGCCAAACTATATGCAAG 6039
 QY 2196 -----LeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGln 2210
 DB 6040 TGTGAGATGATTAATCTCCAGTTGACTAGTAAGAACTTCATGAAGAGCTTGAAGAAATTAAGA 6099
 QY 2211 MetGluLeuArg--AsnGluLysLeuArgAsnTyrGluLysCysGluLysMetAspIle 2229
 DB 6100 ATTGATGCTAAAGAAAGAGATGAGCTTAAGAGAGATTAAGAAAGATCTCTCAAAATGAAA 6156
 QY 2230 MetGluLysGluLysSerValLeuArgLeuMet-----Gln 2241
 DB 6157 AGGACCAATTCATGCAACTTAAGGGAATGATAGTACAGACCCAGACAGAACCAACCA 6216
 QY 2242 AsnGluProGlnGlnGlu-----GluAspAspValAlaGluArgMetAspIleLeuGlu 2259
 DB 6217 GTAATACTGAAAAAGCTTAAGTATGATGACACAAAGCACTTAATGAAAGCCTTGAGA 6276
 QY 2260 SerArgAsnGlnGluIleGlnIleuMetGluLysIleSerAlaValTyrSerGluGln 2279
 DB 6277 GAAAGTCTCTAGATAAAGAGCTTTTGAAGAGATACTCAGAGATG---GATGATCAT 6333
 QY 2280 HisThrLeuLeuSerSerLeuSerGluLeuGlnLysGluThrGluAlaHisLysHis 2299

DB 6334 TATGAGTGTGAATAGATTTGCTCTGTACTGAGAAAGAAATTAATTCACAGAAA 6390
 QY 2300 CysMetLeuAsnIleLysGluSerLeuSerThrLeuSerArgSerPheGlySerLeu 2319
 DB 6390 ----- 6390
 QY 2320 GlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeuLeuAsnLysPheLysVal 2339
 DB 6391 -----ATCATAGAAAGTCAAGCTAT 6411
 QY 2340 Val-----TyrArgThrAlaAlaValLysGluAsnHisSerLeuIleLysAspTyrGlu 2357
 DB 6412 GTGTTAACTATGTTACAAAATAAAGAAAGACAACTGATGATCATTAATTTGAA 6471
 QY 2358 LysAspLeuAlaAlaGluGlnLysArgHisAspGluLeuArgLeuGlnLeuGlnCysLeu 2377
 DB 6472 ATGGAATTTTATGATGAAGTGGAAAAGCAAGAAATGCTTAATTAATAATACAGCACTT 6531
 QY 2378 GlnGlnHisGluArgLysTyrSerPheSerPheLysSerGluGluLysPheCysGluIle 2397
 DB 6532 CAACAAAGAT-----TGTGATGTACCATCCACAGAAATTAAAGGATCTCAAAATGG 6579
 QY 2398 GluPheLeuAsnGluLeuLeuPheLysValAsnIleIleGlnSerValGlnAspAsp 2417
 DB 6580 AACCGAATATGAGATCTA-----CATATTAGGAAATTTCTCAAGAT 6621
 QY 2418 PheSerGluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnGluGluGlu 2437
 DB 6622 TTCTCAGAAAGTGAAG-----TTCCCTAGCATTAAGAACTGAATTTCAACAACTAATAGT 6675
 QY 2438 HisLysLysGluLysPheMetGlnThrLeuGlnGluPheGluAspLeuHisValAspAlaLys 2457
 DB 6676 AATAGAAAAGAAATGACACAGTTTGTGAAGAGTGTGAATATCTGTTTGTATATAGAA 6735
 QY 2458 LysLeuSerGluGluMetGlnGlnGlnLysAsnArgArgIleAlaSerThrIleGlnLeuLeu 2477
 DB 6736 AAGCTTAATAATGCGATCCAGAAAGAAATATGATAGATTTGTCAAGTAACTCTTT 6795
 QY 2478 ThrLysArgLeuLysAlaValAlaGlnSerLysIle-----GlnArgGluIleThr 2494
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 QY 2495 ValTyrLeuAsnGlnPheGluAlaLysLeuGlnGlnCysLysGluGlnAsnLysLeu 2514
 DB 6856 ATA---TCAAGAGATGGAAACAGACCTGAAATCTAGAAAGAAAAAGTGAAGAACTA 6912
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 QY 2535 LeuLeuGluIleLeuLysThrValGlnAspGlu-----SerLysLys 2548
 DB 6967 -----CTTACACACACACAAATAGATTCCTCATGTTATCAATCAAGAGCT 7011
 QY 2549 LeuGln-----SerArgIleLysMetLeuGlnAsnGluLeuAsnLysValLysAsp 2565
 DB 7012 ACACAGTTAACACACAGAAATTCGAGAGCTGGAAATTCACATGCAAGAACTTAAGAA 7071
 QY 2566 AspAlaMetHisLysGluGluLysValAlaIleLeuGlnAspLysLeuLeu--LeuSerArg 2584
 DB 7072 AGTGTATGCTTAAGAAAGCAAGATTTAAAGATGCGAAAGAACTTGAGTGACTAAT 7131
 QY 2585 AsnAlaGluAlaGluLeuAsnAlaMetGlnValLysLeuThrLysLysGlnAspAsnLeu 2604
 DB 7132 GACATTAATAGCAAACTT-----CAAGCCAAAGTTCAATGAATTAATAGCTT 7182
 QY 2605 GlnAlaAlaMetLysGluIleGluAsnLeuGlnLysMetValAlaLysGluAlaValPro 2624
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 Oy 2685 ThrValCysValProLysAspTyrGlnLysAlaSerThrPheProValThrCysGlyGly 2704
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 Oy 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerGluLysAlaAlaLeu 2724
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 Db 7585 -----ATAAAACAAAGATGAATGTTGTAAGCAATATACGACTTT 7626
 Oy 2765 SerHisArgGlySerProHisLysThrGluThrTyrArg-----HisGlyProVal 2781
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 Oy 2802 SerThrLysArgValValSerProAsnArgSerGluIleTyrSerGlnLeuValMetSer 2821
 Db 7708 -----TCT 7710
 Oy 2822 ProGlyLysThrGlyMetHisLysHisIleLeuSerProSerLysValGlyLeuHisLys 2841
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 Oy 2862 LysThrGlyLeuHisLysAsnLeuThrGluSerThrLysPheAsnLeuSerSerPro 2881
 Db 7756 -----TCTCA 7761
 Oy 2882 CysLysGlnGlnLysValGlnLeuAsnLeu-----AsnSerProLysGlyLysLeuPhe 2899
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 Oy 2900 AspValLysSerLysSerMetProTyr---CysProSerGlnPhePheAsnSerLys 2918
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 Oy 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
 Db 7882 TTAGGCTTTTCCAGAGGTGCAAAATGACAGAGACAGAGAGTGATTCACAGCAGT 7941
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FILE REFERENCE: PA-0043 US
 ; CURRENT APPLICATION NUMBER: US/10/071,766
 ; CURRENT FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 144
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 51
 ; LENGTH: 8493
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020192678A1 441283.3
 US-10-071-766-51
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 Pred. No.: 4,456-220 Length: 8493
 Score: 3613.50 Matches: 995
 Percent Similarity: 50.34% Conservative: 573
 Best Local Similarity: 31.94% Mismatches: 932
 Query Match: 24.47% Indels: 615
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 Oy 21 Gln-----GlyAspGlnAlaAsnLeuGlnThrProLysAlaGlyAsnAsnThrIleSerGln 38
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 Db 211 GTTGATGGAATTAATCTTCAATTTGATGCTGCTTCTTCAATGATTAAGAACTACCAA 270
 Oy 59 GlnIleTyrGlnGluIleAlaValProIleIleArgSerAlaLeuGlnGlyTyrAsnGly 78
 Db 271 AATGATGTAAGAAATTAAGCAGCACCAATCATCTGCAATTCAGCAATCAAGCTTCAATG 330
 Oy 79 ThrIlePheAlaTyrGlyGlnThrSerSerGlyLysThrTyrThrMetMetGlyThrPro 98
 Db 331 ACTATATTGCTGCTTGAACAGACTGCTTCAGAAAAACATATACAGATGAGGTTCAAA 390
 Oy 99 AsnSerLeuGlyIleIleProGlnAlaIleGlnGluValPheLysIleIleGlnGluIle 118
 Db 391 GATCATTTGGAGATTATACCCAGGCAATTCATGACATTTTCCAAAAATTAAGAGATT 450
 Oy 119 ProAsnArgGluPheLeuLeuArgValSerTyrMetGluIleTyrAsnGluThrValLys 138
 Db 451 CCTATAGGGAATTTCTTTACGTTATCTTACATGAGAAATATACAAATGAAGCAATTA 510
 Oy 139 AspLeuLeuCysAspAspArgLysLysProLeuGluIleArgGluAspPheAsnArg 158
 Db 511 GATTACTCTGTGCACTCAAAAAATGAACCTTTAATTATTCAGAGAAATGTAAGAG 570
 Oy 159 AsnValTyrValAlaAspLeuThrGlnGluLeuValMetValProGlnHisValIleGln 178
 Db 571 AATGTATATGTTGCTGATCTCACAGAGAAAGTTGATATACATCAGAAATGGCTTGAAA 630
 Oy 179 TrpIleLysLysGlyLysLysAsnArgHisTyrGlyGluThrLysMetLeuAspHisSer 198
 Db 631 TGGATTACAAAGGAGAAAAGAGAGGCAATTATGAGAAAACAAAAGAAATCAAGAGAGC 690
 Oy 199 SerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnAspProThr 218
 Db 691 AGTGCTTCTATACCACTTTAGAGATCTTTGGAAAGCAGAGAGAGAGGAGTCACTTCT 750
 Oy 219 AsnSerGluAsnCysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAla 238
 Db 751 -----AATGTGAAGATCTGTTAAGGTATCCATTGAATTTGGTTGATCTTGA 801
 Oy 239 GlySerGluArgLysSerGlnThrGlyAlaGluGlyValArgLeuLysGluGlyCysAsn 258

RESULT 2 US-10-071-766-51

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 ; Publication No. US20020192678A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huel-Mei Chen
 ; TITLE OF INVENTION: GENES EXPRESSED IN SENSESCENCE

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Db      802  GGCAAGGAAAGAGCTGCTCAAAACAGCGCTGCGCATCGGCTCAAGAAAGCTGTAAT 861
Qy      259  11easnaSergLeuPhe11eug1ygl1val11elysLeuSeraspG1ygl1ala 278
Db      862  ATAAATCGAAGCTTATTTTGGGACAAGTATCAAGAACTTATGATGATGACAACTT 921
Qy      279  G1yG1yPhe11easntYrArgSerLeuThArg11eug1nambserLeuG1y 298
Db      922  GGTTGTTCAATAATATATGAGATGCAAGTTAACGCAATTCCTGCAATTCCTGGGA 981
Qy      299  G1yAsna1a1yThVal11e11eCyThr11eThrProValSerPheaspG1uthrLeu 318
Db      982  GGAATTCGAAGACACGATTTATCTGCACAATTATCTCCAGTATCTTTGATGAACCTT 1041
Qy      319  SerThrLeuGlnPheAlaSerThra1a1ySh1eValArgAntThrProH1eValanglu 338
Db      1042  ACTGCTCTCCAGTTTGCCAGTACTGCTAATATATGAGAAATATCTCTTATGTAATGAG 1101
Qy      339  ValLeuAspAspG1ua1aleuLeu1ySarg1yRarg1yGlu11e1euaSpleu1yS1yS 358
Db      1102  GTATCAACTGATGAGCTCTCTGAAAAGGTATAGAAAAGAAATATGATCTTAAAAA 1161
Qy      359  G1nleuG1uaSpleuG1uSerSerg1uthr1ySAlaG1nAlaMerAla1ySglu1n 378
Db      1162  CAATTAGAG-----GAGCTTCTTTAGAGACCGCGGCTCAGGCAATGAAAAAGACCA 1215
Qy      379  H1strG1nLeu1aG1u11elySg1nLeuH1s1ySg1uArg1uAspArg11etRp 398
Db      1216  TTGGCCCAACTTTTGGAGAAAAGATTGCTTCAGAAAGTACAGATGAGAAATTGAA 1275
Qy      399  H1e1euthrAsn11eVal1a1a1aSerSerg1nG1uSer---G1nG1nAspG1nRgVal 417
Db      1276  AACTTAACACGAGATCTGCTGACCTCTCTCTCCACAGTCAACAGAAATTAAGGCT 1335
Qy      418  1ySarg1ySarg1yValThrTrpAlaPArg1y1yS11eG1nAsnSerLeuH1a1aSer 437
Db      1336  AAAAAGAAAAGAAAGCTTACTGCTGCGCTCGCAAAATTAACAAATGAAAGAACTCAAC 1395
Qy      438  G1yVal1SerAspPheAspMetLeuSerArg1e1uProG1yAsnPheSer1yLe1yAla1yS 457
Db      1396  TATGACAGATCAATTAAT-----ATACCAACAAATATATACAAACAAACACACT 1443
Qy      458  PheSerAspMetProSerPheProG1u11eAspAspSerVal1CyethrG1uPheSerAsp 477
Db      1444  AAGCTTTCTATTAATTTATTTACGAGAAATTTGATGATCTGCTTCAGAGCTGATGTT 1503
Qy      478  PheAspAspAlaLeuSerMetLeuSerAspSerAsnG1y11eAspAlaG1uThrAsnLeu1a 497
Db      1504  TTCAGTAAACACTCTTGATACATTAAGT-----GAGATAGAAATGAGAAATCCAGCA 1551
Qy      498  Ser1ySVal1ThrH1a1aRgG1u1yThrSerLeuH1sG1nSerMet11eAspPheG1yG1n 517
Db      1552  ACAAAAGCTAACTAAATCAGAG----- 1572
Qy      518  11eSerAspSerValG1nPheH1sAspSerSer1ySg1uAsnG1nLeuG1nTyR1eupro 537
Db      1572 ----- 1572
Qy      538  1ySAspSerG1yAspMetAlaG1uCySarg1ySAlaSerPheG1u1ySglu11etHrSer 557
Db      1572 ----- 1572
Qy      558  LeuG1nG1nG1nLeuG1nSer1ySg1uG1nG1u1yS1ySg1uLeuValG1nSerPheG1u 577
Db      1572 ----- 1572
Qy      578  Leu1yS11eAlaG1uLeuG1uG1nLeuSerVal1ySAla1yAsnLeuG1uMetVal 597
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Db      1588  TTGAATCA----- 1596
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Db      1596 ----- 1596
Qy      638  G1nAspSerSerValAspG1y1ySarg1e1uSerSerSerH1eAspG1uCyethr1eG1uH1s 657
Db      1596 ----- 1596
Qy      658  Arg1ySmetLeuG1nG1n1yS11eValAspLeuG1uG1nPhe11eG1uAsnLeuAsn1yS 677
Db      1596 ----- 1596
Qy      678  1ySserG1uAsnAsp1yG1n1ySserSerg1uG1nAspPheMetC1uSer11eG1nLeu 697
Db      1596 ----- 1596
Qy      698  CySg1uAla11eMetAlaG1u1ySAla1aSerLeuG1uG1uLeuAla1e1uMetArgAsp 717
Db      1597 ----- 1605
Qy      718  AsnPheAspAsn11e11eLeuG1uAsnG1uThrLeu1ySarg1u11eAlaAspLeuG1u 737
Db      1606  GACTATGATTAATCTGATTTAGACTATGAAACAACCTACGAAAGAAAGAAATGGA 1665
Qy      738  ArgSerLeu1ySg1uAsnG1nG1uThrAsnG1uPheG1u11eLeuG1u1ySg1uThrG1n 757
Db      1666  TTGAATTTAAAGAAAGAAATGATTTGATGATGATTTGAGGCTCTGAAAGAAACTAA 1725
Qy      758  1ySg1uH1sG1uAlaG1nLeu11eH1sG1u11eG1ySserLeu1ySLeuValG1uAsn 777
Db      1726  AAAGATCAAGAGATGCACTAAATTCATTAATTTGAACTTAAAGAAATTTAGTTAAGCT 1785
Qy      778  AlaG1uMet1yRAsnG1nAsnLeuG1uAspLeuG1uThr1ySThr1ySLeuLeu1yS 797
Db      1786  CGAGAAATATTAATCAAGATCTTGAGAAATGAACTCACTTCAAAAGTAAAGCTTTGA 1845
Qy      798  G1uG1nG1u11eG1nLeuAlaG1uLeuArg1ySarg1a1aAspAsnLeuG1n1ySLeuVal 817
Db      1846  GAAAAGGAAAGCCAGATTAAAGATACAGAAATCATAGACTCTCAAAAGCTAAGAAAT 1905
Qy      818  ArgAsnPheAspLeuSerValSerMetC1yAspSerG1u1ySLeuCyG1uG1u11ePhe 837
Db      1906  ATAAAAATGACTTGTCACTACTG-----GAAAGCTTGAAGAACCCAAAA 1953
Qy      838  G1nLeu1ySg1nSerLeuSerAspAlaG1uAla1yThrArgAspAlaG1n1ySLeuCyS 857
Db      1954  CAATGAGACAGACTCTTGTGATGCTGAAACTGAGCCCTTGATGCCAAGAGAAATCA 2013
Qy      858  SerPheLeuArgSerG1uAsnLeuG1uLeu1ySg1u1ySmetG1uAspThrSerAsnTrp 877
Db      2014  GCCTTTCTTAAGAGAAATCTGAGATTGGAAGGAAAGAAAGAAAGAACTTGCAACTCA 2073
Qy      878  TyRAsnG1n1ySg1u1ySAla1aSerLeuPheG1u1ySg1nLeuG1nThG1u1ySser 897
Db      2074  TACAAACAAATGGAATGATATTCAGTTATATCAAAACCAATTTGAGGCAAA----- 2127
Qy      898  AsnTyR1yS1ySmetG1uAlaAspLeuG1n1ySg1uLeuG1nSerAlaPheAsnG1u11e 917
Db      2128 ----- 2181
Qy      918  AsnTyR1euaSng1yLeuLeuAlaG1y1ySVal1ProArgAspLeuLeuSerArgValG1u 937
Db      2182  ACAAAAGCTCACCTCTTATGATGAGCAAAAGTTCCAAAAGATTTGCTCTGTAATTTGGA 2241
Qy      938  LeuG1u1yS1ySValSerG1uPheSer1ySg1nLeuG1u1ySAla1e1uG1uG1u1ySAsn 957
Db      2242  TTGGAAAGAAAGATTACTGATCTTCAGAAAGAACTTAATTAAGAAAGTTGAAAGAAATGA 2301
Qy      958  AlaLeuG1uAsnG1uVal1yThrCyethSerSerg1uTyR1ySPhelPProAsnG1uValG1u 977
Db      2302  GCTTTGGGGAAGAGTATTTGCTTTCAAAATTTGAATCTTTACCTTTGAAAGTAA 2361

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QY 978 CysLeuLysAsnGlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGlnGlu 997
 Db 2362 AGCGTACGAGAAAGATACCAAGCAAAATCTGAAGAGCTCCATATATATAACATCAAGAAAA 2421
 QY 998 GluHisSerAlaSerIleIleSerLysGlnGluIleIleMetGlnGlnSerGluGln 1017
 Db 2422 GATAAATGTTTTCTTAAGTACTCTTAAGAGAGTACAGATTCGAAGTTTACTGGAAGAA 2481
 QY 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnGlnThrGluGlu 1037
 Db 2482 ATTTGGAAAAACAAGAGATGACCTAGCACTACACAGCTGCAATTTAAAAAGACGTATCA 2541
 QY 1038 GlnTyrLeuGlnMetLysLysMetHisAspAspLeuPheGluLysTyr----- 1053
 Db 2542 GAATTCCTAAATTTCTAAACCCCTTCATATGACTTTTGACCAAAAGTATTAAGTGTCTCT 2601
 QY 1054 -----IleArgAsnLysSerGluIleGluAspLeuLeuArgGluMetGlnLysLeu 1070
 Db 2602 GAGGAGATGAGAGATGCAATGACAGAAATAGTAAATCTCTCTAAAGAAAGCCCAAAATTT 2661
 QY 1071 LysGlyThrMetGlnSerValGluValLysIleAlaAspThrLysHisGlnLeuGlnGlu 1090
 Db 2662 GATTCGAGTTTGCGCTTTGAAGACCGAGCTTTCTTCAAGAACCCCAAGAACTTCAGAG 2721
 QY 1091 ThrIleArgAspLysGlnGlnLeuLeuHisGlnLysLysTyrThrPheGlnAlaMetGln 1110
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 QY 1111 ThrIlePheProIleThrProLeuSerAspSerLeuProProSerLysLeuValGlnGly 1130
 Db 2782 AAT-----AGAGATTCTCCGCTGCAGAACTGTAAGAAAGGAGAAACAACCTATTACGAG 2835
 QY 1131 AsnSerGlnAspProIleGluIleAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
 Db 2836 AAACGTGCAGCAAACTTTAGAA-----GAACTTAAACCTTTAACTCAAGAAAAAGATGAT 2889
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 Db 2890 CTAAACAACAACCTCAAGAAAGCTTGCAAAATTGAGAGAGCCAACTCAAAAGTAAATTCAC 2949
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 Db 2950 GATACGTGTAACATGAATATAGATCTCAAGAACCAATTAACGAATATGCTTGAAGCTCTG 3009
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 Db 3010 AAACAACAACCAAGAAACAATTAACTACCTAAATTCGAAATTTCTGAG--GAAGTTTCC 3066
 QY 1203 LeuLeuLeuGlnMetGlnLeuLeuLysGlnHisLeuThrAsp-----SerGln 1218
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 QY 1219 LeuSerIleGlnLysLeuGlnLeuGlnLysAsnLeuGlnValThrGlnLysLeuGlnThrLeu 1238
 Db 3127 GTTGGCATTAGATTAATAAAAAACAG-----GATTGGAA--CCTAAATAATCCCAAAACACTA 3177
 QY 1239 GlnGlnGlnMetLysAsnIleThrIle----- 1247
 Db 3178 ACTGCAGATGTGTAAGATATAGAGATTAATTGAGCAACAAGGAAGATATTTCTTTAATA 3237
 QY 1248 ---GluArgAsnGlnLeuGlnThrAsnPheGlnAspLeuLysAlaGlnHisAspSerLeu 1266
 Db 3238 CAGAGGAAAAATGAACTCCAAACAATGTTNAGAGCTGTTNAGCAGAAAGAAACAATTTG 3297
 QY 1267 LysGlnAspLeuSerGlnAsnIleGlnGlnSerIleGlnThrGlnAspGlnLeuArgAla 1286
 Db 3298 AAGACTGACTTAAAGGAAATATTTGAATGCACTTGAACAACCGAAGAAATTTAAGCTT 3357
 QY 1287 AlaGlnGlnGlnLysLeuArgGlnGlnLysGlnLeuValAspSerPheArgGlnGlnLeu 1306
 Db 3358 CTTCGGGATGAACTTAAAAAGCAACAGAGATAGTTGCAACAGAAAAAGAACATGCCATA 3417

QY	1307	AspCySerValGlyIleSerSerProAsnHisAspAlaValAlaAsnGlnGluVal	132
Db	3418	AAG---AAGAAGGAGAGCTTTCTAGACCTGTGACAGACTGGCAAGATTAAAGAAAA	347
QY	1327	SerLeuGlyGluValAsnSerLeuGlnSerGlnMet-----LeuArgGly	134
Db	3475	CTAAAGAAAAGAGCCAGACAACTCCAGAAAAACAGCAACAACCTTTAATGTACAGAA	353
QY	1342	GluArgAspGlnLeuGlnThrSerCysIysAlaLeuValSerGlnLeuGlnLeuArg	136
Db	3535	GAGATGAGGAGATGATGAGAAAAAG-----ATTAAATGAATATGAGAAATTAAAG	358
QY	1362	AlaHisValIleSer-----ValGlnGlyGlnAsnLeuGlnIle	137
Db	3589	AATGAAATTAAAGAACAAAGAAATTGACATTGGAACTATGGAAACAGAGGCTTGAGTTG	364
QY	1375	ThrIysIysLeuAsnGlyLeuGlnIysGlnIleLeuGlyIysSerGlnLeuSerGluVal	139
Db	3643	GCTCGAAAACCTTAATGAAATATTAATGAGAAAGTAATCTATTAACCAAGAAAGAAAGTT	370
QY	1395	LeuIysSerMetLeuGlnIysAsnLeuIysGluIysAsnAsnIysLeuIysGlnAlaGlu	141
Db	3703	CTAAAGGAATTACAGAGCTATTGTAACAGAGAGAGACCACTTAAGGAGATAT-----	375
QY	1415	GluIYrSerSerIysGluAsnGlnPheSerLeuGlnGluValPheSerCylSerGlnIys	143
Db	3757	-----ATAAGAAATTTGAAGCTACAGCCTACAA	378
QY	1435	LeuValAspGluIleGluValLeuIysAlaGlnLeuIysAlaAlaGlnGluArgLeuGln	145
Db	3787	ACCAAGAGAAGAACTAAAAATGGCTCATATTGACCTTAAAAAGAACCAAGAAACTTTGAT	384
QY	1455	IleIysAspArgAspIYrPheGln---LeuValGlnThrAlaAsnThrAsnLeuValGlu	147
Db	3847	GAACTAAAGAAGAGCGTATCTGAGAAGACAGCTCAATATATATATATCTAGAGCTTAAGA	390
QY	1474	GlyIysLeuGlnIYrProLeuGlnAlaAsp-----HisGlnGluAsp-----	148
Db	3907	---AATCCCATACCAAAATTACAAGAGAGATCCAGCTTCATGAGAAACAAGATTAA	396
QY	1488	-----SerIleAspArgIYrSerGlnMet---GlnIleuValLeu	150
Db	3964	CTGCTTAATGCAAAAAAGTCAGTGAAGACTCAGAGAAACAATGAATGAATGGAGTTATTA	402
QY	1502	GlyIuIys---LeuGluArgAsnGlnIYrLeuLeuGlnIYrArgLeuGlnGlnIysLeu	152
Db	4024	ACAGAAACGTCACCAACCAAGAGACTCAACACATCGGCAAGATTAAGAAATGAAAGCGTC	408
QY	1521	GluIysSerAsnIysLeuGlnIleLeuGlnIysGlnMetGluThrSerValLeuLeuIys	154
Db	4084	AGGTTGAATGAAAAATTTCAAGAAAGTCAGGAAGATAAAAATCTTTAACCAAGAAAGA	414
QY	1541	AspAspLeuGlnGlnIysLeuGlnIYrSerLeuLeuSerGlnIleIleLeuIysGlnIys	156
Db	4144	GACAACTTAAACGATTAAGAAAGAGAGCCCTTGAACTTAAACATGACGACGTAAGAAACAT	420
QY	1561	IleAspThrThrLeuIysHisHisSerAspThrGlnAlaGlnLeuGlnIysThrGlnGln	158
Db	4204	ATTGAGAGAACTTTG-----GCTAAATCCAGAGATCTCCAAAGC	424
QY	1581	GluLeuGlnLeuAlaIysAsnLeuAlaIleAlaIleSerAspAsnCysProIleThrGln	160
Db	4243	AAACAAAGACGCTCTTAATATATATAAAGAAAGAAACAAATGAATACCAAAATGTGAGT	430
QY	1601	GluIysGlu-----ThrSerAlaAspCysValHisProLeuGlnGluIleLeu	161
Db	4303	GAGATGAGCAATTTCAAAACCAAGAGATTGACACTAAGATAGATGAATGGAATGCTC	436
QY	1618	LeuLeuThrGlnGlnIysHisGlnIysThrAsnGlnGlnIysIysLeuLeuHisGlnIys	163
Db	4363	GGATTGTCCAAAGACTTCAAGAAAGCATGATGATTAAGATTTGATGCTTAAGAGAAAGAA	442
QY	1638	AsnGluLeuGlnGlnAlaGlnValGlnLeuIysCysGluValGlnHisIleMetIysSer	165

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4423 GATGACCTACAGAGCTGCAAGAACTTCTTCAATCTGAAAGTACAGAGCTC----- 4473
QY 1658 MetTleugLysSerSerLeuLysLeuGlnHisGlnLysHisAspThrGln 1677
Db 4474 -----AAAGAAAACATAAAGAAATGTGACTAAACCTGGAACCTGAAGAG 4521
QY 1678 GlnLeu-----LeuAlaLeuLysGlnGlnMetGlnValValThrGlnLys 1693
Db 4522 GAACCTAAAGTTGCTGATTTGCTGCTGAAGAAAGAGAACTATATATGATTAA 4581
QY 1694 LysGlnLeuGlnGlnThrHisGlnHisLeuThrAlaGlnValAspHisLeuSerGln 1713
Db 4582 GTGAATCTTTCAGAGAAAGAA-----ACGAAATATCAACCTTCAAAAGCAG 4629
QY 1714 TleGlu---LeuGlnLysLeuAspPheLysAspGlnAlaGlnGlnLysThrThrLysGln 1732
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Db 4690 CAATTT-----AATTAATAACAATTAAGTGAAGTTCAAGAAAAGTGAAT--GAAC 4740
QY 1753 GlnGlnLeuMetLysSerLeuLysAspLysGlnSerAlaLeuGlnThrLeuLysGln 1772
Db 4741 AAACAATTCAGAGAGATCGCAAGCCAGATTCAGCACTACAAAGTATA----- 4791
QY 1773 GlnGlnLysValLleAsnLeu-----AsnGlnGlnMetGlnMet 1785
Db 4792 GAAATGATGATCTGAGTTGACCAACAGACTTCAAGAAAGTCAAGAAAGTAAACAAAT 4851
QY 1786 ValMetLeuGlnMetGlnGlnLysLeuLysAspSerGlnArgThrValLleAlaGlnArg 1805
Db 4852 AGGATTAAAGAAAGAAAGAAATGAAAGAGTACAGAGAGCCCTTCAAGTAAAGAGAGAC 4911
QY 1806 GlnLeuGlnAspAspLeuLysGlnSerValGlnMetSerLleGlnThrGlnAspLeu 1825
Db 4912 CAACCTGAAAGAAACCTAAAGAAATTTGCTAAATAAGAAAGAACTCAAGAA----- 4965
QY 1826 ArgLysAlaGlnAlaLeuGlnGlnGlnLysAspLysValGlnGlnLeuThrSerGln 1845
Db 4966 AAAGATATCAAGTTCTTAAGATGACAGCTGCAATGAGACTCAGAGAAATGTGTGA 5025
QY 1846 TleSerValLeuGlnGlnLysLleSerLeu-----LeuGlnAsn----- 1858
Db 5026 ATAGAACACTTGAAAGCAATTTGAGACCAGAACTTAACCTGGAACCACTAGAAAG 5085
QY 1859 -----GlnMetLeuLys---AsnValAlaThrValLysGlnThrLys 1871
Db 5086 GAGAAATTAAGGTTGACTCAGATTAAGTACTGAAACCTTGAAGAAATGAGATCTGAACA 5145
QY 1872 SerGlnArgAspAspLeuAspGlnSerLysGlnHisLeuPheSerGlnLleGlnThrLys 1891
Db 5146 AAAGAAAGAGATGACTTAAGAGTGTGAGAGAGACTCAAAAGTGAAGAGAGACAGCTC 5205
QY 1892 SerLeuSerLeuLysGlnLys---GlnPheAlaLeuGlnAlaGlnLysAspLys--- 1909
Db 5206 AAGAAACCTTAGAGAACTTAACCTAGAGACTTAGAAACCAAGAGAGCTTAAGAAAT 5265
QY 1910 -----AlaAspAlaAlaArgLysThrLleAspLleThrGlnLysLleSerAsn 1925
Db 5266 GTTCACATGATCTGAAGAGACCAAGAACTTATGAT-----AAACTTAAGAGAG 5316
QY 1926 TleGlnGlnLysLeuLysGlnAlaThrAsnLeuLysGlnThrLys---TyrGlnArg 1944
Db 5317 ATTGTTTCAGAGAAACAAATGAAATATCAATATGCAAAAGAGACTTGAACACCTCAAT 5376
QY 1945 GlnSerLeu-----TleGlnCysLysGlnGlnLysLeuAlaLeuAsnThrGlnHis 1960
Db 5377 GATGCTTAAAGACACAGAGATCTGAATAATACAAAGAGAACTAAGATGCTCACATGAT 5436
QY 1961 LeuArgGlnThrLeuLysSerLysAspLeuAlaLeuGlnLysMetGlnGlnGlnArgAsp 1980
1980

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Db 5437 CTGAAAGACAGACAGAAACCTATGACAAACTCAGAGAAATTTGTTCTGAGAAACAGAT 5496
QY 1981 GlnAlaAlaAsnLysValLleAlaLeuThrArgLysLysMetSerSerLeuGlnGlnTle 2000
Db 5497 AAACATCAAAATATGCAAAAGATTTAGCAAAATTCAMATGCTAAATTTACAAAGAAAT 5556
QY 2001 AsnGlnAsnValThrThrLeuLysGlnGlnGlnGlnLysGlnLysGlnThrPheThrLeuGln 2020
Db 5557 CAAGAA-----CTTAAGCCAAATGAAACATCAACTTAATTAAGCTTAAGAAAGAT 5604
QY 2021 ArgProSerLysGlnGlnSerSerSerGlnMetGlnGlnLysLeuArgLysLeuLysThr 2040
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QY 2041 LysAspLeuGlnLeuGlnGlnAlaGlnLysGlnLleSerGlnAlaThrAsnGlnLys 2060
Db 5665 CAACCTTAACCTGAGTAAATTA-----GAAATAGAG 5697
QY 2061 AsnLeuThrAlaLysLleSerSerLeuGlnGlnGlnLleGlnHisAsnLleSerLleLeu 2080
Db 5698 AATTTA-----AATTTGCTCAAGAACTTCAAGAAACCTTGAAGAAATG 5742
QY 2081 AsnGlnAlaValSerGlnArgLysLeuAsnLeuArgHisSerLysGlnGlnLeuValSerGln 2100
Db 5743 AAATCTGTAATGAAGAAAGAGATATCTAAGAGAGTGAAGAGACACTCAAACTGAGAG 5802
QY 2101 LeuGlnGlnLysSerLeuThrLys-----LysSerArgAspHisAlaPheAlaGln 2117
Db 5803 AGAGACCAACTCAAGAAAGCCCTGCAGAAACCAAGCTAGAGATCTGGAATTAACAACAG 5862
QY 2118 -----SerLysArgLysLys-----AspGlnAlaVal 2126
Db 5863 GAACCTAAAACTGCTCGATGCTATCAAAAGAACCAAGAAACCTGTTGATTAACCTTGA 5922
QY 2127 AsnLysIleAlaSerLeuAlaGlnGlnLysLysLleLeuThrLysGlnMetAspGlnPhe 2146
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QY 2147 ArgAspSerLysGlnSerLeuGlnGlnGlnLysSerHisLeuSerGlnGlnLysCysThr 2166
Db 5980 -----TCAAAAGATGAATTAACGAAAAAGATCCAAAGAACTTCAG----- 6018
QY 2167 TyrLysThrGlnLeuGlnMetLeuLysGlnGlnLysGlnAspLleAsnAsnLysLeuAla 2186
Db 6019 ---AAAAAGAACTTCAACCTGCTTGA---GTGAAGAGAGATGCAATTAATGACT---CAT 6069
QY 2187 GlnLysValLysGlnValAspGlnLeu----- 2195
Db 6070 AAAAAAATTAATGAATGGAACAGTTGAAGAAAGCAATTTGAGCCAAACTATCTATGCAAG 6129
QY 2196 -----LeuGlnHisLeuSerSerLeuLysGlnGlnLysAspGlnTleGln 2210
Db 6130 TGTGAGATGATTAACCTTCACTGACTGAAGAAACCTTGAAGAGCTTGAAGAAATTAAGA 6189
QY 2211 MetGlnLeuArg---AsnGlnLysLeuArgAsnThrArgLysCysGlnLysMetAspLle 2229
Db 6190 ATTGATCTTAAGAAAGAGATGAGCTTAAGAGATTAAGAAATCTTCAAAATGGA--- 6246
QY 2230 MetGlnLysGlnLleSerValLeuArgLeuMet-----Gln 2241
Db 6247 AGGCAACATTCATAGCAACTTAAGGAAATGATAGCTAGAGACCAGACAGAACCAACCA 6306
QY 2242 AsnGlnProGlnGlnLys---GlnAspAspValAlaGlnArgMetAspLleLeuGln 2259
Db 6307 GTAAACCTGAAAAAGGTTACTAAGTATGAGACAAACAGCACTTATGAAAGCTGAGAG 6366
QY 2260 SerArgAsnGlnGlnLleGlnGlnLysMetGlnLysLleSerAlaValTyrSerGlnGln 2279
Db 6367 GAAAGTCTCTAGAAATTAAGAGCTTTTGAAGAGATATCTCAGAGACT--GATATCAT 6423
QY 2280 HisThrLeuLysSerSerSerSerGlnLeuGlnLysGlnThrGlnAlaHisLysHis 2299
Db 6424 TATGAGCTCTTGAATGATTTGCTTGAAGAGAAAGAAATTTGAATTCACAGAG--- 6480

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QY 2300 CysMetLeuAsnIleLysGluSerLeuSerThrIleuSerArgSerPheGlySerLeu 2319
 Db 6480 ----- 6480
 QY 2320 GluThrGluHisValLysLeuAsnThrGlnLeuGlnThrIleuLeuAsnLysPheLysVal 2339
 Db 6481 -----ATCATGAGAAATCGAAGTAT 6501
 QY 2340 Val-----TyrArgThrAlaAlaValLysGluAspHisSerLeuIleLysAspTyrGlu 2357
 Db 6502 GTGTTAGCATGTTTCAAAAATAAAGAGAACACATGATGATCATATAATTGAA 6561
 QY 2358 LysAspLeuAlaAlaGluGlnLysArgHisAspGluLeuArgLeuGlnLeuGlnCysLeu 2377
 Db 6562 ATGGATTATTAATTGATGAAGTGAAAGCAAAAGAAATTCCTAATTAATAACAGCACCTT 6621
 QY 2378 GluGlnHisGlyArgLysTrpSerAspSerAlaSerGluGluLeuLysPheCysGluIle 2397
 Db 6622 CAACAAAGAT-----TGCGATGTAACATCCAGAGAAATTAAGGATCTCAAAATGG 6669
 QY 2398 GluPheLeuAsnGluLeuLeuPheLysAlaAsnIleIleGlnSerValGlnAspAsp 2417
 Db 6670 AACCAAGATATGATCTCA-----CATATTGAGGAATTCCTCAAGAT 6711
 QY 2418 PheSerGluValGlnValPheLeuAsnGlnValGlySerThrIleuGlnGluLeuGlu 2437
 Db 6712 TTCTCGAAAGTCAG-----TTCCCTAGCATTAAGACCTGAATTCACAAAGTACTAAGT 6765
 QY 2438 HisLysLysGlyPheMetGlnTrpLeuGlnGluPheGlyAspLeuHisValAspAlaLys 2457
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 QY 2458 LysLeuSerGluGlyMetGlnGlnGlnLeuAsnArgArgIleAlaSerThrIleGlnLeuLeu 2477
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 QY 2478 ThrLysArgLeuLysAlaValAlaGlnSerLysIle-----GlnArgGluIleThr 2494
 Db 6886 AATTAACAGATATATTTGCCATTAATGAATCAACACAGCTTGAAGAAAGAAAGTGTCTAC 6945
 QY 2495 ValTyrLeuAsnGlnPheGluAlaLysLeuGlnGlnLysGluGlnAsnLysGluLeu 2514
 Db 6946 ATA-----TCCAAAGAGTGGGACACGACCTGAATATCTGAAAGAGAAATATAAAACTA 7002
 QY 2515 MetArgArgMetGluHisIleGlyProSerAlaSerValMetGluGlnGluAsnAlaArg 2534
 Db 7003 TTTAAAACTACCAACATTTGAAGACTTCTTGCGCATCTGTGCCAGGTTAAT----- 7056
 QY 2535 LeuLeuGlyIleLeuLysThrValGlnAspGlu-----SerLysLys 2548
 Db 7057 -----CTTACCAACACAGCAATTAAGATCTCTCATGTTACCAAGAGCT 7101
 QY 2549 LeuGln-----SerArgIleLysMetLeuGlnGlnLeuAsnLeuValLysAsp 2565
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 QY 2566 AspAlaMetHisLysGlyGlyLysValAlaIleLeuGlnAspLysLeu-----LeuSerArg 2584
 Db 7162 AGTGTATGCAATACAGAAAGCAAGATTTAAAGATGACAGAAAGAACTTGAGGTGACTAAT 7221
 QY 2585 AsnAlaGluAlaGluLeuAsnAlaMetGlnValLysLeuThrLysLysGlnAspAsnLeu 2604
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 QY 2625 TyrLysGluGluLysAspAsnLeuLysThrLysValValLysIleGlnMetGluLysIle 2644
 Db 7333 TATAAAGAAAGAAATGAAGATCTCAAAATGAAGCTTTGAAATAATGAGACCTAGAGAAATG 7392

QY 2645 LysTyrSerLysAlaThrAspGlnGluIleAlaTyrLeuLysSerCysLeuGluAspLys 2664
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 QY 2665 GluGluGlyLeuAlaArgLeuLysGluGluLeuAlaGlnAlaGlnAlaAspAsnAspThr 2684
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 QY 2685 ThrValCysValProLysAspTyrGlnLysAlaSerThrPheProValThrCysGlyGly 2704
 Db 7513 TCAGTATATATCGAACATATGATGATCTTCAGCTTCAAAATTAACCTTATCTTGAGAGT 7572
 QY 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerGluLysAlaIleLeu 2724
 Db 7573 GGCACGGCATTTGTCAAAACACAAAGCTTTATTTGAAAGAGTAAATGATTAAGGCTA 7632
 QY 2725 GluArgGluLeuSerHisTyrLysLysLysTyrHisIleLeuSerArgThrMetSerSer 2744
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 QY 2765 SerHisArgGlySerProHisLysThrGluThrTyrArg-----HisGlyProVal 2781
 Db 7717 TCCAAATGAGGTCAAAACTTGGAGAGAGAAAGAACCTTTAAAGAGAGGCTCACAAACAAAGTA 7776
 QY 2782 ThrProGluArgSerGluMetProSerLeuHisIleuGlySerProLysLysSerGluSer 2801
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 QY 2802 SerThrLysArgValLysSerProAsnArgSerGluIleTyrSerGlnLeuValMetSer 2821
 Db 7798 -----TCT 7800
 QY 2822 ProGlyLysThrGlyMetHisLysHisIleLeuSerProSerLysValGlyLeuHisLys 2841
 Db 7801 CCTAAAGTACTGGAACA-----GCTTCTTAA 7827
 QY 2842 LysArgAlaLeuSerProAsnArgSerGluMetProThrGlnHisValIleSerProGly 2861
 Db 7828 AAGAAACAATTAACACC----- 7845
 QY 2862 LysThrGlyLeuHisLysAsnLeuThrGluSerThrLeuPheAsnLeuSerSerPro 2881
 Db 7846 -----TCTCA 7851
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 QY 2900 AspValLysSerLysSerMetProTyr-----CysProSerGlnPhePheAspAsnSerLys 2918
 Db 7912 GATAGCCGATTAAGTCTTTACATCAATCACTCATCACTGCTATTTTGATTAATCAAGT 7971
 QY 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
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 QY 2939 TrpTrpTyrGluAlaLysGluThrAlaProGluLysLysThr 2953
 Db 8032 CTTTGGACCGCTCTCTCAGGCAAGAGATGTCCTGAGTGCAAAACT 8076

RESULT 3
 US-10-037-270-130
 ; Sequence 130. Application US/10037270
 ; Publication NO. US20030104529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie

QY 518 ILSerAspSerValGlnPheHISAspSerSerIysGluAsnGlnLeuGlnTyrLeuPro 537
 Db 1572 ----- 1572
 QY 538 LysAspSerGlyAspMetAlaGluCysArgIysAlaSerPheGluIysGluIleThrSer 557
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 QY 598 ThrAsnSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluIysGluVal 617
 Db 1588 TTGAATCTCA----- 1596
 QY 618 ValArgIysGluMetSerValLeuGluIysAspSerGlyTyrAsnAlaSerAsnSerAspLeu 637
 Db 1596 ----- 1596
 QY 638 GlnAspSerSerValAspGlyIysArgLeuSerSerSerHisAspGluCysIleGluHis 657
 Db 1596 ----- 1596
 QY 658 ArgGlyMetLeuGlnGlnIysIleValAspLeuGluGluPheIleGluAsnLeuAsnIys 677
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 Db 1726 AAAGATCAAGAGATGCACTAAATTCATGAAATTTGCAACTTAAAGAAATTTAGTAAAGAT 1785
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 QY 858 SerPheLeuArgSerGluAsnLeuGlnLeuIysGluIysMetGluAspThrSerAsnTyr 877
 Db 2014 GCCTTTCTTAGAAGTGAATCTGAGATTGAAAGGAAATGAAGAACTTGCAACTACA 2073

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 Db 2074 TACAAGCAAAATGAAAATGATATTCAGTTATATCAAGCAATTCGAGGCAAAA----- 2127
 QY 898 AsnTyrIysIysMetGluAlaAspLeuGlnIysGlnLeuGlnSerAlaPheAsnGluIle 917
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 QY 918 AsnTyrLeuAsnGluIysLeuAlaGluIysValIleProArgAspLeuSerArgValGlu 937
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 Db 2482 ATTGGGAAAACAAAAGATGACCTTACCAACTACACAGTGAATTTTAAAGACATGATCAA 2541
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 Db 2836 AAATGCAAGCAAACTTTAGAA-----GAACTAAAACTTTAACTCAAGAAAAAGATGAT 2889
 QY 1151 ArgAsnAsnIleMetValCysLeuGluThrGluIysArgSerLeuIysGluGlnVal-- 1169
 Db 2890 CTTAAACAACTCCAAAGAAAGCTTGCAAAATGAGAGGAGCAACAACCTCAAAAGATGATATCAC 2949
 QY 1170 -----IleAspLeuAsnThrGlnLeuGln-----SerLeuGlnAlaGln 1182
 Db 2950 GATCTGTTAAATGATATATGATATCTCAAGAAACAATTTAGAAATGCTTTGAGTCTCTG 3009
 QY 1183 SerIleGluIysSerAspLeuGlnIysProIysGlnAspLeuGlnGluGluIysGluValIys 1202
 Db 3010 AAACAACATCAAGAAACAATTAATATACACTAAATTCGAATTTCTGAG--GAAATTTCC 3066
 QY 1203 LeuLeuLeuGluMetGluLeuLeuIysGlyHisLeuThrAsp-----SerGln 1218
 Db 3067 AGGAATTTGATATTTGGAGAAATATACAGAGAAACTTAAGATGAATTTTCAGAAAAAGATG 3126
 QY 1219 LeuSerIleGluIysLeuGlnLeuGluAsnLeuGluValIleThrGluIysLeuGlnThrLeu 1238

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Db      3127 GTTGCATGATGAAAAACAG-----GATTGGAA--GCTAAAAATACCAAAACACTA 3177
Qy      1239 GInGluGluMeLysLeuAsn1LeThr1Le----- 1247
Db      3178 ACTGCAGATGTTAAAGATTAATGAGCAACAAGAGATATTTCTTAAATA 3237
Qy      1248 ---GluArgAsnGluLeuGlnThrAsnPhenGluAspLeuAlaGlnHisAspSerLeu 1266
Db      3238 CAGGAGAAATGAAATCCAAACAATGTTAGAGAGTGTATAGCGAAAGAAACAATGG 3297
Qy      1267 LysGlnAspLeuSerGluAsn1LeGluGlnSer1LeGluThrGlnAspGluLeuArg1a 1286
Db      3298 AAGACTGACCTTAAGAGAAATTTGTAATGACCATTTGAAACAGAGAAATTAAGACT 3357
Qy      1287 AlaGlnGluGluLeuArgGluGlnLysGlnLeuValAspSerPheArgGlnGlnLeu 1306
Db      3358 CTTGGGATGAACTTAAAGCAACAGAGATAGTTGCACAAGAAAGAACCATGCCATA 3417
Qy      1307 AspCysSerValGly1LeSerSerProAsnHisAspAlaValAlaAsnGlnLysVal 1326
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Qy      1337 SerLeuGlyGluValAsnSerLeuGlnSerGluMet-----LeuArgGly 1341
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Qy      1342 GluArgAspGluLeuGlnThrSerCysGlyAlaLeuValSerGluLeuGlnLeuArg 1361
Db      3535 GAGATGAGTGAATCAGAAAAAG-----ATTAATGAATAGAGAAATTAAG 3582
Qy      1362 AlaHisValLysSer-----ValGluGlyGluAsnLeuGluLe 1374
Db      3583 AATGAATTAAGAAACAAGAAATTGACATTGAAACATATGAAACAGAGAGCTTAGTGG 3642
Qy      1375 ThrLysLysLeuAsnGlyLeuGlnLysGluLeuGlyLysSerGlnLysSerGluVal 1394
Db      3643 GCTCGAAATCTTAAGAAATTTATGAGAGAGTGAATCTATTAACCAAGAAAGAAAGTT 3702
Qy      1395 LeuLysSerMetLeuGlnAsnLeuLysGluAspAsnAsnLysLeuLysGlnGlnAlaGlu 1414
Db      3703 CTAAGGAAATTAACAAGACTTATGAAACAGAGAGACCACTTAAGAGATAT----- 3756
Qy      1415 GluTyrSerSerLysGluAsnGlnPheSerLeuGluGluValPheSerGlySerGlnLys 1434
Db      3757 -----ATMAAGAAATTAAGAGCTTAACAGCCCTAACAA 3786
Qy      1435 LeuValAspGluLeuGluValLeuLysAlaGlnLeuLysAlaAlaGlnGluLysLeuGlu 1454
Db      3787 ACCAAAGAAAGAACTAAATAATGCTCATATTCACTTAAGAAACACCAAGAAATTAATGAT 3846
Qy      1455 IleLysAspArgAspTyrPheGlu---LeuValGlnThrAlaAsnThrAsnLeuValGlu 1473
Db      3847 GAACTAAGAAGAGCGTATCTGAGAAAGACGCTCAATAATTAATCTCAGAGACTTAAGA 3906
Qy      1474 GlyLysLeuGluThrProLeuGlnAlaAsp-----HisGluGluAsp----- 1487
Db      3907 ---AAATCCCATACCAAAATTACMAAGAGATCCAGTGCCTTCATGAGAGAACAGAGTTA 3963
Qy      1488 -----SerIleAspArgArgSerGlnGluMet-----GluIleLysValLeu 1501
Db      3964 CTGCCTAATGTAAGAAAAAGCTGAGACTCAGGAAACAATGAATGAATGAGTTATTATA 4023
Qy      1502 GlyLysLys---LeuGluArgAsnGlnTyrLeuLeuGluArgLeuGlnGluLysLeu 1520
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Qy      1521 GluLeuSerAsnLysLeuGlnLysGlnLysGlnMetGluThrSerValLeuLysLys 1540
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Qy      1541 AspAspLeuGlnGlnLysLeuGlnSerLeuLeuSerGluAsn1LeIleLysGluLeu 1560

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Qy      1561 IleAspThrThrLeuLysHisHisSerAspThrGlnAlaGlnLeuGlnLysThrGlnGln 1580
Db      4204 ATTAGAGAAACTTGT-----GCTAAATATCAGAGAGCTCAAAAGC 4242
Qy      1581 GluLeuGlnLeuValAlaLysLeuAlaIleAlaLysSerAspAspCysPro1LeThrGln 1600
Db      4243 AAACAAGAAACAGCTCTTAATATGAAAGAAAAAGCAATGAATACCAAAATCTCGACT 4302
Qy      1601 GlyLysGlu-----ThrSer1AspCysValHisProLeuGluGluLys1Leu 1617
Db      4303 GAGATGAGAGCAATTAACACCAAGATTCAGACATACTAAGGATGAATGAATGAGCTC 4362
Qy      1618 LeuLeuThrGlnGluLeuHisGlnLysThrAsnGlnGlnGlnLysLeuLeuHisGluLys 1637
Db      4363 GGATGTCCAAAGACCTTCAAGAAAGTATGATGAATGAATGTGTAGTGAAGAGAA 4422
Qy      1638 AsnGluLeuGluGlnAlaGlnValGluLeuLysCysGluValGlnHisLysMetLysSer 1657
Db      4423 GATGACCTACAGAGCTGCAAGAGACTTTCATATCTGAATGAGCAGCTC----- 4473
Qy      1658 MetIleGluSerLysSerSerLeuGluLysLeuGlnHisGluLysValAspThrGluGln 1677
Db      4474 -----AAGAAACATAAAGAAATTTGATGACTTAACACCTGAAACCTGAAGG 4521
Qy      1678 GlnLeu-----LeuAlaLeuLysGlnGlnMetGlnValAlaThrGlnLys 1693
Db      4522 GAACCTTAAGTGTCTCATGTTGTGCTGTAAGAAACAGAGAGAACTTAATGACATTAAGA 4581
Qy      1694 LysGluLeuGlnGlnThrHisGlnHisLysThrAlaGlnValAspHisLysLysGluLeu 1713
Db      4582 GTGAATCTTTACAGAGAGAA-----ACTGAATATTCACCACTTCAAAAGCAG 4629
Qy      1714 IleGlu---LeuGlyLeuAsnPhenLysAsnGlnAlaGlnGlnLysThrLysGluGln 1732
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Qy      1733 CysLeuLeuAsnGluAsnLysGluLeuGlnGlnSerGlnHisValGluLeuGlnCysGluLe 1752
Db      4690 CAACCT-----AATATTAACAAATAGTACAGTTCGAGAAAGAACTAAT---GACCTG 4740
Qy      1753 GluGluLysMetLysSerLeuLysAspLysArgGlnSerAlaLeuGlnThrLeuLysGluSer 1772
Db      4741 AAACAATTCAGAGACATCGCAAGAGCCAAAGATTCAGACATTAACAAGTATA----- 4791
Qy      1773 GluGlnLysValIleAsnLeu-----AsnGlnLysMetGluMet 1785
Db      4792 GAAGTAAAGATGCTCGAGTTGACCAACAGACTTCAGAAAGTCAAGAAATTAACAATT 4851
Qy      1786 ValMetLeuGluMetGluGlnLysLeuLysAsnSerGlnArgThrValIleAlaGluArgAsp 1805
Db      4852 ATGATTAAAGAAAAAGAGAAATGAAAGATACAGAGAGGCCCTTCAGATGAGAGAGAC 4911
Qy      1806 GlnLeuGlnAspAspLeuLysGluSerValGlnLysSer1LeGluThrGlnAspAspLeu 1825
Db      4912 CAACGAAAGAAACACTTAAGAAATTTGACTTAATAATGAAGAAATTCAGAA----- 4965
Qy      1826 ArgLysAlaGlnGlnAlaLeuGlnGlnGlnLysAspLysValGlnGlnLysThrSerGln 1845
Db      4966 AAAGAAATTCAGTTTCTTAATGATGACAGCTGCAATGACAGCTGAGGAGAAAAATGCTGA 5025
Qy      1846 IleSerValLeuGlnGluLysIleSerLeu-----LeuGluAsn----- 1858
Db      5026 ATAGAAACACTTGAAGAGACAATTTGAGACCCAGAAAGTTAAACCTGAGAAACATAGAAAGC 5085
Qy      1859 -----GlnMetLysLys---AsnValAlaThrValLysGluThrLeu 1871
Db      5086 GAGAAATTAAGCTTGAATCAATATCTACATATAAAACCTTGAAAGAAATGAGATCTGTAACA 5145
Qy      1872 SerGluArgAspAspLeuAsnGlnSerLysGlnHisLysLeuPheSerGlu1LeGluThrLeu 1891
Db      5146 AAAGAAAGATGACCTTAGAGAGTGTGAGAGAGACTCAAAAGTAAAGAGAGACAGCTC 5205

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OY 139 AsnLeuLeuCyAspAspArgArgLysLysProLeuGluIleArgGluAspPheAsnArg 158
Db 511 GATTACTCTGTGGCACTCAAAAATGAACTTTAATTATTCGAGAAAGATGCTCAATAGG 570
OY 159 AsnValTyrValAlaAspLeuThrGlnGluLeuValMetValProGluHisValIleGln 178
Db 571 AATGGTATGTGGCTGATCTCAAGAAAGAGTTGATATACATAGAAATGGCTTGGAA 630
OY 179 TrpIleLysGlyGluLysAsnArgHisTyrGlyGluThrLysMetAsnAspHisSer 198
Db 631 TGGATTCAAAAGGAGAAAAGACAGGCATTTATGGAGAACAAAATGATCAAGAGAC 650
OY 199 SerArgSerHisThrIlePheArgMetIleValGluSerArgAspArgAsnProThr 218
Db 691 AGTGGTCTCATACCATCTTTAGATGATTTTGGAAAGCAGAGAGAAAGGCTGAACCTTCT 750
OY 219 AsnSerGluAsnCyAspGlyValAlaMetValSerHisLeuAsnLeuValAspLeuAla 238
Db 751 -----AATTGTGAAGATCTGTTAAGTATCCCATTTGAAATTTGGTTGATCTTGCA 801
OY 239 GlySerGluArgAlaSerGlnThrGlyAlaGluGlyValArgLeuLysGlnGlyCysAsn 258
Db 802 GGCAGTAAAGAGAGCTGCTCAAAAGCGCTGAGAGTGTGCGGCTCAAGAGAGCTGTAA 861
OY 259 IleAsnArgSerLeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAla 278
Db 862 ATTAATTCGAAGCTTATTATTATTTGGGACAAAGTATCAAGAACTTGTGTGACAAAGTT 921
OY 279 GlyGlyPheIleAsnTyrArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGly 298
Db 922 GGTGGTTTCATTAATTTATTCAGATAGCAAGTAAACAGAAATTTTCAGAAATTCCTTGGA 981
OY 299 GlyAsnAlaLysThrValIleIleCysThrIleThrProValSerPheAspGluThrLeu 318
Db 982 GGAATTCCAAGACAGATATTTATCTGCACAAATTAATCCAGATCTTTGATGAAACTCTT 1041
OY 319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValAsnGlu 338
Db 1042 ACTGCTCTCCAGTTTCCCACTACTGCTTAATATATAGAAATATCTCTTATGTATATAG 1101
OY 339 ValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLysLys 358
Db 1102 GATATCAACTGATGAACTCTCCGAAAGGTATAGAAAGAAATATATGATCTTAAAAA 1161
OY 359 GlnLeuGluAsnLeuLysSerSerGluThrLysAlaGlnAlaMetAlaLysGluGlu 378
Db 1162 CAATTAGAG-----GAGGTTCTTTAGAGCGCGGCTCAGCAATGCAAAAAGACCA 1215
OY 379 HisThrGlnLeuLeuAlaGluIleLysGlnLeuHisLysGluArgGluAspArgIleTrp 398
Db 1216 TTGGCCCACTTTTGGAGAAAAGATTTGCTTCAGAAAGTACAGAAATGCAAAATTTGAA 1275
OY 399 HisLeuThrAsnIleValAlaLysSerGlnGluSer--GlnGlnAspGlnArgVal 417
Db 1276 AACTTAACCGAGATGCTGTGACCTTCTTCCCTCAGCTTGCAACAGAAATTAAGGCT 1335
OY 418 LysArgLysArgArgValThrTyrAlaProGlyLysIleGlnAsnSerLeuHisAlaSer 437
Db 1336 AAAAGAAAAGAGAGTTACTGTGCGCTTGCAAAATTAACAAAATAGAAAGACCAAAAC 1395
OY 438 GlyValSerAspPheAspMetLeuSerArgLeuProGlyAsnPheSerLysLeuAlaLys 457
Db 1396 TATGCAGATCAATTAAAT-----ATACCAACAATATATACAAACAAAACACAT 1443
OY 458 PheSerAspMetProSerPheProGluIleAspAspSerValCysThrGlnPheSerAsp 477
Db 1444 AAGCTTTCTAATAATTTATTCAGAGAAATGATGATGTCTGTTCAGAGCTGATGATTT 1503
OY 478 PheAspAspAlaLeuSerMetMetCysSerAsnGlyIleAspAlaGluThrAsnLeuAla 497
Db 1504 TTCAGTACACCTCTTGATACATTAAGT-----GAGATAGAAATGAAATCCAGCA 1551
OY 498 SerLysValThrHisArgGluLysThrSerLeuHisGlnSerMetIleAspPheGlyGln 517

OY 1552 ACAAAGCTACTAATATAGAG----- 1572
OY 518 IleSerAspSerValGlnPheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuPro 537
Db 1572 ----- 1572
OY 538 LysAspSerGlyAspMetAlaGluCysArgLysAlaSerPheGluLysGluIleThrSer 557
Db 1572 ----- 1572
OY 558 LeuGlnGlnGlnLeuGlnSerLysGlnGluGluLysGlyLeuValGlnSerPheGlu 577
Db 1572 ----- 1572
OY 578 LeuLysIleAlaGluLeuGlnGluGlnLeuSerValLysAlaLysAsnLeuGluMetVal 597
Db 1573 -----AATATGAAAGTGAAG 1587
OY 598 ThrAsnSerArgGluHisSerIleAsnAlaGluValGlnThrAspValGluLysGluVal 617
Db 1588 TTGAATCTA----- 1596
OY 618 ValArgLysGluMetSerValLeuGlyAspSerGlyTyrAsnAlaSerAsnSerAspLeu 637
Db 1596 ----- 1596
OY 638 GlnAspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHis 657
Db 1596 ----- 1596
OY 658 ArgLysMetLeuGlnGlnLysIleValAspLeuGlnGluPheIleGluAsnLeuAsnLys 677
Db 1596 ----- 1596
OY 678 LysSerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeu 697
Db 1596 ----- 1596
OY 698 CysGluAlaIleMetAlaGluLysAlaAsnAlaLeuGlnGluLeuAlaLeuMetAlaGAsp 717
Db 1597 -----CTTCTGTGCT 1605
OY 718 AsnPheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuGlu 737
Db 1606 GACTATGATATCTGATATAGACTATGAAACAATCGAACAACAAAAGAAAGAAATGCAA 1665
OY 738 ArgSerLeuLysGluAsnGlnGlnGlnGluThrAsnGluPheGluIleLeuGluLysGluThrGln 757
Db 1666 TTGAATTTAAAGAAAAGAAATGATTTGGATGAAATTTGAGAGCTCTAGAAAAGAAACTTAA 1725
OY 758 LysGluHisGluAlaGlnLeuLeuIleHisGluIleGlySerLeuLysLysLeuValGluAsn 777
Db 1726 AAAGATCAAGAGATGCACTTAATTCATGAAATTTGCAACTTAAGAATTTAGTTAAGCAT 1785
OY 778 AlaGluMetTyrAsnGlnAsnLeuGlnGluAspLeuGluThrLysThrLysLeuLeuLys 797
Db 1786 CGAAGATATATATCAATCAATCTTGGAATGAACTCAGTTCAAAAGTAGAGCTGTAGAA 1845
OY 798 GlnGlnGluIleGlnLeuLeuAlaGluLysArgValAlaAspAsnLeuGlnLysVal 817
Db 1846 GAAAGAGAGAGACAGATTTAGAGAGCTACAGAAATCATAGATCTCAAAAAGCTTAAGAAAT 1905
OY 818 ArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeuCysGluGluThrPhe 837
Db 1906 ATTAATAATGACCTTGTCAATCATG-----GAAAGCATTTGAAGAACCAAAA 1953
OY 838 GlnLeuLysGlnSerLeuSerAspAlaGluAlaValThrArgAspAlaGlnLysGluCys 857
Db 1954 CAAATGAAAGCAGACTCTGTTGATGCTGAAACTGTAGAGCTTTGATGAGCCAAAGAGAAATCA 2013
OY 858 SerPheLeuArgSerGluAsnLeuGluLysGluLysMetGluAspThrSerSerTrp 877

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Db	2014	GCCTTTCTTGAAGTGAATCTGGAGTTGAAGAGAAATGAAGAACTTGCAATACA	2073
Oy	878	TyrAngInGlnYsGluYLeuAlaAlaSerLeuPheGlnYsGlnLeuGluThrGluYLeuSer	897
Db	2074	TACAAGCAAAATGGAAAAATGATATTCAGTTATATCAAGCCAAATTGGAGGCAAAA-----	2127
Oy	898	AsnYrYsYsMetGluAlaAspLeuGlnYsGlnLeuGlnSerAlaPheAsnGluIle	917
Db	2128	-----AAGAAAAATGCAGTTGATCTGGAGAAAGAAATTACAATCGCTTTTAATAGATA	2181
Oy	918	AsnYrYsLeuAsnGlyLeuLeuAlaGlyYsYsAlaProAlaGAspLeuLeuSerAlaGlyAlu	937
Db	2182	ACAAAACCTCACCTCCCTTATATGATGGCAAAATGCCAAAAGATTGGCTCTGTAATTGGAA	2241
Oy	938	LeuGlnYsYsValSerGluPheSerYsGlnLeuGlnYsAlaLeuGlnGluYsLeuAsn	957
Db	2242	TTGGAAAGAAAGATTACTGATCTTCAGAAAGAACTAAATTAAGAATTGAAAGAAATGAA	2301
Oy	958	AlaLeuGlnAsnGluValThrCysLeuSerGluYrYsPheLeuProAsnGluValGlu	977
Db	2302	GCTTTGCGGGAAGAAGATCTTTGCTTCAGAAATTGAAATCTTTACCTTGGAAGTAGAA	2361
Oy	978	CysLeuYsAsnGlnIleSerYsAlaSerGluGlnIleMetLeuLeuYsGlnGluYs	997
Db	2362	AGCGTTAGGAAAGAGATCAAGACAAACTAGAGCGCCATATATATATCAATCAGAAAA	2421
Oy	998	GluHisSerAlaSerAlleSerYsGlnGluIleMetGlnGlnGlnSerGlnGln	1017
Db	2422	GATTAATTTGTTTCTGAAGTAGTTCATAGAGAGTAGAGTAGTTCAAGTTTACTTGAAACA	2481
Oy	1018	IleLeuGlnLeuThrAspGluValThrHisThrGlnSerYsValGlnGlnThrGluGln	1037
Db	2482	ATTGGGAAAAAACAAGATGACCTAGCAACTACACAGTCGAATTATTAAGACACTGATCA	2541
Oy	1038	GlnYrYsLeuGlnMetYsYsMetHisAspAspLeuPheGluYsYrYs-----	1053
Db	2542	GAATTCCAAAATTTCCAAAACCTTCATATGACTTGGACCTTGGACAAAAGTATTAAGATGCTCTT	2601
Oy	1054	-----IleArgAsnYsSerGlnAlaGlnAspLeuAlaGlyGluMetGluAsnLeu	1070
Db	2602	GAGAGAAATGAGAAATGATACAGAAATAGTTAATCTCTTAAGAAAGCCCAAAATTT	2661
Oy	1071	LeuGlnYsThrMetGlnSerValGluValYsIleAlaAspThrYsHisGluLeuGlnGlu	1090
Db	2662	GATTCGAGTTGGGGGCTTGAAGCGAGCGCTTCTTACAGACCCAAAGAACTTCAGSAG	2721
Oy	1091	ThrIleArgAspYsGluGlnLeuLeuHisGluYsYsYrYsPhePheGlnAlaMetGln	1110
Db	2722	AAAAACAGCTGAGCTTCAAGAAAGACTTAATAGATGCAACGTCGAGAAACAATTTGAA	2781
Oy	1111	ThrIlePheProIleThrProLeuSerAspSerLeuProProSerYsLeuValGluGly	1130
Db	2782	AAT-----AGAGATTCTCCGCTGCAAACTGACAAAGGAGAAACACTGATTACTGAG	2835
Oy	1131	AsnSerGlnAspProIleGluIleAsnAspYrYsHisAsnLeuIleAlaLeuAlaThrGlu	1150
Db	2836	AAACTGCGCAAACTTTAGAA-----GAATAAAACTTTAAGTCAAGAAAAAGATGAT	2889
Oy	1151	ArgAsnAsnIleMetValCysLeuGluThrGluYsAsnSerLeuYsGluGlnVal--	1169
Db	2890	CTAAACAAACTCCAAAGAAAGCTTCCAAATTGAGAGGCGCAAACTCAAAAGATGATTCC	2949
Oy	1170	-----IleAspLeuAsnThrGlnLeuGln-----SerLeuGlnAlaGln	1182
Db	2950	GATCTGTTAACATGATATTAATGATATCTCAGAACAACTTACGAAATGCTCTTGAATCTGTG	3009
Oy	1183	SerIleGluYsSerAspLeuGlnYsProYsGlnAspLeuGlnGlnGluGlnGluValYs	1202
Db	3010	AAACAAACATCAAGAAACAATTATATACCTAAATCGAAAAATTCGTGAG--GAATTTCC	3066
Oy	1203	LeuLeuLeuGlnMetGluLeuLeuYsGlyHisIleuThrAsp-----SerGln	1218
Db	3067	AGGAATTTGCAATATGGGAAAAATACAGGAAACCTAAAGATGATTAATTCAGCAAAAGATG	3126

[illegible]

OY	1541	AspAPLeuGlnGlnIleuLeuGluSerLeuSerGluAsnIleIleuLeuGluAsn	1560
Db	4144	GACAACCTTAAACGATAAAGAGAGCCCTTGAAGTTAAACATGACGACCTGAAGACAT	4203
OY	1551	IleAspThrThrLeuLeuSniSniSerAspThrGlnIleGlnLeuGlnIlyThrGlnIln	1580
Db	4204	ATTGAGAGAACTTTG-----GCTAAATATCCAGAGAGCTCAAGC	4242
OY	1581	GluLeuGlnLeuAlaLeuAsnLeuAlaIleAlaIleSerAspAsnCyProIleThrGln	1600
Db	4243	AAACAAGAACGACTCCTTAATATGAAAGAAAAGCAATGAATCAACAAATCGTGAGT	4302
OY	1601	GluIlySglI-----ThSerAlaAspCyValIlnIProLeuGluIlySniIleLeu	1617
Db	4303	GAGATGAGGACCAATTCAAACCCAAAGATTCAGACCATTAAGAGATGAATGAATGCTC	4362
OY	1618	LeuLeuThrGlnGluLeuSniSniGlnIlyThrAsnGlnGlnIlyLeuLeuSniIleGluIlyS	1637
Db	4363	GGATTGCTCCAAAAGACTTCACAAAGAAAGTCATGATGAATGAATCTGTGCTAAGAGAAA	4422
OY	1638	AsnGluLeuGlnGlnIleGlnIleValIleuLeuCySglIValIleGlnIleLeuMetLysSer	1657
Db	4423	GATGACCTTACAGAGCGCTCGAAGAACTTCTCAATGCGAAAGGACCACTC-----	4473
OY	1658	MetIleGluSerLysSerLeuGluSerLeuGlnIlnIleGluIlySniIleAspThrGluGln	1677
Db	4474	-----AAAGAAAACATTAAGAAATTTAGCTTAAACACCTGGAACCTGAAGAGAG	4521
OY	1678	GlnLeu-----LeuAlaLeuSglGlnIlnMetGlnIValIleThrGlnIlyS	1693
Db	4522	GAACTTAAAGTTGCTCATTTGTTGCTGTAAGACCAAGAGAACTATTATGAGTTAAGA	4581
OY	1694	LysGluLeuGlnGlnIlnThrIleSglIlnIleuThrAlaGluValaAspSniLeuGluAsn	1713
Db	4582	GTGAATCTTTGACAGAAAGAA-----ACTGAATATATCAACATTCAAAAGAG	4629
OY	1714	IleGluI-----LeuGluLeuAsnProPheLeuAsnGluValaGlnIlySniThrThrLysGluGln	1732
Db	4630	TTAGAAAGCAATCAATGATTAATTTACAGAAACAAGATTCACAGAGATTATGAGAAAGAGAA	4689
OY	1733	CysLeuLeuAsnGluAsnIlySglIleuGluGlnIlnSerGlnIlnIleSargLeuGlnIlyGluIle	1752
Db	4690	CAATTT-----AATATAAACAATATTGTCAGCTTCAGAAACGTAAT--GAAGCTG	4740
OY	1753	GluGluLeuMetLysSerLeuLysAspLysGluSerAlaLeuGluThrLeuLysGluSer	1772
Db	4741	AAACCAATTCAGAGACATCGCAAAAGCCAAAGATTCAGCATCAACAAAGTAT--	4791
OY	1773	GluGlnIlyValIleAsnLeu-----AsnGlnIlnMetGluMet	1785
Db	4792	GAAAGTAAGATGCTCGAAGTTGACCAACAGACTTCACAGAAAGTCAAGAAATTCAAATTT	4851
OY	1786	ValMetLeuGluMetGluGluLeuLysAsnSerGlnIlnArgThrValIleAlaGluArgAsp	1805
Db	4852	ATGATTTAAGGAAAAAGAGAAATGAAAAAGATACAGAGAGCCCTTCAGATGAGAGAGAC	4911
OY	1806	GlnLeuGlnAspAspLeuArgGluSerValaGluMetSerIleGluThrGlnAspAspLeu	1825
Db	4912	CAACTGAAAGAAAACATTAAAGAAATTTAGCTAAATGAAAAGATTCACAGAA--	4965
OY	1826	ArgLysAlaGlnGluAlaLeuGlnGlnIlnIlyAsnLysAspLysValaGlnIlyLeuThrSerGln	1845
Db	4966	AAAGAAATTCAGTTTCTTAAGATGACAGCTGTCATGATGAGACTCGAGAAAAATGTGGAA	5025
OY	1846	IleSerValLeuGlnIlyLysIleSerLeu-----LeuGluAsn--	1858
Db	5026	ATAGAAACCTTGAAGAGCAATTTGAGACCCAGAAATTAACTCGGAAACATGAGAAACG	5085
OY	1859	-----GlnMetLeuLys--AsnValaIleThrValIlySglIThrLeu	1871
Db	5086	GAGAAATATTAAGCTTGACCTCAAGATCTACATGAACAACTTGAAGAAATGAGATCTGTACA	5145
OY	1872	SerGluArgAspAspLeuAsnGlnSerLysGlnIlnIleuPheSerGluIleGluThrLeu	1891

Db	5146	AAAGAAAGAGTGA	CTTGAAGAGTGTGAGAGGAGACTCTCAAGTGAAGAGACCAAGCTC	5205
OY	1892	SeuSerLeuLysGluLys--	GluDheAlaLeuGluGlnAlaGluLysAspLys--	1905
Db	5206	AAGGAAAACTT	AGAAACCTATACCTATACCTAGACACCTGAAAAAACAAGAGAGCTTAAAAATT	5265
OY	1910	-----Ala	AspAlaAlaArgLysThrIleAspIleThrGluLysIleSerAsn	1925
Db	5266	GTTCACTGCATCTGA	AGAGACCAACCAAACTATTGAT-----AAACTAAGAGG	5318
OY	1926	IleGluGluGlnLeuLeuGlnGlnAlaThr	AsnLeuLysGluThrLeu--TyrGluArg	1944
Db	5317	ATTGTTTCAGAGAAA	CAAAATGAAATATCAAAATATGCAAAAGCACTTGAACACCTCAAT	5376
OY	1945	GluSerLeu-----	IleGlnCysLysGluGlnLeuAlaLeuAsnThrGluHis	1966
Db	5377	GATGCTTAAAGCA	CAGAGACTGTGAAATATACAAAGAGAACTAAGATTGCTCACATGCAT	5435
OY	1961	LeuArgGluThrLeuLysSerLysAspLeuAla	LeuGluLysMetGluGlnLysArgsp	1988
Db	5437	CTGAAGAGCAGCAG	GAACCTATTGACAACTCAGAGGAATTTGTTCTGAGAGACACAT	5496
OY	1981	GluAlaAlaAsnLysValIleAlaLeuThr	GluLysMetSerSerLeuGluGlnIle	2000
Db	5497	AAACTATCAAAATATG	CAAAAAGATTGAAAAATTCAAAATGCTAAATTCAAGAAAAAGATT	5556
OY	2001	AsnGluAsnValThrThrLeuLysGluGlnGluGluGlnGluLysGluThr	PhetYrLeuGln	2022
Db	5557	CAAGAA-----	CTTAAGCAAAATGAACATCACTTATTACCTTAAAAAAGAT	5608
OY	2021	ArgProSerLysGlnGlnSerSerGlnMetGluLeuLeuArgGluSerLeuLysThr		2040
Db	5605	GTCATATGAGACAC	AGAAAAAGTGCTGAAATATGAGCACTTAAAGAAAACAATATAAAGAC	5664
OY	2041	LysAspLeuGlnLeuGluAlaGluLysIleSerGluAlaThr	AsnGluLysLys	2066
Db	5665	CAAAAGCTTAAC	TCTGAGTAAATA-----GAAATTAAG	5697
OY	2061	AsnLeuThrAlaLysIleSerSerLeuGlnGluGlnIleLeuGlnAsnAlaSerIleLeu		2080
Db	5698	AATTTA-----	AATTGGCTCAAGAACTTCATGAAACTTGAAGAAATG	5742
OY	2081	AsnGluAlaValSerGluArgGluAsnLeuArgHiserLysGlnGlnLeuValSerGlu		2100
Db	5743	AAATCTGTAAAGAA	AGAAAGAAATCTTAAGAAAGATGAGGAGACCTCAAACTGGAG	5802
OY	2101	LeuGlnGlnLeuSerLeuThrLeu-----	LysSerArgAspHisAlaPheAlaGln	2117
Db	5803	AGAGACCACTCA	AGGAAGCGCTCCAGAAACCAAGAGTAGAGATCTCGAAATATCAACAG	5866
OY	2118	-----	SerLysArgGluLys-----AspGluAlaVal	2128
Db	5863	GAACATAAAAC	TGCTGTATGCTATCAAAACAAACAAAGAAACGTGTTGAATATCTTAGA	5922
OY	2127	AsnLysIleAlaSerLeuAlaGluGlnIleLysIleLeuThrLysGluMetAspGluPhe		2146
Db	5923	GAAAAAATTTAG	AAAAAGACATTTCAAAATTTTCAGACATTCAAAGAGATTTAGATAA--	5979
OY	2147	ArgAspSerLysGluSerLeuGlnGlnGlnSerSerHisLeuSerGluLeuCysThr		2166
Db	5980	-----TCAAAAGATGA	ATTATCAAGAAAAAGATCCAAAGAACTTCAG-----	6018
OY	2167	TyrLysThrGluLeuGlnMetLeuLysGlnGlnLysGluAspIleAsnAsnLysLeuAla		2186
Db	6019	-----AAAAAGAACTT	CAACCTGCTTAGA--GTGAAAGAGATGTCATATATGAGT--CAT	6069
OY	2187	GluLysValLysGluValAspGluLeu-----		2189
Db	6070	AAAAAAATTTATGA	AAATGAAGAACTTGAAGAGCAATTTAGCCAAATCTATCTATGCAG	6129
OY	2196	-----LeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGln		2210

Db 6130 TGTGATGATGAATCACTTCAGTGAAGAACTTCATGAAAGCTTGAGAAATAGA 6189
 Qy 2211 MetGluLeuArg---AsnGluIysLeuArgAsnTyrGluLeuGlyMetAspIle 2229
 Db 6190 ATTGTAGCTAAAGAAAGAGATAGCTTAAGAGAGATAAAGAAATCTCTCAAAATGGA--- 6246
 Qy 2230 MetGluIysGluIleSerValLeuArgLeuMet-----Gln 2241
 Db 6247 AGGACCAATTCATTCAGCAACCTTAAGGGAATGATAGCAGAGACCGACAGAACCACTCA 6306
 Qy 2242 AsnGluProGlnGlnGlu-----GluAspAspValAlaGluArgMetAspIleGluGlu 2259
 Db 6307 GTAAACCTCGAAGAAAGCTTACTTAAGTGAACAACAGACCTTAATGAAAGCCCTGAGA 6366
 Qy 2260 SerArgAsnGlnGluIleGlnGluMetGluIysIleSerAlaValTyrSerGluGln 2279
 Db 6367 GAAAGAGCTCTAGAATAAAGAGCTTTGAAAGAGTACTCAGAGTGTG---GATGATCAT 6423
 Qy 2280 HisThrLeuSerSerLeuSerSerGluLeuGlnIysGluThrGluAlaHisIysHis 2299
 Db 6424 TATGAGTCTTAATAGATTTCTCTCTGACTTGAGAGAGAAATTTGAATTCACAGAG--- 6480
 Qy 2300 CysMetLeuAsnIleIysGluSerLeuSerSerThrLeuSerArgSerPheGlySerLeu 2319
 Db 6480 ----- 6480
 Qy 2320 GlnThrGluHisValIysLeuLeuAsnThrGlnLeuGlnThrLeuLeuAsnIysPheIysVal 2339
 Db 6481 -----ATCATGAGAAAGTGAAGTAT 6501
 Qy 2340 Val-----TyrArgThrAlaAlaValIysGluAspHisSerLeuIleIysAspTyrGlu 2357
 Db 6502 GTGTTAAGCTATGTTATCAAAAATTAAGAGAAACACATGATGCATCAATAATTGAA 6561
 Qy 2358 LysAspLeuAlaIleGluGlnIysArgHisAspGluLeuArgLeuGlnLeuGlnIysLeu 2377
 Db 6562 ATGATTTTATGATGAAGTGAAGAAAGCAAAAGATTCCTAATTAATAACAGACCTT 6621
 Qy 2378 GlnGlnHisGlyArgIysTyrSerPheSerAlaSerGluGluLeuIysPheCysGluIle 2397
 Db 6622 CAACAAAGAT-----TGATATGACCATCCAGAGAAATTAAGGATCTCAAAATG 6669
 Qy 2398 GluPheLeuAsnGluLeuLeuPheIysIysAlaAsnIleIleGlnSerValGlnAspArg 2417
 Db 6670 AACCAAGATATGGAATCTA-----CATATGAGAAATTTCTCAAAAGT 6711
 Qy 2418 PheSerGluValGlnValPheLeuAsnGlnValIysSerThrLeuGlnGlnIysLeuGlu 2437
 Db 6712 TTCTCAGAAAGTGAAG-----TTCCTAGCAATAAAGACTGAATTTCAACAAGTACTTAA 6765
 Qy 2438 HisIysIysGlyPheMetGlnTyrPheGluGlnIysPheGlyAspLeuHisValAspAlaIys 2457
 Db 6766 AATAGAAAGAAATGACACAGATTTTGGAGAGTGTAAATATCTGTTTGATATAGA 6825
 Qy 2458 LysLeuSerGluGluMetGlnGlnGlnIysAsnArgGluIleAlaSerThrIleGlnLeuLeu 2477
 Db 6826 AAGCTTAAATAATGCGATCCAGAAAGAAATGATAGAGATTTGTCAAGTGAATAACTTCTT 6885
 Qy 2478 ThrIysArgLeuIysAlaValAlaGlnSerIysIle-----GlnArgGluIleThr 2494
 Db 6886 AATAACAGATATATGCTCATATATGAATGAATCAACAGACTTTGAGAGAAAGAGTCTTACC 6945
 Qy 2495 ValTyrLeuAsnGlnPheGluAlaIysLeuGlnIysValIysGluGlnAsnIysGluLeu 2514
 Db 6946 ATA---TCCAAAGAGTGGGAACAGACCTGAATATCACTGAAGAGAAATAATGAATACTGA 7002
 Qy 2515 MetArgGluMetGluHisIleGlyProSerAlaSerValMetGluGlnGluAsnAlaArg 2534
 Db 7003 TTTAAACCACTCAACAACTTGAAGACTTCTTGCGATCTGCTGCCAGGTAAAT----- 7056
 Qy 2535 LeuLeuGlyIleLeuLeuThrValGlnAspGlu-----SerIysIys 2548
 Db 7057 -----CTTACACACAGACATAGAAATCTCATGTTATCATCAAGACT 7101

Qy 2549 LeuGln-----SerArgIleIysMetLeuGluAsnGluLeuAsnLeuValIysAsp 2565
 Db 7102 ACACGTTTAACACACAGAAATAATTCAGAGCTGGAAATTCATCTCATGAACTTAAGAA 7161
 Qy 2566 AspAlaMetHisIysGlyGluIysValAlaIleLeuGlnAspIysLeu---LeuSerArg 2584
 Db 7162 AGTCTTATGCATTAAGAAAGCAAGATTTAAAGATGACGAAGAAAGAACTTGAGTGAAT 7221
 Qy 2585 AsnAlaGluAlaGluLeuAsnAlaMetGlnValIysLeuThrIysIysGlnAspAsnLeu 2604
 Db 7222 GACATATATGCAAACTT-----CAAGCCAAAGTCTGATCAATTAATGCTTT 7272
 Qy 2605 GlnAlaIleMetIysGluIleGluLeuLeuGlnIysMetValAlaIysGluValAlaPro 2624
 Db 7273 GAAAAAAGAAAGACAACTTCAACTCTCAGCAAAAGTCTTGTGAGACTTAAGCCA 7332
 Qy 2625 TyrIysGluGluIleAspAsnLeuIysThrIysValValIysIleGluMetGluIysIle 2644
 Db 7333 TATAAGAAAGAAATTTGAAGATCTCAAAATGAAGCTTGGAATAATGACCTGAGAGAAATG 7392
 Qy 2645 LysTyrSerIysAlaThrAspGlnGluIleAlaTyrLeuIysSerCysLeuGluAspIys 2664
 Db 7393 AAAAATGCCAAAGAAATTTGAAGAGAAATCAGTCTACAAAGCCACTGTAATATATCA 7452
 Qy 2665 GlnGluGluIysLeuArgArgLeuIysGluGluIysArgAlaGlnAlaAspAsnAspThr 2684
 Db 7453 AAGGAAGTTATAGGCTATTAAGAGAAATTCAGAAAGAGCAACAGCCCAAGATACCC 7512
 Qy 2685 ThrValCysValProIysAspTyrGlnIysAlaSerThrPheProValThrCysGlyGly 2704
 Db 7513 TCAGTGAATATGAAACATACATGATCTTCAGGCTTCAATTAACCTTAACTTGTGAGCT 7572
 Qy 2705 GlySerGlyIleValGlnSerThrAlaMetLeuValLeuGlnSerGluIysAlaLeu 2724
 Db 7573 GCGACGCGCATTTGTAACAAACAAAGCTCTTATTTTGAAGAAAGCAATAGAGCTA 7632
 Qy 2725 GluArgGluLeuSerHisTyrIysIysIysArgIysHisIleLeuSerArgThrMetSerSer 2744
 Db 7633 GAAAAAGAAATTTCTAAGTTAAAGCGCAAAATGAACAGCTA----- 7674
 Qy 2745 SerGluAspArgIysIysThrIysAlaIysSerAspAlaHisSerSerHisThrGlySer 2764
 Db 7675 -----ATTAACCAAGATGAATGTTTAAGCAATATACAGATCTT 7716
 Qy 2765 SerHisArgIysSerProHisIysThrGluThrTyrArg-----HisGlyProVal 2781
 Db 7717 TCCATGAGTCAAAACTTGGAGAGAAAGAACCTTAATAAGAGAGCTCACAAACAGTA 7776
 Qy 2782 ThrProGluArgSerGluMetProSerLeuHisIleuGlySerProIysIysSerGluSer 2801
 Db 7777 ACTTGCTGAG-----AATTTCTCAAG----- 7797
 Qy 2802 SerThrIysArgValIserProAsnArgSerGluIleTyrSerGlnLeuValMetSer 2821
 Db 7798 -----TCT 7800
 Qy 2822 ProGluIysThrGlyMetHisIysHisIleLeuSerProSerIysValGlyLeuHisIys 2841
 Db 7801 CCTTAAGTACTGGAACA-----GCTTCTTAA 7827
 Qy 2842 LysArgAlaLeuSerProAsnArgSerGluMetProThrGlnHisValIleSerProGly 2861
 Db 7828 AAGAAACAAATTAACACC----- 7845
 Qy 2862 LysThrGlyLeuHisIysAsnLeuThrGluSerThrLeuPheAspAsnLeuSerSerPro 2881
 Db 7846 -----TCTCA 7851
 Qy 2882 CysIysGlnGlnIysValGlnGluAsnLeu-----AsnSerProIysGlyIysLeuPhe 2899
 Db 7852 TGCAAGGAAGCAAGATTTTCAAGATCTCTGTGCCAAAGAAATCACCAAAATCTTGTTTT 7911

QY 2900 AspValLysSerLysSerMetProTyr---CysProSerGlnPhePheAspAsnSerLys 2918
 Db 7912 GATACCCGATCAAAAGCTTTTACCATCACCCTCATCCAGTTCGCTATTGTAATACTCAAGT 7971
 QY 2919 LeuGlyAspPheSerGluLeuAsnThrAlaGluSerAsnAspLysSerGlnAlaGluAsn 2938
 Db 7972 TTAGCCCTTTGCCAGAGGTGCMAAATGCAGAGCAGAGAGTTCGATTCTCAGCCAGCT 8031
 QY 2939 TrpTyrGluAlaLysGluGluThrAlaProGluCysLysThr 2953
 Db 8032 CCTTGACAGCCCTCCTCAGCAAGAGATGTGCTGATGCAAACT 8076
 RESULT 5
 US-09-960-253-145
 ; Sequence 145: Application US/09960253
 ; Patent No. US20020123619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Mohamed, Michael J.
 ; APPLICANT: Mohamed, Michael J.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.556
 ; CURRENT APPLICATION NUMBER: US/09/960,253
 ; NUMBER OF FILING DATE: 2001-09-20
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 145
 ; LENGTH: 10300
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-960-253-145

Alignment Scores:
 Pred. No.: 1.6e-63 Length: 10300
 Score: 1153.00 Matches: 675
 Percent Similarity: 39.53% Conservative: 651
 Best Local Similarity: 20.13% Mismatches: 1170
 Query Match: 7.81% Indels: 858
 DB: 10 Gaps: 138

US-09-724-584-1 (1-2954) x US-09-960-253-145 (1-10300)

QY 110 GluValPheLysIleIleGlnGluIleProAsnArgGluPheLeuLeuArgValSerTyr 129
 Db 559 GAAATGAAAGATTAAACATAAGCTCCAGAGAGAGAGAACTATC----- 606
 QY 130 MetGluIleTyrAsnGluThrValLysAspLeuLeuCysAspAspArgLysLysPro 149
 Db 607 -----AGCACTTGCAGGCCAGCTTACTCAGGACAGGACAGCAACAACCT 651
 QY 150 LeuGluIleArgGluLysPheAsnArgAsnValTyrValAlaAspLeuThrGluGluLeu 169
 Db 652 GCACAGAGTTCACAGAGATG-----GAAAGATT 681
 QY 170 ValMetValProGluHisValIleGlnThrLysLysGluLysAsnArgHisTyr 189
 Db 682 GTTAATGATCAACCAACAGCTC-----CAGGAGAAGAGAAATTCTT 723
 QY 190 GlyGluThrLysMetAsnAspHisSerSerArgSerHisThrIlePheArgMetIleVal 209
 Db 724 AGCACTTTACAAAGCCAGCTCAGCCAGACACAGGAGCAAGCTGCACACAGAGTGTCTC 783
 QY 210 GluSerArgAspArgAsnAspProThrAsnSerGluAsnGlyAlaValMetVal 229
 Db 784 CGAGAGAAAGATGCCCGTTGAAACACACAGATGCTCTTCAAGAGATGAGCTT----- 837
 QY 230 SerHisLeuAsnIleValAspLeuAlaGluSerGluArgLysArgGlnThrGlyAlaGlu 249
 Db 838 -----CTTCAAGTATTAACCCAGCAGATGTGAGACAGAGATGCAA----- 879
 QY 250 GlyValArgLeuLysGluGlyCysAsnIleAsnArgSerLeuPheIleLeuGlyGlnVal 269

Db 880 -----CAGAAATTGAGGCTGTCGCAAGAG 906
 QY 270 IleLysLysLeuSerAspGlyGlnAlaGlyLysPheIleAsnTyrArgAspSerLysLeu 289
 Db 907 CTGGAGAAACAGAAAGAACTTGTGTGGC-----CGTGCTCAGTTC 948
 QY 290 ThrArgIleLeuGlnAsnSerLeuGlyGlnAlaLysThrValIleIleCysThrIle 309
 Db 949 GTTGACTTCTGCAACAGAGCTGCTGCTGTCGAGAGAA----- 990
 QY 310 ThrProValSerPheAspGluThrLeuSerThrLeuGlnPheAlaSerThrAlaLysHis 329
 Db 991 -----AACAGATTCTCTCTCAGCAGCTTACAGCAGATGGAAGCTGAGCAT 1035
 QY 330 -----ValArgAsnThrProHisValAsnGluValLeuAspArgGluAlaLeuLys 347
 Db 1036 AATACTTGAAGAACACTGTGAA--ACAGAAAGAGAGAGTCCAAAGATTCTACTGGA 1092
 QY 348 ArgTyrArgLysGluIleLeuAspLeuLysLysGlnLeuGluAsnLeuGluSerSer 367
 Db 1093 AAGATGAACTTGAAGTGCAGAGAGAAATTTATCTTCCATTAATCTGCGAAGAAATC 1152
 QY 368 -----GluThrLysAlaGlnAlaMetAlaLysGluGluHisThr 380
 Db 1153 CATGATCTTTTGAACAGATTGACCAAGCAGGCCAGCCAGCTGAAGTAACTAGAG----- 1206
 QY 381 GlnLeuLeuAlaGluIleLysGlnLeuHisLys---GluArgGluAspArgLysThrHis 399
 Db 1207 TCTGGTATAGTCTCTTGGAGCAGACAGCAAGCAAGAAATGAGAGAGAGCTTCTCAT 1266
 QY 400 LeuThrAsnIleValAlaLysSerGln----- 409
 Db 1267 ATTTGAGTCTTCAAAAGACTGCACAGAGCTGCAGTCTGCTGATGCTTAAAGAT 1326
 QY 410 -----GluSerGlnGlnAspGlnArgValLysArgLysArgVal 423
 Db 1327 CAAAATTCAAAGCTTCTCCAGATTAAGATGAACAGGACCTTCAGCAGCCAGACATT 1386
 QY 424 ThrTrpAlaProGluLysIleGlnAsnSerLeuHisLysSerGlyValSerAspPheAsp 443
 Db 1387 CAGCACTGGAAGATCAAGCTCCAGCAAAA-----TCCAAAGAAATTTGCCAATTT--- 1437
 QY 444 MetLeuSerArgLeuProGluLysAsnPheSerLysLysAlaLysPheSerAspMetProSer 463
 Db 1438 ---CTAATAGACTGCC-----TTGCAACAACATGAAGAACACACTCTCAGACTCT 1485
 QY 464 PheProGluIle-----AspAspSerValCysThr--- 473
 Db 1486 TTCCAGATGTTTATATGAGGACACAGGCCAGTCACTGAGAGAAATTCCTTCTTTG 1545
 QY 474 -----GluPheSerAspPheAspAspAla-----LeuSerMetMetAsp 486
 Db 1546 CAGAGAGAGTGTAGATGATGAGATGAAGAGGAGCTTGTCTCTTATAGAG 1605
 QY 487 SerAsnGlyIleAspArgLys---TrpAsnLeuAlaSerLysValThr----- 501
 Db 1606 CTGAGAGAGCTGAAGCTGAATGAATGAATGAATGATGCTTCTCAGATTACTCTCTAGAGCT 1665
 QY 502 -----HisArgGluLysThrSerLeuHisGlnSerMetIleAsp 514
 Db 1666 CAGAAATAGAACTGGGAGGACAGACAGAGAAAGTCAAGTGAATC-----AGCTTTTAT 1719
 QY 515 Phe-----GlyGlnIleSerAspSerValGln 523
 Db 1720 ATTGCCAACAGAGAGCTTTCTGTGAGAAAGTGAACAA-----GATGTTCTAAGAA 1773
 QY 524 PheHisAspSerSerLysGluAsnGlnLeuGlnTyrLeuProLysAspSerCylAspMet 543
 Db 1774 AACACATTTTCTCAGAAACATTAAGATTAATAGTTTA-----TTG 1815
 QY 544 AlaGluCysArgLysLysSerPheGluLysGluIleThrSerLeuGlnGlnLeuGln 563
 Db 1816 TTGAAATGAAGAGAGCT-----CAAGAGAAATTCATTTCTTAATTAACAGCTCAG 1869

QY 564 SerIys-----GluGluGluIuIySlySgluIeuValGlnSerPheGluIeuIleAla 581
 DB 1870 GGAAGGAGGGCTGAGAGCAGATCATGAGGCTCTTGACCAAGAAAGAAAGAGATG 1929
 QY 582 GluLeuGluGluGlnIeuSerValIySAlaIyS-----Aen 593
 DB 1930 GAGGGGTAGGAAATAGCTCCATTTAAATGAAAGTATTTCTTAAGATACAGGCAAGT 1989
 QY 594 LeuGluMetValThrAsnSerArgGluHisSerIleAsnAla-----GluValGlnThr 611
 DB 1990 TTCCCTTAATGCCAAAT--GAAGAGACAGCTCTCCAGACGTTGAAAGAAAGACAGGGC 2046
 QY 612 AspValGluIySgluValValArgIySgluMetSerValIeuGluIySAspSerGlyThrAn 631
 DB 2047 AGCACTGAACATCAAGTAGAAATCTGAGAAATATCTTTAAATATGCTGGAGTA--- 2103
 QY 632 AlaSerAsnSerAspLeuGlnAspSerSerValAspGlyIySArg----- 646
 DB 2104 -----GAATTGAATCAACAAGACAGATGGTATTAATCCTTCTGCTGA 2151
 QY 647 -----LeuSerSerSerHisAspGluIySleGlu----- 656
 DB 2152 CCAGATATTGTCAGTGTCTATCAGATGATGTGAAAGGTTAAAGTCAAATTTTGAG 2211
 QY 657 -----HisArgIyMetIeuGluIyS--- 664
 DB 2212 CTCGACTTAACCTTTCATTAAGACACAGAAATCTATGAGAAATTAATATAGAAAGCT 2271
 QY 665 -----IleValAspLeuGluGluPheIleGluAsnLeuAsnIySAspSerGluAsnAsp 682
 DB 2272 AAGAAATTAAGCACTTAACCAAGTTGATGAGAGACTTAAAGAAATGCTGACAAAC 2331
 QY 683 IySgluIyS-----SerSerGluGlnAspPheMetGluSerIleGlnIeuIyS 698
 DB 2332 AGCAGTGCATTCAGCTCTTGTCTGTAAGAAAGACAGCTCTCTCT---CAGGTGAG 2388
 QY 699 GluAlaIleMetAlaGluIySAlaAsnAla---LeuGluGluIeuAlaIeu----- 714
 DB 2389 GAACCTTAGCATGTAAACGAATTAGAGGCTCAGGTAAACCACTGGAATTAACCTTGCA 2448
 QY 715 -----MetArgAspAsnAspAsnIleIle 723
 DB 2449 GAGCAAGAAAGCAAGAAAGACTTGTATTGAAAGCAATGCTCCATGACAACTGCTGC 2508
 QY 724 LeuGluAsn----- 728
 DB 2509 ACTGAACAGATCCATAGTCTCAGCATAGAAAGCAATTAAGATGTGAAATTTGAAGT 2568
 QY 729 LeuIySArgGluIleAlaAspLeuGlu-----Arg 738
 DB 2569 TTACAGAAATGAACCTGATGATGTGCAGCTTTCAGTCTGAGCAGAGTACCTGATTA 2628
 QY 739 SerLeuIySgluAsnGlnIuThrAsnGluPheGluIleGluGluIySgluThrGlnIyS 758
 DB 2629 ACCCTGCAAGCCAGCTGCAGAAATTAAGAAAGTGAAGCTTGAAGGGGCGACAACTGTA 2688
 QY 759 GluHisGluAlaGlnIeuIleHisGluIleGlySerLeu-----LysIySLeuValGlu 776
 DB 2689 AGGCATATCTCAAGTAAAGTGAAGAACTGCCAGACCTTTCAACAGAAAGAACTGGA 2748
 QY 777 AsnAlaGluMetIySAsnGlnAsnLeuGluIyS-----AspLeuGluThrIySThrIyS 794
 DB 2749 ATTAACAAGAAATGATCAGCTCTTACTAGAAAGAAAGAGATGTGAAACCTCCAAACA 2808
 QY 795 LeuLeuIySgluGlnGluIleGlnIeuAlaGlu----- 805
 DB 2809 ACCATGAGAGAGAGATCAACAAGTACAGAAATAGCTTTAGTACTGAGAAATG 2868
 QY 805 ----- 805
 DB 2869 GTTCAGCTTAATGAGAGAGATTTTCTTGGGGTTGAATTAAGACTCTTAAGAAACAG 2928

QY 806 -----LeuArgIySArgAlaAspAsnLeuGlnIySlyValArgAsnPheAspLeuSer 823
 DB 2929 CTAAATTTATTTATCCAGAGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2988
 QY 824 ValSerMetGlyAspSerGluIySleuIySgluGluIlePheGluIeuIySgluSer--- 842
 DB 2989 GTTCTCTTCGCG-----CTTAAACAAATATAT 3015
 QY 843 -----LeuSerAspAlaGluAlaValThrArg---AspAlaGlnIySgluIySAspPhe 859
 DB 3016 GATGAGATGAGCCACAGCAGCAATTAAGTAAAGAAAGTTCACATGATTAATTTGACTT 3075
 QY 860 LeuArgSerGluAsnLeuGluIeuIySgluIySmet----- 871
 DB 3076 CTGAAGAAAGAAATGACAGCAAGAAAGAAAGCTCCAGCAGCTTTATTAAACAGAAAG 3135
 QY 872 -----GluAspThrSerAsnTrpIySAsnIyS 881
 DB 3136 GAGCTTCTGCAAGAGTCAGTAGATTGGAAGAAATTAAGCACTTGAAAGATGAAATCT 3195
 QY 882 GluIySAlaAlaSerLeuPheGluIyS-----GlnLeuGluThrGluIySAsn 898
 DB 3196 AAGAAAGAAATCCACCTCAGTACAGTACAGAGGAGAAAGTGAAGAAATTAAGAAAG 3255
 QY 899 TyrIySlyMetGluAlaAspLeuGlnIySgluIeuGlnSerAlaPheAsnGluIleAsn 918
 DB 3256 AAGAAATCTCAGAA-----AAATGTGACTTCTTAAGTCCAAAGAAATTAAGAA 3303
 QY 919 ---TyrLeuAsnGluIySleuAlaGluIyS-----ValProArgAsp 931
 DB 3304 ATTTATTTTAAACAGACATATCTGAGAAAGAAAGTGAACCTACACATTAAGAAAGAT 3363
 QY 932 LeuLeuSerArgValGluIeuGluIySlyValSerGluPheSerIySgluIeuGluIyS 951
 DB 3364 TTGGAAGAAAGCTGCAGCTGAGAGCAATTCACGCTCTGTCGAAACAGATGATCA 3423
 QY 952 AlaIeuGluGluIySAsnAlaIeuGluIySAsnIySValThrCysLeuSerGluIySlyPhe 971
 DB 3424 ACCTTGCAAGATTAACA----- 3441
 QY 972 LeuProAsnIySAlaGluIySlyValAsnGlnIleSerIyS----- 985
 DB 3442 -----AACCAATAGATTGCTCCAGCAGCAATTCAGTGAAGAAACCAAGCAATTTCCAG 3495
 QY 986 -----AlaSerGluGluIleMetLeuLeuIySglu 995
 DB 3496 AAGTTAATCACAAGTAAACAGATGCAAGTATGAGGAGCTCCGCTGACACTTTGAAGAA 3555
 QY 996 GluGluGlnHisSerAlaSerIleIleSerIySgluGluIleIleMetGlnGluIySAsn 1015
 DB 3556 ACAGTGTGATTAAGTCCACCTTTGTACAGTACTAGTAACACTGGAACCAAGAACTAGAA 3615
 QY 1016 GluGlnIleLeuGlnIeuThrAspGluValThrHisThrGlnSerIySlyValGln----- 1033
 DB 3616 GAAAGATATCTGCCCTTGAAGAAAGAAAGCAAACTTCAAAAGACGTACAGAAAGCC 3675
 QY 1034 -----GlnThrGluGluGlnIySleu----- 1040
 DB 3676 TTAACCTCCCGCAAGCAATTTTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3735
 QY 1041 GluMetIySlyMetHisAspAspLeuPheGluIySlyThrIleArgAsnIySAspSerGluAla 1060
 DB 3736 GAGCTTAAGCAACAGAAAGATGAC-----TATTAATGCTTGCAGAAACAGATT 3783
 QY 1061 GluAspLeuLeuArgIySmetGluAsnLeuIySgluIySmetGluSerValGluValIyS 1080
 DB 3784 GATGAGCAAGCAAGCAAGAAATAGAAATATGAGACCAAGCTTAAGCAACTCCAGATTCA 3843
 QY 1081 IleAlaAspThrIySHisGluIeuGluGluIuThrIleArgAspIySgluIleuIeuHis 1100
 DB 3844 GTTAAGGAAATCC----- 3855
 QY 1101 GluIySlySlyThrPhePheGlnAlaMetGlnThrIlePheProIleThrProLeuSerAsp 1120


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Db      3856 -----ATGACGGA 3864
QY      1121 SerLeuProSerLeuValGluGlyAsnSerGlnAspProIleGluIleAsnAsp 1140
      |||||  ::|||  |||  |||
Db      3865 AACTCCAGACACAGCCAGCAATCGTGTCTTCCACTCA-----GGT 3912
QY      1141 TyrHisAsnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThr 1160
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      3913 TTAGAAGAACTTATTCAAGCCACAGAACACATCACACTCACTGTTTAGAGTCC 3972
QY      1161 -----GluArgAsnSerLeuLys-----Glu 1167
Db      3973 AACTGTGCCAGACGTGGCTTCTCACTTGTGAAGATCGAGTCTGTGACGGCGGAAGT 4032
QY      1168 GlnValIleAspLeuAsnThrGlnLeuGlnSerLeuGlnAlaGlnSerIleGlu----- 1185
      |||||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4033 TCTGTTGCCAGATTAAAGCCCGACGTGAAGAAATAGAGCTTGAAGAAAGATTAGAA 4092
QY      1186 -----LysSerAspLeuGlnLysProLysGlnAsp-----Leu 1196
Db      4093 TTGAAGATTAGTTCTCAACAAGTAGAGCTTACTTAAATAATCAGAAAGAGATTTCAGTTA 4152
QY      1197 GluGluGluGlyValValLysLeuLeuLeuGluMetGluLeuLeuGlyHisLeuThrAsp 1216
      |||||  |||||  |||||  |||||  |||||  |||||
Db      4153 CAGAGCACAGATTAAATATAACAGGGTTTAAAGATCGAAGATCTTAAAGACATATCCATGAA 4212
QY      1217 SerGlnLeuSerIleGluLysLeuGlnLeuGluAsnLeuGluValThrGluLysLeuGln 1236
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4213 GCTGAAGTCCATGCCGAAAGCCCTGCAG-----CAGAAATTTGGA 4251
QY      1237 ThrLeuGluGluGluMetLysAsnIleThrIleGluArgAsnGluLeuGlnThrAsnPro 1256
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4252 ACCAGCCAACTCAAAATGTGCTGCTAGAACATCTAAGA---GAATGCAACCTTAAACG 4308
QY      1257 GluAspLeuLysAlaGluHisAspSerLeuLysGlnAspLeuSerGluAsnIleGluGln 1276
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4309 GATGAATCTCAAAACTCTAATAGCAAAAGAAAGAAAGAGCTTAAAGCTTCTTGACAA 4368
QY      1277 SerIleGluThrGlnAspGluLeuArgAlaAlaGlnGluGluLeuArgGluGlnLysGln 1296
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4369 CTTAGTGAGAAAGAACACAGCTCTCAATAAATACACAGAGATATATAGAACAGAAAGT 4428
QY      1297 LeuValAspSerPheArgGlnGlnLeuLeuAspCysSerValGlyIleSerSerProAsn 1316
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4429 TTAAATTAAAGCTCTGCATACACAGCTA-----GAATGCAACCCAAAGAG 4473
QY      1317 HisAspAlaValAlaAsnGlnGluLysValSerLeuGluGluValAsnSerLeuGlnSer 1336
      |||||  |||||  |||||  |||||  |||||  |||||
Db      4474 CATGATGAGAGATTAAAGCAGCTACAGGTGAACTTTGTGAATAGAACAAACCAGAA 4533
QY      1337 GluMetLeuArgGlyGluArgAspGluLeuGlnThrSerCysLys-----AlaLeu 1353
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4534 GAGATTGAGAAAGAAAGTAGACAAAGCAAAATACAAAGAAACCTGACCTGCCCTT 4593
QY      1354 ValSerGluLeuGluLeuLeuArgAlaHisValLysSerValGluGlyGlu----- 1370
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4594 ATTTCCCGAAAGAAAGCACTAAAGAAAC---AAAGTCTCAAGAGAAATGTCTTTG 4650
QY      1371 -----AsnLeuGlu---IleThrLysLysLeuAsnGlyLeuGlnLysGlnIleLeu 1386
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4651 GCCAAGAGTACCATTTGAACGTCTCACCAAGTCTCTGGCAGATGTGGAAAGCCAAAGTTTCT 4710
QY      1387 GlyLysSerGluGluSerGluValLeuLysSerMetLeuGluAsnLeuLysGluAspAsn 1406
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4711 GCTCAAAATTAAGAAAGATACGGTCTTAGAAGTTAGCTCTTCTTCAAGAAAGAAAGA 4770
QY      1407 AsnLys-----LeuLysGluGluAlaGluGluIleThr 1417
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4771 GACCAAACTCATTAAGAAATGACAGGTCTTATTGAAATCAAGAGTCTCAGCAGCTCC 4830
QY      1418 SerLysGluAsnGlnPheSerLeuGluGluValPheSerGlySerGlnLysLeuValAsp 1437
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
      *  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||

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Db      4831 TGTGAAGCTTAAAACTAGCTCTAGAGGGTCTTACTGAAGACAAAGAAAAGTTAGTAAG 4890
QY      1438 GluIleGluValLeuLysAlaGlnLeuLysAlaIleGlu-----GluArg 1452
      |||||  |||||  |||||  |||||  |||||  |||||
Db      4891 GAATTGTAATCTTTAAATCTTTCT---AAGATTGCAGAAAGTACGTAGTGCAGAGAA 4947
QY      1453 LeuGluIleLysAspArgAspThrPheGluLeuValGlnThrAlaAsnThr----- 1469
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      4948 CACAAGGAGCTACAAAGAGATGAATAATCTTTCGACGTCTATGAGATGTTAGTAAT 5007
QY      1470 -----AsnLeuValGlu----- 1473
Db      5008 GAAGCAAGAAAGATTACACATGTGTGGAGCTGTGACGCAAGAAACAAAGACTGTAT 5067
QY      1474 GlyLysLeu-----GluThrProLeuGlnAlaAspHisGlu 1485
      |||||  |||||  |||||  |||||  |||||  |||||
Db      5068 GCGCAATTAAGACAGACAGAGCAACAAAGAAAGAGACAGAAAGCACTGTGCAGAACT 5127
QY      1486 GluAspSerIleAspArgArgSerGluMet----- 1496
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5128 GAGCAAGAAATGAGAGAAATGAAAGAAAGATGAGAAAGTTGCTTAATCTAAACAGCAG 5187
QY      1497 -----GluIleLysValLeuGly 1502
Db      5188 AAATCTTAGAGCTGAAGAAAGAAAGATGACCGGCTTAGGCGAGAGGTGCACCTGCAGGA 5247
QY      1503 GluLys-----LeuGluArgAsnGlnTyrLeuLeuGluArg 1514
      |||||  |||||  |||||  |||||  |||||  |||||
Db      5248 GATACAGCTAAAGAGTAGTATGGAACACCTTTCTTCCATGCGCAGATAGAAAGAA 5307
QY      1515 LeuGlnGluGluLysLeuGluLeuSerAsnLysLeuGluIleGluGlnLysGluMetGlu 1534
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5308 CTGGAAGGCTCAAAATGAG---TATGAACCCCTTTCTTAAAGAAAGTTTTCAG 5355
QY      1535 ThrSerValLeuLeuLysAspAspLeuGlnGlnLysLeuGlnSerLeu-----Leu 1551
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5356 TCTTTAATGTGTGAAGAAAGCTCTTAACTAGTAAGAGGTTCAGATTTAAAGCATCAGATA 5415
QY      1552 SerGluAsnIleIleLeuLysGluAsnIleAspThrThrLeuLysHisSerAspThr 1571
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5416 GAAGTATATGATGTAAACAAAGCTAACCTAGAGCCACCGAAACATGATTAACCAAGC 5475
QY      5416 GAGTATGAGCAGACAGACCTACATGT-----TCAGATGTGTTCCATCAGCGAAGAGT 5586
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5586 AGTATGAGCAGACAGACCTACATGT-----TCAGATGTGTTCCATCAGCGAAGAGT 5586
QY      1589 AlaIleAlaIleAspAsnCysProIleThrGlnGluLysGluThrSerAlaAspCys 1608
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5587 GCCAACCCTGTGTAAAGTAAAGGATTTCAGCTCACATGATGAATAATAT----- 5634
QY      1609 ValHisProLeuGluGluLysIleLeuLeuLeuThrGlnGluLeuHisGlnLysThrAsn 1628
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5635 -----AACCACTTACAGCAGATGAT-----CAGCTCAA 5664
QY      1649 CysGluValGluHisLeuMetLysSerMetIleGluSerLysSerSerLeuGluSerLeu 1668
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5665 GAAAGAAATGTGTGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5724
QY      5725 GAAATGAGAAAGAAATACCTTACTGATCAGATATCAACAAAGATGTGAACTTAAATG 5784
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5785 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5841
QY      1705 AlaGluValAspHisLeuLysGluAsnIleGluLeuLeuLysLeuAsnProLysAsnGluAla 1724
      ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db      5842 TCCAGAGTTACCAAACTTAAAGAGACAGCAGAA----- 5874

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OY	1725	GlnGlnIuYrThrThrLysGlnGlnCysLeuLeuAenGluAenIuYsGluLeuGlnGlnSer	1744
Db	5875	GAAAGCAAAAGATGATTTGGAAAGAGCGCTTATGATTCATTAATGACGAAGAACTTAATGGAAGC	5934
OY	1745	GlnHisArgLeuGlnCysGlnIuIleGlnIuIuMetIuYsSerLeuLeuAspIuYsGlnSer	1764
Db	5935	-----ATTGGGAATTACTGTCAGGATGTTTACAGATGCCCAATA	5973
OY	1765	AlaLeuGlnIuThrLeuLysGlnSerGlnGlnIuYsValIleAenLeuAenGlnIuMetGln	1784
Db	5974	AAAAATAGCGTATTGCG--GAATCTGAAATGAAAG-----AACCTTAAAAAG-----	6015
OY	1785	MetValMetLeuGlnMetGlnGlnIuLeuLysAsnSerGlnArgThrValIleAlaGluArg	1804
Db	6016	-----TGCTGAGTGAATTTGGAAGAAAGAAAGCAGCATTTGTCAGAGGAAAAA	6063
OY	1805	AspGlnIuLeuGlnAspAspLeuArgGlnSerValGlnMetSerIleGlu-----	1820
Db	6064	ACTAAGGTGGATCGAATATCGAAATCGAAAGAAATTTGGAGAAAAAATACAGAGTCTCAGAAA	6123
OY	1821	-----ThrGlnAspAspLeuArgLysAlaGlnGluAlaLeuGlnGlnIuYsAsp	1837
Db	6124	GAACCCGGAATTAAGAGCCATGACAAAGGAACCTTCAGAACCTGTTAAGAAAGAAACAAACA	6183
OY	1838	LysValGlnGlnIuLeuThrSerGlnIleSerValLeuGlnGlnIuYsIleSerLeuLeuGln	1857
Db	6184	GAAGTAAAGCAGCTACAGAGACCTGCATCGATACGATACAGAGAAATTAAGTGCCTGAG	6243
OY	1858	AsnGlnMetLeuTyrrAsnValAlaThrValIys-----GluThrLeuSer	1872
Db	6244	AGA-----ACTGTTAAAGCTCTACGATTTGTTCAACTGAATCT	6282
OY	1873	GluArgAspAspLeuAenGlnSerIleGlnIleHisLeuPheSerGluIleGlu-----	1889
Db	6283	CAAAAA--GATTTGGAATATACCAAGAAATATGCTCTCAAGCAGTTGAACACCGCAA	6339
OY	1889	-----	1889
Db	6340	AAGGCACAGACGAAATTAGTACGTTCCAAATCCTCGTACAGTACGACCTCAAGGAAAGCA	6399
OY	1890	-----ThrIuSerLeuSerLeuIuYsGlnIuYsGlnIuPheAlaLeuGlnGlnAlaGluIuYs	1907
Db	6400	GCAAGGCTCTACAGACAGACATCTCAAGTTGAAAAAGAACTTCAGTCAATTAAGAAATCA	6459
OY	1908	AspLysAlaAspAlaAlaArgLysThrIleAspIleThrGluIuYsIleSerAsnIleGln	1927

Qy	2033	GIUleuAArgGIuSerLeu-----	2038
Db	6871	GAATTAAAGATTAAACATTTCAGGCTTGAAACATGACAAGACAGATTGGAGTCCAAAGCC	6930
Qy	2039	-----LyeThrLysAsp	2042
Db	6931	CAGACAGAGGTCCAGCTTCACGACAAGGTCTGTGTACTCTACAGGGGGAACAAAGAA	6990
Qy	2043	Leu-----GlnLeuGlnGluAlaGlnLysGlnLysSerGlnLysAlaThrAsnGlnLys	2060
Db	6991	CTTTGTGCCAGCTGAGAAAGACAGACGCCACTTATACCAAGCTCTCAGAAATGAATTAGCT	7050
Qy	2061	AsnLeuThrAlaLysLysSerSerLeuGlnGlnLysLeu-----LeuGlnAsnAla---	2077
Db	7051	AAGTTGGAAATCAGAACTTTAAGAGTCTCAAAAGACAGATTGACTGATTTTAACTCTTTA	7110
Qy	2078	-----SerLeuAsnGlnAlaValSerGln	2086
Db	7111	GAAAAATTAAAGAAACAAAAGAAACTTGGAAGGATCATAGGCGAAGCAAGAGCTGAT	7170
Qy	2087	ArgGlnAsnLeuArgHisSerLysGlnGlnLeuValSerGlnLysGlnLysLeuSerLeu	2106
Db	7171	ATTCAAAATTCTAAGTTACGTTATGAACAACTGAGAGCTGATCTT---CAGGCTCCAGA	7227
Qy	2107	ThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArgGlu-----	2121
Db	7228	GAACTGACCACTAGGCTGCTCATGAAGAAATTAATATGAAAGACAAAAGATTATTAAGCTG	7287
Qy	2122	-----LysAspGlnAlaValAsn---LysIleAlaSerLeuAlaGln-----	2134
Db	7288	CTTCTGCGAAAGAAAGAGCAATCCAAATGACTATTCCTGAACGCTCAGCAACATGAT	7347
Qy	2135	---GlnIleLys-----IleuThrLysGlnLysAspGlu-----Phe	2146
Db	7348	AAAGAAATTAAGAAGCTCGAAAACTGCTGTGCCAGAGGAAGAGCAATATGTTT	7407
Qy	2147	ArgAspSerLysGlnSerLeuGlnGlnLysSerSerHisLeuSerGlnLysLeuCysThr	2166
Db	7408	GAAGCGAAGAACAAAGAGCTGTTGAATAAACCAATCAGCTTATGAGAAACACTGAAAACC	7467
Qy	2167	TyrLysThrGlnLeuGlnMetLeuLysGlnGlnLysGlnLysLeuAsnLysLeuAla	2186
Db	7468	ATCAAA-----AAGAAAACTTACGCAAAAG-----	7494
Qy	2187	GlnLysValLysGlnValAspGlnLeuLeuGlnGlnHisLeuSerSerLeuLysGlnGlnLeu	2206
Db	7495	-----GCACAGTTGATCTCTTGTTAATCCATGCTCTTCTCTCCAAATGATCGA	7545
Qy	2207	AspGlnIleGlnMetGlnLeuArgAsnGlnLysLeuArgAsnTyrGlnLeuCysGlnLys	2226
Db	7546	GACCGCATAGGGGAGCTATCAACAGGTGGAAGACGACATCTCTCTATA-----	7596
Qy	2227	MetAspIleMetGlnLysGln-----IleSerValLeuArgLysMetGlnAsnGlnPro	2244
Db	7597	-----ATCTTGGAAAAAAGACCAATCATCCAGAGGCTGCTGCAGAAATTAATAGCTT	7650
Qy	2245	GlnGlnGlnGlnLysAspArgValAlaGlnArgMetAspIleLeuGlnLysArgAsnGlnGln	2264
Db	7651	AAAGAGAAATATCAGAGCTTGAGAAAGTCATATGGATATCTCAATTGTGAGAAATGCCAAG	7710
Qy	2265	Ile-----GlnGlnLysMetGlnLysIleSerAlaValTyrSer	2277
Db	7711	CTAGATGCAGAACTGATCCAAATATAGAGAGAGACTGAACCAAGATATCAATTAAGAC	7770
Qy	2278	GlnGlnHisThrLeuLeuSerSerLeuSerSerSerGlnLysGlnLysThrGlnAlaHis	2297
Db	7771	AGCCACAAAGACAGCTTCTTGAAGTTCAATTCAGCAAAATATAGAGCTGGAA---AAT	7827
Qy	2298	LysHisCysMetLeuAsnLys-----GlnSerLeuSerSerThrLeuSer	2313
Db	7828	AAATATGCTTAATATGAAGAAAGAAAGCTGAGAGAAATCTGAGAGCAAAATGAGATCTCGG	7867
Qy	2314	ArgSerPheGlnSerLeuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeu	2333

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Db      7868  |||||  ....  |||  |||  .....  |||  7947
      AGCTCTTAAATGCTTACAGAGAGAAACAAGATTATCTAAAGAGATTGAGATTG
Qy      2334  ---LeuAsnLysPheLysValValTyrArgThrAlaAlaValLysGluAsp----- 2349
      |||||  .....  |||  |||  .....  |||  |||
Db      7948  AAAGATATCATATCCAGCTTAACAAGACAAGTAACGCTTCAAGAAAGAGTACTTTA 8007
      |||||  .....  |||  |||  .....  |||  |||
Qy      2350  -----HisSerIleuLysAspTyrGluLysAspLeu----- 2360
      |||||  .....  |||  |||  .....  |||  |||
Db      8008  GGACTCTATCATGCCAGCTTAAAGTAAAGTAAGAGAGAGTACACAGCTTAAAGCTTTG 8067
      |||||  .....  |||  |||  .....  |||  |||
Qy      2361  ---AlaAlaGluLysArgHisAspGluLysLeuArgLysLeuGlnCysLeuGluGln 2379
      |||||  .....  |||  |||  .....  |||  |||
Db      8068  TTTTCTCTCTCTCAAAAGCAATTCGACAACTGGAAGAAATGTTGTTGTTCAAAAG 8127
      |||||  .....  |||  |||  .....  |||  |||
Qy      2380  HisGlyArgLysTyrSerAspSerAlaSerGluLysLysPheCysGluIleGluPhe 2399
      |||||  .....  |||  |||  .....  |||  |||
Db      8128  GAAGCTGCCAAGAGTAGTGAATAATGAAGATTAAGATTAAGCTGAG---AAAGATTAAGCAT 8184
      |||||  .....  |||  |||  .....  |||  |||
Qy      2400  LeuAsnGluLysLeuPheLysLysAlaAlaValIleGlnSerValGlnAspAspSer 2419
      |||||  .....  |||  |||  .....  |||  |||
Db      8185  CTTTCATCATGATGACAGGATTAATGAGAAATGAACTGAAACGACAGACAGAGTGGCA 8244
      |||||  .....  |||  |||  .....  |||  |||
Qy      2420  GluValGlnValPheLeuAsnGlnValGlySerThrLeuGlnGluLysLys 2439
      |||||  .....  |||  |||  .....  |||  |||
Db      8245  GAGCTAGCAGAGATTTGGTGAGATGACAGAAATTAATCTCATGCTCACCAAGAAAT 8304
      |||||  .....  |||  |||  .....  |||  |||
Qy      2440  LysGlyPheMetGlnThrLeuGluLysPheGly-----AspLeuHisValAsp 2455
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Db      8305  AAAGCTCTACAGCAAAATTCAGCTTTTGGAAAGCTATGAGTTCTTGCAGAAATAGT 8364
      |||||  .....  |||  |||  .....  |||  |||
Qy      2456  AlaLysLysLeuSerGluLysMetGlnGlnLysAsnArgArgIleAlaSerThrIleGln 2475
      |||||  .....  |||  |||  .....  |||  |||
Db      8365  AGAGATCATGCCAATGAGAACTTGATGAACTGAAAGAAATATGATGCTCAGCTGAG 8424
      |||||  .....  |||  |||  .....  |||  |||
Qy      2476  LeuLeuThrLysArgLeuLysAlaValIleGlnSerLysIleArgGluIleThrVal 2495
      |||||  .....  |||  |||  .....  |||  |||
Db      8425  GAATTGGCA---CAGTTGAAGAA-----CAGGACCTTTAAACAGACAGAGATGCT 8475
      |||||  .....  |||  |||  .....  |||  |||
Qy      2496  TyrLeuAsnGlnPheGluAlaLysLeuGlnLysLysGluGlnAsnLysGluMet 2515
      |||||  .....  |||  |||  .....  |||  |||
Db      8476  CTTCTTTCTGAAACCGCTTTTCAATGAACTCCACTGAGCAAGATTAAGCTTCTCAGCT 8535
      |||||  .....  |||  |||  .....  |||  |||
Qy      2516  ArgArgMetGluHisIleGlyProSerAlaSerValMetGluGluLysAlaAlaArgLeu 2535
      |||||  .....  |||  |||  .....  |||  |||
Db      8536  GAGAACTTAACCAACAG-----CTCTATCCAAAGATGAGCAATTG 8577
      |||||  .....  |||  |||  .....  |||  |||
Qy      2536  LeuGlyIleLeuLysThrValGlnAspGluSerLysLysLeuGlnSerArgLys 2554
      |||||  .....  |||  |||  .....  |||  |||
Db      8578  CTTCACTTGCTCTCACAACCTAAGATTTCTTAACCAAGTCAAGTCTTTTCCAAAGCT 8637
      |||||  .....  |||  |||  .....  |||  |||
Qy      2555  ---MetLeuGluAsnGluLysAsn-----LeuValLysAspAspAla 2567
      |||||  .....  |||  |||  .....  |||  |||
Db      8638  ATGCCACTGTGCAAGATGAGAGATCACTGTGGAATGAGCTGAGAAATTTGCAAG 8697
      |||||  .....  |||  |||  .....  |||  |||
Qy      2568  MethLysGlyGluLysValAlaIleLeuGlnAspLysLysLeuSerArgAsnAlaGlu 2587
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Db      8698  TCAGAGGAAGGAGACAGAGCTGCTGACGCTCAGCTTCC-----ACGAGCCCA 8745
      |||||  .....  |||  |||  .....  |||  |||
Qy      2588  AlaGluLeuAsnAlaMetGlnValLysLeuThrLysLysAspAsnLeuGlnAlaAla 2607
      |||||  .....  |||  |||  .....  |||  |||
Db      8746  GCTGAAGTACAGAGCTTAAAAAACCTATGCTTCACTCCAAATGACAGACAGACTA 8805
      |||||  .....  |||  |||  .....  |||  |||
Qy      2608  MetLysGluLysLeuAsnLeuGlnLysMetValAlaLysGlyAlaValProTyrLysGlu 2627
      |||||  .....  |||  |||  .....  |||  |||
Db      8806  CTGAAGGATTAAGAAATCTGACAGACCAATAC-----TTACAGATTAATCA 8853
      |||||  .....  |||  |||  .....  |||  |||
Qy      2628  GluIleAspAsnLeu-----LysThrLys 2635
      |||||  .....  |||  |||  .....  |||  |||
Db      8854  GAGATCACTGAGTTACATCCACTGAAGGCTCAACTTCAGAGATTAACAGATTAAGCA 8913
      |||||  .....  |||  |||  .....  |||  |||
Qy      2636  ValValLysIleGluMetGluLysLysLysLysLysLysLysLysLysLysLysLys 2654
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Db      8914  GCATTTCATTATGCAAGAGAGCTCAGGACGAGAAACCTCTCTGACAGATGAGCTG 8973
      |||||  .....  |||  |||  .....  |||  |||
Qy      2655  AlaTyrLeuLys----- 2658
      |||||  .....  |||  |||  .....  |||  |||
Db      8974  CATCAGCTCAGAGATGAGAGAGATTCTGGAAATATACATGAGAGAGATGAGAGAG 9033
      |||||  .....  |||  |||  .....  |||  |||
Qy      2659  ---SerCysLeuGluLysArgLysGluLysLeuArgLysLeuGluLysLeuArg 2676
      |||||  .....  |||  |||  .....  |||  |||
Db      9034  TACCTTATGCTTATCTCAGATTAAGATGAGAGCTCAGCTCATCTGCAAAATCTTAAG 9093
      |||||  .....  |||  |||  .....  |||  |||
Qy      2677  ArgAlaGlnAlaAspAsnAspThrThrValCysValProLysAspTyrGlnLysLaser 2696
      |||||  .....  |||  |||  .....  |||  |||
Db      9094  GAATTGAGGTCTTCTCTCTCCAGACTCAGGCTCCTCAAGTGCATTAACAAAGAGCA 9153
      |||||  .....  |||  |||  .....  |||  |||
Qy      2697  ThrPheProValThrCysGly-----GlyLysSerGlyIleValGlnSerThrAla 2713
      |||||  .....  |||  |||  .....  |||  |||
Db      9154  TCC---CCAGAGACATCAGCTTCCCAAGATGGTCAAAATCTGTTATGACACAGA 9210
      |||||  .....  |||  |||  .....  |||  |||
Qy      2714  MetLeuValLysLeuSerGluLysAlaAlaLeuGluLysArgLysLeuSerHisTyrLys 2733
      |||||  .....  |||  |||  .....  |||  |||
Db      9211  CTTTCAGAGCCCAAGCTCAATGACAGCTTA-----AAAGAAATTCACCAAAAGAG 9264
      |||||  .....  |||  |||  .....  |||  |||
Qy      2734  LysTyrHisLysLeuSerArgThrMetSerSerSerGluAspArgLysLeuThr----- 2751
      |||||  .....  |||  |||  .....  |||  |||
Db      9265  AGAATTCAGCAACTGAACAGAACTTCTCTCAGTACTGAGAGAGAGAGAGAGAGAG 9324
      |||||  .....  |||  |||  .....  |||  |||
Qy      2752  ---LysAlaLysSerAspAlaHisSerSerHisThrGlySerSerHisArgLysSer--- 2769
      |||||  .....  |||  |||  .....  |||  |||
Db      9325  ATTCACTCTGCGATACAGTACAGTCTGCTGAGAACCCAGACACTATGATGACCTT 9384
      |||||  .....  |||  |||  .....  |||  |||
Qy      2770  -----ProHisLysThrGluThrTyrArgHisGlyProValThr 2782
      |||||  .....  |||  |||  .....  |||  |||
Db      9385  TTAATCATCTGCTGCTTGGAGAGAGAGCTTCAAGAGCTGACGCGGCGGCTTAAT 9444
      |||||  .....  |||  |||  .....  |||  |||
Qy      2783  ProGluArgSerGlu---MetProSerLeuHisLeuGlnLysSerProLysLysSerGlu 2801
      |||||  .....  |||  |||  .....  |||  |||
Db      9445  ATGATGTGTTCCAGAGAGCTCCAGAGAAAGATGAGTTACAGAAAGAGTACCT 9504
      |||||  .....  |||  |||  .....  |||  |||
Qy      2802  SerThrLysArgValValSerProAsnArgSerGluLysLysGlnLeuValMetSer 2821
      |||||  .....  |||  |||  .....  |||  |||
Db      9505  GAGNACTAAGGAAACCCAGCAAAAGCTTTCTGAAAGTCCAGACACTATGCAACAC 9564
      |||||  .....  |||  |||  .....  |||  |||
Qy      2822  ProGlyLysThrGluMetHisLysHisIleLeuSerProSerLys----- 2836
      |||||  .....  |||  |||  .....  |||  |||
Db      9565  AGACAGAGATGATGAATTAAGAGAGCTGCGAAGAGAGACAGACCAAGAGAGTGC 9624
      |||||  .....  |||  |||  .....  |||  |||
Qy      2837  -----ValGlyLeuHisLysLysArgAlaLeuSerProAsnArgSerGluMet 2852
      |||||  .....  |||  |||  .....  |||  |||
Db      9625  GCTGAAGATGCTCTCTGTCGCGAGAGAGATCAGACGTTAAGACAGACAGTGAATGG 9684
      |||||  .....  |||  |||  .....  |||  |||
Qy      2853  ProThrGlnHisValIleSerProGlyLysThrGlyLeuHisLysAsnLeuThrGluSer 2872
      |||||  .....  |||  |||  .....  |||  |||
Db      9685  GACTCTTCCCGACTCTATCATTTGGCTCTGTGGCACTCAGAG-----CAGCA 9735
      |||||  .....  |||  |||  .....  |||  |||
Qy      2873  ThrLeuPheAspAsnLeuSerSerProCysLysGlnGlnLys 2886
      |||||  .....  |||  |||  .....  |||  |||
Db      9736  CTGTTAATGATCTTACAGCAACAGTTGTGAAAGAGACCCGG 9777
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RESULT 6
US-09-960-253-163
; Sequence 163, Application US/09960253
; Patent No. US20020123619A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Lodes, Michael J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.556
; CURRENT APPLICATION NUMBER: US/09/960.253
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 163
; LENGTH: 10096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-960-253-163

Alignment Scores:
Pred. No.: 1,8e-63 Length: 10096
Score: 1152.00 Matches: 740
Percent Similarity: 37.41% Conservative: 563
Best Local Similarity: 21.25% Mismatches: 1160
Query Match: 7.80% Indels: 1022
Gaps: 140

US-09-724-584-1 (1-2954) x US-09-960-253-163 (1-10096)

QY 81 PheAlaTYrGIgInThrSerSerGIyYrThrTYrThrMetMetGIyThrProAnsSer 100
Db 465 TTCGAGGAAGGACACTGAACTGACAGCAAA----- 494

QY 101 LeuGIyIleIleProGIAlaIleGIInGluValPheYsIleIleGIInGluIleProAns 120
Db 495 -----AAACAATATGAAAACTGAAACAGGAACTTAAAG 530

QY 121 ArgGIuPheLeuLeuArgValSerTYrMetGIuIleTYrAnsGIuThrValYsAepLeu 140
Db 531 TGTAAATGTGAGCTTGAAAGAACCAACAGCTGGCAGCTGCGAGATCTCTCTGAAT 590

QY 141 LeuCyAAspArgArgLyS-----LYsProLeuGIuIleArgGIuAAspAAsn 157
Db 591 CCATCATATACACCAAAAAATTTTACAACTCCACTCAACACCAAGTCATATATAGT 650

QY 158 ArgAnValTYrValAlAAspLeuThrGIuGIuLeuValMetValProGIuHisValIle 177
Db 651 GGTTCCAAGTAT--GAAGATCTAAAGAAAAATATATAAAGAGTTGAA----- 698

QY 178 GIuTrIleLySlyGIyGIuYsAAsnArgHisTYrGIyGIuThrLYsMetAAspHis 197
Db 699 -----GAAAGAAAAAGATTAGAGGCAAGAGTTAAAGCCCTTGCAAGCT 740

QY 198 SerSerArgSerHisThrIlePheArgMetIleValGIuSerArgAsp-----ArgAAsn 215
Db 741 AAAAAAGAGGCAAGCTCTCCACAGCCACATGATACCGGAGACATTCGCCGCGCAT 800

QY 216 AspProThrAAsnSerGIu--AAsnCyAAspGIyAlaValMetValSerHisLeuAAsnLeu 234
Db 801 CAGGCTTCATCATCTGTGTCTTCATGCGACAGAAAGAACCCCAAGTCATCTTCA-- 857

QY 235 ValAAspLeuAlaGIySerGIuAArgAlaSerGIuThrGIyAlaGIuGIyValArgLeuYs 254
Db 858 -----TCATATCTCAAGAACT----- 875

QY 255 GIuGIyCyAAsnIleAAsnArgSerLeuPheIleLeuGIyGIuValIleYsLySLeuSer 274
Db 876 -----CCAATTAGAGAGATTTCTCT 896

QY 275 AAspGIyGIuAlaGIyGIyPheIleAAsnTYrArgAAspSerLYsLeuThr----- 290
Db 897 GCATCTTACTTTTCTGGGGAATAGAGGTGACTCCAACTGCATCAACTTTCGCAATAGAG 956

QY 291 ---ArgIleLeuGIuAAsnSerLeuGIyGIyAAsnAlaYsThrValIleIleCySerThrIle 309
Db 957 AAAAGAGATGCTATAGCAAGTTCTTTCGCAATTTTACC----- 995

QY 310 ThrProValSerPheAAspGIuThrLeuSerThrLeuGIInPheAlaSerThrAlaYsHis 329
Db 996 AGTCTCATCTTTTGAT-----CATTTAAAGCCCAAGATCAAG 1037

QY 330 ValArgAAsnThrProHisValAAsnGIuValLeuAAspArgGIuAlaLeuLeuLYsArgTYr 349
Db 1038 CTAAGAAAC-----AAGATTATATAGTTG-----GAACTACGCTCGCAAGAGCAT 1082

QY 350 ArgLySGIuIle-----LeuAAspLeuLYsGIInLeuGIu-- 361

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Db 1083 GAAAAAGAAATGAAGGCCAAGTGAATAGTTTCAAGAACTCCAACTGAGAGAA 1142
QY 362 ---AAsnLeuGIuSerSerSerGIuThrLYsAlaGIuAlaMetAlaLYsGIuIleThr 380
Db 1143 GCAAAAGTGAATTAATTGAAGAAAGATTTTGAACAAATGTAGGATGATCACTAGT 1202

QY 381 GIuLeuLeuAlaGIuIleLYsGIuLeu-----HisLYsGIuAArgGIuAAspArgIle 397
Db 1203 AGAAACACGACCAATAGACAGCGGCTGCACCAAGTATCTGCACTTGGAAACAAACTG 1262

QY 398 TrpHisLeuThrAAsnIleValAlaAAspSerGIuIleSerGIuIleSerGIuIn----- 413
Db 1263 AAAAAATTTGACGGAAGATTTGATGCTGCAGGACAAATGCAAGAAAGTCCAGATGTTCT 1322

QY 414 ---AAspGIuAArgValLYsArgLYsArgValThrTrpAlaPro--GIyLYsIleGIu 431
Db 1323 CTGAAACGAAAAATTAAGAAAGAAAGAGATTTCAAGAGAGACTCTCCGTCACAG 1382

QY 432 AAsnSerLeuHisAlaSerGIyValSerAAspPheAAspMetLeuSerArgLeu-ProGIyAs 451
Db 1383 GCTTCTTTCCAAACACTGAGACCGAGTGCATCCAGATGAAGGCCAGACTCACCGAGAG 1442

QY 451 nPheSerLYsLYsAlaLYsPheSerAAspMetProSerPheProGIuIleAAspAAspSerVa 471
Db 1443 TTACAGCAAG-----CCAAGAAAT 1460

QY 471 LYsThrGIuPheSerAAspPheAAspAlaLeuSerMetAAspSerAAsnGIyIleAs 491
Db 1461 ATGCACAAAGCTCTGCAGAGCTGAACTGGATTAACATCAGATCAGTAAACCAACAGCTAGAA 1520

QY 491 PAlaGIuThrAAsnLeuAlaSerLYsValThrHisAArgGIuLYsThrSerLeuHisGIInSe 511
Db 1521 AACAAATTGGAAGATTTAAAGCAAAAGTTGTC--AGACTGAACAGGGCTTCCAGCGAG 1579

QY 511 MetIleAAspPheGIyGIuIleSerAAspSerValGIuInPheHisAAspSerSerLYsGIuAs 531
Db 1580 TCAGATCAAGAGAGATAGACTGAGAGAGAAAGCATGAG--GAAATCAAGCAAGAA 1633

QY 531 nGIuLeuGIuInTYrLeuProLYsAAspSerGIyAAspMetAlaGIuCyAArgLYsAAspSerh 551
Db 1634 CAACCTCTTAAAGATCACTCTGAGCAAAAGGCCAGAAAGTCTCCACTGAGAGCGCA 1693

QY 551 eGIuLYsGIuIleThrSerLeuGIuInGIuInLeuGIuInSerLYsGIuGIuLYsGIu 571
Db 1694 ACTCAAGAAACATCAAAAGCTTTAAATCAAGCCAGAAATTTTGCAAGAAATGAAGC 1753

QY 571 uLeuValGIuInSerPheGIuLeuLYsIleAlaGIuLeuGIuGIuInLeuSerValLYsAl 591
Db 1754 GAAAGATACCTCTCAGGAAACCATGTTAAGAGATCTTCAAGAAAAATTA----- 1802

QY 591 aLYsAAsnLeuGIuMetValThrAAsnSerArgLIuHisSerIle----- 605
Db 1803 -----AATCAGCAAGAAAACTCTTGAATTAAGAAAACTGAA 1840

QY 606 -----AAsnAlaGIuValGIuThrAAspValGIuLYsGIuValAlaArgLYsGI 621
Db 1841 GCTTCTGTGCTGCTAGTGTGAAAAAGCAGCGAGATTTGTTCAAGACCTTTTGAAGAAAG 1900

QY 621 uMetSerValLeuGIuAAspSerGIyTYrAAsnAlaSerAAsnSerAAspLeuGIuInAAspSerSe 641
Db 1901 A-----GAACATCACTTGAACAACTTAATATATAGTTAAGCAAGACAGCA 1945

QY 641 rValAAspLYyArgLYsLeuSerSerHisAAspGIuCyIleGIuHisArgLYsMetLe 661
Db 1946 GAAAGAGTCAAAAGCTTGTGATGCT-----TT 1975

QY 661 uGIuGIuLYsIleValAAspLeuGIuGIuPheIleGIuAAsnLeuAAsnLYs----- 677
Db 1976 AGAGTTAAAGAAAGAAATATGAAGAAATTAAGAAAGAAAGAACTGTGTTTCTTGTG 2035

QY 678 -LYsSerGIuAAspLYs-----GIuLYsSerSerGIuInAAspPheMetGIuSe 694

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Db 2036 GAAAAAGTAAACGAAAACTTTAACTCAGATGGATCAGAAAAAGAAAACTTGACAG 2095
 QY 694 T-----11leuLeuCys----- 698
 Db 2096 TAAATTAATCACTTGGAACCTTGCTGACAGACAGCAATAAAGATCAATGATCAAA 2155
 QY 699 -----GluAla11MetAla11GluLysAlaAsnAlaLeuGluLysLeuAlaLeu 715
 Db 2156 CGAGAGAGTAAAGAACGCTGAGATGACAGAGAAAACTTAAGTGTCCAGATTCAGAAACCT 2215
 QY 715 LArgAspAsnIleAspAsnIle11LeuGluAsnGluThrLeuLysArgGlu11Ala11 715
 Db 2216 TCACAGAGCTTTACACAGTAAGTACAGTGAAGTAGAGACCAGAACTTACCTTAATGTA 2275
 QY 735 PLeuGluArgSer----- 739
 Db 2276 GCTACACAGCAAAAGCTGAGTTCTCAGATCAGAAACATCAGAGAAATAGAAAAATATGTC 2335
 QY 740 -LeuLysGluAsnGluLysThrArgGluLysPheGlu11LeuGluLysGluLysGlu 759
 Db 2336 TTGGAGACATCTTCAGCTTACTGCGCAAGTTGAAGATCTA-----GA 2377
 QY 759 uH1sgLysAlaGluLeuLysIleHisGluLysSerLeuLysLeuValGluAsnAlaG 779
 Db 2378 ACACAAAGCTTCAGTTACTGTCA-----AATGAAATTAATGACAAAGACCG 2422
 QY 779 uMetTyrAsnGluAsnLeuGluLysPheGluLysThrLysLeuLysGluLys 799
 Db 2423 GTGTTAC--CAAGACTTGATGCGCAATATGAGAGCTCAGAGATCTGTAAATCCAA 2479
 QY 799 ngLys11LeuLys----- 803
 Db 2480 AGATGCTCTCTCTGTGACAAATGAATCATCAGAGAAGCTTTGGCTTTGATCAGCA 2539
 QY 803 ----- 803
 Db 2540 GCCTGCATGATCATCTCTTGCATAATTAATTTGAGAAACAAGAGATGCTTCAGA 2599
 QY 804 ----AlaGluLeuArgLysArgAlaAspAsn-----LeuGluLys 815
 Db 2600 GAGAGAGTAAATGCTGTTAGAACGACAGACCAAGTCCGAAAAATTCGCCATCTCAAAA 2659
 QY 815 sLysVal1ArgAsnPheAspLeuSerValSerMet-----GlyAspSerG 830
 Db 2660 TAGAGTTGATCATCTGAATTTTCATTAGAGTCTCAAAAACAGATGACATGCACTGCA 2719
 QY 830 uLysLeuCysGluGluLysPheGluLeuLysGluSerLeuSerAspAlaGluAlaValTh 850
 Db 2720 AAAGCAGTGTGAAGTTGGTCCAAATCAAGAGAAATAGAA-----GAAATCTCAT 2773
 QY 850 rArgAspAlaGluLysGluCysSerPheLeuArgSerGluAsnLeuGluLysGluLys 870
 Db 2774 GAAACGACAGACAGATGATCAAAAGTTTGTGCTCAAAACAGTCAAGCCATTAGTAAGT 2833
 QY 870 sMetGluAspThrSerAsnTyrAsn-----G 880
 Db 2834 ACAGAGAAACCTTGTCTCACCAGAAATGTTGCTGAAACCTTAAGTGCCTTGAGAA 2893
 QY 880 nLysGluLysAla11AspLeuPheGluLysGluLeuLysGluLysSerAsnTyrLys 900
 Db 2894 CAAGAGAAAAAGAGCTGCAACTTTTAATGATTAAGTAAAGAACTGACGAGAGAGATTC 2953
 QY 900 sLysMetGlu-----AlaAspLeuGluLysGluLeuGlu----- 911
 Db 2954 AGAATTAATAAAAGAGACACATCTTACGAAAGCTCTTAAGAGAGCTACCACTTTATC 3013
 QY 912 -----SerAl 913
 Db 3014 GGAACCTTAAGCTTGAGAAAGAAAGAAATGATTCATCTTAAATTAAGAGCA 3073
 QY 913 aPheAsnGluLysAsnTyrLeuAsnGluLysLeu-----AlaGlyLys 927
 Db 3074 AATTAAGAGAGCTGACCCAGAGATGGAGCTCTTAAGAAATTAATGATCTTAAATCA 3133

QY 927 sValProArgAspLeuSerArgVal-----GluLeuG 939
 Db 3134 AGAGAGATGAACTTAATTCAGAAAAAGTGAAGTTTGCAAACTATATGATGAAGAGCA 3193
 QY 939 uLysLysValSerGluPheSerLysGluLeuGlu----- 950
 Db 3194 GAAAGACATTTACAGATTATCTGATCAGTACAGCAAGAAAACTTATTTACTACAAAG 3253
 QY 951 -----LysAlaLeuGluG 955
 Db 3254 ATGTAAGAAACCGAAATGATATGAGATCTTAATGCAAAATATCAAGACAGACAGCA 3313
 QY 955 uLysAsnAla-----LeuGluAsnGluValThrCysLeuSerGluTyrLysPh 971
 Db 3314 AAAGATTTCTAAATTAGATCTTGCTTAAAGAAATGCACTGCTCTTGTGAAAAATAGG-- 3371
 QY 971 eLeuProAsnGluValGluCysLysLeuLysAsnGlu11LeuSerLysAlaSerGluLys 991
 Db 3372 ----AAATATGAGTTGGAACAGCTTAAAGAGCAATTCGCAAGAGCAACCAAGAAATTC 3427
 QY 991 tLeu----LeuLysGluGluGluLysSerAlaSerLys11LeuSerLysGluGlu11 1010
 Db 3428 AACAAATTAACATTTGCTGAAGAAAGAAATCAGAAATCTGATGAGTTGAGACAGT 3487
 QY 1010 eMetGln-----GluLysSerGlu----- 1016
 Db 3488 GCAGCAAGCTTGAGATCTGATGACAGATTAACCAAAACATTTTAAGACGCGCTGCG 3547
 QY 1017 -----GluLysLeuGluLysThrAspGluValThn11ThrGlnSerLysVal 1032
 Db 3548 TGGTTTAAAGCAAAATATCATGACTTTAAAGAAAGCAAAACAAATGCAAAAGCAAGT 3607
 QY 1032 1-----GlnGlnThrGluGluGluLysThrLeuGluMetLysLysMetHisAsp-- 1047
 Db 3608 TAATGATTTATTAACAGAAAGTAAACGCTGATGAAGTAAAGCTTAACATGATGATG 3667
 QY 1048 ----AspLeuPheGluLysTyr11LeuArgAsnLysSerGluAlaGluAspLeuLysG 1066
 Db 3668 TCAAATCTAGATCAAGAACCAATTAAGAACTGTGTAAGAAAGAGAGAGTGAAGAA 3727
 QY 1066 uMetGluAsnLeuLysGluLysThrMetGlu----- 1075
 Db 3728 TCATGTAATTTTAAACCTCAGATGATCTTGAAGTTAAAGAAATTTCTAGATATGTA 3787
 QY 1076 -----SerValGluValLys11Ala11AspThrLysHisGluLeuGluG 1090
 Db 3788 TAATGCGCACTTGCTCAATTAAGACTATGCTTAAGAAATTAAGAAATTAAGAACTT 3847
 QY 1090 uThr11LeuArgAspLysGluGluLysLeuLysGluLysLysTyrPhePheGluAlaMetG 1110
 Db 3848 AAGTGAAGAGAGAAAGAGAGTGTGCGCATGAA-----TTACA 3886
 QY 1110 nThr11LeuPhePro11LeuThrProLeuSerAspSerLeuProProSerLysLeuValG 1130
 Db 3887 GACAAAT-----AGAGCAATCTTGAACACGCAATTTCCAAAGACAT 3928
 QY 1130 yAsnSerGlnAspPro11LeuLysAsnAspTyr----- 1141
 Db 3929 GCAGTACAAAGAAATTAAGTGCCTTAAAGACGTGTAATATGATGCGGAAGAAAGATAT 3988
 QY 1142 -----HisAsnLeu11AlaLeuAlaThrGluArgAsnAsn11MetValCysLe 1158
 Db 3989 TTCAGGCGCTCATGAGTTGTCAACAAGTCAAAACAGACATGACACTTCAGTGTCTCT 4048
 QY 1158 uGluThrGluArgAsnSerLeuLysGluGluVal11LeuAspLeuAsnThrGlnLeuG 1178
 Db 4049 GCAACCAACAAATGAACAGCTGAATGAG-----CTAGCAAAATATGTGGAAT 4096
 QY 1178 tLeuGlnAlaGlnSer11Leu-----LysSerAspLeuG 1190
 Db 4097 ACTGAGAGGCTGAAAGTAACTGTAAGCTGATGATGATGATGATGATGATGATGATGAT 4156

1190 nlyseProlyseGlnAspLeuGluGlyGluValIysLeuLeuGluMetGluLeu 1210
 4157 CACAGCAACTAGGAAATGCGAGAAAGAGTAGGAACTAATTAAGTAATTAAT 4216
 1210 uLyseGly----- 1212
 4217 AAATGATGACAGATGCTTCTTCATGTGAGTTAGTGAAGACATACCAGAGTGAATT 4276
 1212 ----- 1212
 4277 TGTGTAACAACCAATGAAACAGACACCTGTGTCTTGGCTCATTTGAGAGATTAATTC 4336
 1213 -----HisLeuThrAspSerGlnLeuSerIleGluIysLeuGlnLeuGlu 1230
 4337 CTACAGACACTTGAACA-----TTGTACAGACAAAGAAAGTTCAAAATGACATTGGCCA 4387
 1230 uValThrGluIysLeuGlnThrLeuGlnGluIleuMetIysAsnIleThrIleGluArgAs 1250
 4388 ATTGCAGAGAAATTTCTTATCTTTTCAAAAGTAAACAAAATTTTATCATGATGACAGACTG 4447
 1250 nGluLeuGlnThrAspMetGluAspLeuIysAlaGluHisAspSerLeuIysGlnAspLe 1270
 4448 TCAGATGAGCTCTTAATATGTCAGAGCTGACACTATGTTGACTATTAAAG----- 4499
 1270 uSerGluAsnIleGluGlnSerIleGluThrGlnAspGluLeuArgAlaIleGlnGlu 1290
 4500 -GCCGAAAATTGGTCTGTCTCA-----ACGAATCTGAGAACTTTCAAGGTGA 4546
 1290 uLeuArgGluGlnIysGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerVa 1310
 4547 CTGTGTGAGAGAGATGACAGCTG-----GGCTTGAGAGAGGGGCTGTTCCATCCCTGTC 4600
 1310 IGIlyLeuSerProAsnHisAspAlaValAlaAsnGlnIlyValSerLeuGlyG 1330
 4601 ATCCCTTGCTGTGCTGACAGCTGACCTTAAGTCTTAGC-----AGTTTGGGAGA 4645
 1330 uValAsnSerLeuGlnSerGluMetLeuArgGlyGluArgAspGluLeuGlnThrSerCy 1350
 4646 C---TCCCTCTTTTACAGAGCTCTTTTGA-----CAGACAGAGAGA 4684
 1350 sLyseAlaLeuValSerGluLeuGlu----- 1358
 4685 TATGTCTCTTTTGAATTAATTTAGAAAGGGCTTTTACAGCAACAGTGCAGTGAATGA 4744
 1359 -----LeuLeuArgAlaHisValIysSerValGluGlyGlnAsnLeuGlu 1374
 4745 AGTATTTTGCAGACAGCTGACAGCTGATGTGACTTAAGAGCGCAAAATTTGTCT 4804
 1374 eThrIlyIysIleuAsnGlyLeuGlnIlyLeuGlyIysSerGlu-----G 1391
 4805 GTCAACGATCTGAGAACTTTCAAGGTGACTTGTGAGAGAGATGACAGCTGGCTTGA 4864
 1391 uSerGluValLeuIysSerMetLeuGlnAsnLeuIysGluAspAsnIlyLeuIys-- 1410
 4865 GGAGGGGCTGCTTCATCCCTGTCTCTTGTGTGCTGACAGCTGACGCTTATGACAG 4924
 1411 -----GluGlnAlaGluIlyrSer----- 1417
 4925 TTTGGAGAGCTCCTTTTACAGAGCTCTTTTACAGACAGAGAGATATGCTCTTTT 4984
 1418 -----SerIysGluAsnGlnPheSerLeuGluGluValPhe----- 1429
 4985 GAGTAATTTAGAAAGGGTGTGTTTCAAGCAACAGTGCAGTGAAGTATTTTTCAG 5044
 1430 -----SerGlySerGlnIlyLeuVal 1436
 5045 CAGTGTGACAGAGAGATCTCAACAGAAAGAAACCTTGGGCCCAAGCAAGAGGTGT 5104
 1436 IAspGluLeu-----GluValLeuIysAlaGlnLeuIysAlaIleGluGluArg 1452
 5105 TGAAGAGCTTGAGTCCCTCTGTGAGAGGTGAACGGAGCTCCTCGAAGAGCTGAAGAGAGA 5164
 1452 glLeuGlu-----IleIysAspArgAspIlyrPheGluLeuValGlnThrAlaAs 1468

5165 AATGAAAGTCAAGGATTTATGAAAATAGAAATTCAGAGGCTCGAGAGTTATTAAG 5224
 1468 nThrAsnLeuValGlu---GlyIysLeuGluThrProLeuGlnAlaAspHisGlu----- 1485
 5225 TTTGTAAGGCAAGAGCTTGACCTGCTTGAAGAGAGATTTTGTAGAAAATGAACAGCTG 5284
 1486 -GluAspSerIleAspArgSerGluIleuMetGluIlyValIysValIysGlyIysLe 1505
 5285 GCAACAGAACTGCAACAGCTGACCTGTGAGATGAGTCCAAAGTTGGGGCGCAAAAAGAA 5344
 1505 uGluIysArgAsnIlyrLeuLeuGlu-----ArgLeuGlnGlnIlyIysLeuG 1521
 5345 ACAGACGGAAACATCTGCACTTGAAGCTGAGAGTACAGACAGCTCCAGATCAAGAGTCTGA 5404
 1521 uLeuSerAsnIlyIysLeuGluIleuGlnIlyAspGluMetGluThrSerValLeuLeuIys 1541
 5405 CTTAAGTCTCGG-----TCTTGTCTTGGCAT 5431
 1541 PAspLeuGlnGlnIlyIysLeuGluSerLeuLeuSerGluAsnIleIleLeuIysGluAsnI 1561
 5432 CGACACAGAAAGTCTTATTCAGGC-----CGAAATGAGAGCTG 5470
 1561 eAspThrThrLeuIysHisIleSerAspThrGlnAlaGlnLeuGlnIlyIys----- 1577
 5471 TGACATATCAAAAGAACATCTCTGAAACTACAGAAAGAACACCAAGAGCATGCTTCA 5530
 1578 -----ThrGlnGlnIlyLeuGlnLeu-----AlaIly 1586
 5531 TCAGATTTGTGATAAGATGCTCAGACAGAGCTCAATGACTGACATTCAGAAATTAATCA 5590
 1586 eAsnLeuAlaIleAlaIleAspArgAsnProIleThrGlnIlyIysGluThr----- 1604
 5591 GACTGTGCAAGTAAACCCACAGAGAGTCTGTGGGAAAGTCCCAAGATACCAATTA 5650
 1605 -----SerIleAspCysValHisProLeu----- 1612
 5651 TGAGCTCCAGGGAGATTAACCCAGAGGCTCTTCAAGATTCATTTGCAATTTGTCATT 5710
 1613 -----GluGlyIysIleLeuLe 1618
 5711 TTTGCTCTTAAGCTTTGTGATCTATGATGATTTCTCGGGGAATCGAGAAATATCCATTA 5770
 1618 uLeuThrGluGluLeuHisGlnIlyrThrAsnGlnGlnIlyIysLeuHisGluIysAs 1638
 5771 TCTTAACTCGCGGTAAGAGACATCAAAATGAGATTTGAGATTACTTCATGTATGA 5830
 1638 nGluLeuGluGlnAlaGlnValIleGluLeuIysCysGluValGluHisIleMetIysSerMe 1658
 5831 GCACCTGACAG-----AAAGTTGAAGTTGCTTAATGAAT 5869
 1658 rIleGluSerIysSerSerLeuGluSerLeuGlnHisGluIlyHisAspThrGluGlnG 1678
 5870 GAAGAGATTAAGCTCAAAATC-----CATTTACAGAGAGTACA 5908
 1678 nLeuLeuAla-----LeuIysGlnGlnMetGlnValIleThrG 1691
 5909 ACTAATGACCAAAATTTGAAGCATGATGAATTTGAAAATAGTTGGGAATTAAGAA 5968
 1691 nGluIlyIysGluGlnGlnThrHisGluHisIleuThrAlaGluValAspHisGluIly 1711
 5969 AGAAAACACAGATTAAGTGAAGAAATTTGAAATATTTTCTGTGTATGACACAGAGATTA 6028
 1711 sGluAsnIleGluLeu-----GlyLeuAsnPheIysAsnGluAlaGln---GlnIlyrTh 1728
 6029 CCAGAGATTAAGAACTTGAAGGCTCAATTTGATTTAGAAATGATGACAGATTAATC 6088
 1728 rThrIysGluGlnCysLeuLeuAsnGluAsnIly----- 1739
 6089 ATCAGGTGAGATTAATGAGATTAATGTCGCAAGGTGATGACAGCTGAAAGAGAGATT 6148
 1740 ---GluLeuGlnGlnSerGlnHisArgLeuGlnCysGlu----- 1751

Db 6149 TCTTATGTGAAAAAGTACGATGATCGAGAAAGCTAGCTGACATGCA 6208
 Qy 1752 -----1leGlulLeuMeLysSerLeuYsApLysGluSerAlaLeuGluTh 1768
 Db 6209 AGCCCTTACCTGAGGGCTGATGAGGTATGCAACAGAGAGCTATGTTTGA 6268
 Qy 1768 rLeuLysGluSerGluGluGluValIle---AsnLeuGluGluGluMetValMe 1787
 Db 6269 AGACAATGAAATGACAGAAAGTATGCTGCTTGAAGAAAGCTCTGAGTGC 6328
 Qy 1787 rLeuGluMetGluGluLeuLeuYsSerGluThrValIleAlaGluArg- 1804
 Db 6329 AAGTAGAGAAACCCAGCTTCGTGAGAAATTAATGATCTATGCAAAAAAACAGGCACT 6388
 Qy 1805 -AspGluLeuGluAspLeuArgGluSerValGluMetSerIleGluThr- 1821
 Db 6389 CGATCAGTTGCTGTAAGAAATGAGAGAAACACAA---GAGCTTGAAGTCTCATCAAG 6445
 Qy 1822 -----GlnAspLeuArgGluValGluGluAlaLe 1832
 Db 6446 TGAGTGTCTCCATTCATTCAGTGGCAGAGGAGGTGAAGAAAGAGGAACTCT 6505
 Qy 1832 uGluGluGluYsApLysValGluGluLeuThrSerGluIleSerValLeuGluGlu 1852
 Db 6506 TCAGACTTGTCTCTGATGATGAGCTGTTAAAGACAAACCTCATCTCCAGGAAA 6565
 Qy 1852 sIleSerLeuLeuGluAsnGluMetLeuYsAsnValAlaThrValGluThrLeu 1872
 Db 6566 GCTGAGAGTTTGAAGAAAGACTCAAGAGCTGCTTTGACAAATGAGAGCTGAAA 6625
 Qy 1872 rGluArgAspLeuAsnGluSerGluIleGluThrLeu 1892
 Db 6626 CCAAAATTCGACAACTGAATTAAGAAAGATGCTTGTCAAGAAATCTGAAGCTGCA 6685
 Qy 1892 rLeuSerLeuYsGluYsGluPhe-----AlaLeuGluAla 1905
 Db 6686 GGCAGAGTGAATGATGATTAAGAAAGCTGAATGCTCCAGGCTTGGAGCCGC 6745
 Qy 1905 aGluYsApLysAlaAspAlaAlaArgYsThrIleAspIleThrGluYsIleSer 1925
 Db 6746 ACTGCTGAGAAAGGAGTGCATTTGAGCTGAGCTCAACAGAGAGAGATGCATCA 6805
 Qy 1925 nIle-----GluGluGluLeu 1931
 Db 6806 GCTGAGAGAGCATCGAGAAACCTGAGAGTTCGATGAGCCGATGAAGAAAGACAGCT 6865
 Qy 1931 uGluGluAlaThrAsnLeuYsGluThrLeuYsGluArgGluSerLeuIleGluYs 1951
 Db 6866 GCACATTCGACAGAAAGCTGAAGAAAGCGAGCGGAGAAATGATTCATT- 6916
 Qy 1951 sGluGluLeuAlaLeuAsnThrGluIleLeuArgGluThrLeuYsSerYsAspLeuAl 1971
 Db 6917 GATTAAGTGAAGAAAGCTGAAGAAAGGAAATTCAGAGATGCAAGAAAGCAAGAGCTAGT 6976
 Qy 1971 aLeuGluYsMetGluGluGluArgAspGluAlaAlaAsnYsValIleAlaLeuThr 1991
 Db 6977 GATT-----CTTGATGCGGAGAAATTCAGAAAGCA- 7004
 Qy 1991 uLysMetSerLeuGluGluGluIleAsnGluAsnValThrThrLeuYsGluYs 2011
 Db 7005 -GAACTAGAGCTTAAGAAACCAATTAAGAAAGATGCGCAGAGAGCTTAAGATTGCA 7063
 Qy 2011 u-----GluYsGluThrPheYrLeuGluArgProSer 2024
 Db 7064 ATTAGACCTTCACAGTTAAGTCTGAAGAAAGAAATTCAGAAACCAATTAAGAAAGAA 7123
 Qy 2024 sGluGluSerSerGluMetGluGluLeuArgGluSerLeuYsThrYsAspLeu 2044
 Db 7124 ACAAGGTCAAGTGTGAGAACTGAGAAAGTACTCTCTTCAATTAAGAAAGCTGTTAGAGA 7183
 Qy 2044 nLeuGluGluAlaGluYsGluIleSerGluAlaThr----- 2056
 Db 7184 -AAAGAGCAAGAGATTCAGATCAAGAGAAATCTTAAGAAAGCTGAGAGATGCTTCA 7243

Qy 2057 -AsnGluLeuYsAsnLeuThrAlaYsIleSerSerLeu-----GluGluGluIle 2074
 Db 7244 GAATCAGTTAAAGAGCTTAATGAGGCGAGTGCAGCCCTGTGTGTGACCAAGAAATTA 7303
 Qy 2074 uGlu-----AsnIleSerIleLeuAsnGluAlaValSerGluArgGluAsnLeuArgHis 2093
 Db 7304 GAAAGCCACAGAAACAGATCTAGACCCCAATAGAGAAAGAGCTACGCTGAGAAATAG 7363
 Qy 2093 rLysGluGluLeuValSerGluLeuGlu-----GluLeuSerLeuThrLe 2108
 Db 7364 CATTGAAGAGCTGAGAGCCCGCTTGAAGCTGATGAAAGAAAGAGAGCTGTGTGCTTACA 7423
 Qy 2108 uLysSerArgAspHisAlaPheAlaGluSerLeuYsArgGluYsAspGluAlaValAsn 2128
 Db 7424 ACAAGTGAAG-----GAAAGAGAGATCATGCAAGTTTCAATTAAGGTTAG 7468
 Qy 2128 sIleAlaSerLeuAlaGluGluIleYsIleLeuThrYsGluMetAsp----- 2144
 Db 7469 AGTGAGAACCTTGAAAGAGAGCTAGAGATGAGCCAGCAAAACCAAGAGCATGCACTCT 7528
 Qy 2145 -GluPheArgAspSerYs-----GluSerLeuGluGluGluSerHisLeu 2161
 Db 7529 TGAGGCAGAGAAATTCAGAAAGAGAGTGAAGACCTTAAGCAAAATAGAAAGGATGAC 7588
 Qy 2161 rGluGluLeuYsThrYrYsThrGluLeuGluMetLeuYsGluGluValAspIle 2181
 Db 7589 CCAAAAGTGAAGAGCTGAGATTAAGATGTTGTTACTTAAGGTCAGAAAGAAAGATCT 7648
 Qy 2181 eAsnAsnYsLeuAlaGluYsValYsGluValAspGluLeuLeuGluIleSer 2201
 Db 7649 GACAAATGAATTAACAAAGAGCAAGAGCAATATCTGAATTA- 7691
 Qy 2201 rLeuYsGluGluLeuAspGluIleGluMetGluLeuArgAsnGluYsLeuArgAsn 2221
 Db 7692 -----GAAATATAATTAATTCATTCATTTGAAAT- 7718
 Qy 2221 rGluLeuYsGluYsMetAspIleMetGluYsGluIleSerValLeuArgLeuMet 2241
 Db 7719 -----ATTGTCAGAAAGAAAGAA 7735
 Qy 2241 nasGluProGluGluGluAspAspValAlaGluArgMetAspIleLeuGluSerArg 2261
 Db 7736 GCAGAGAAAGTACGATGAAAGAAATCAAGCACTGCCATGAGATGCTTCAACA- 7793
 Qy 2261 gAsnGluIleGluGluLeuMetGluYsIleSerAlaValYsSerGluGluIleHis 2281
 Db 7794 -----CAATTAAGAGCTCAATGAGAGAGTGCAGCCCTGCATTAATGACAA- 7841
 Qy 2281 rLeuLeuSerSerLeuSerSerGluLeuGluYsGluThrGluAlaHisYsHisCys 2301
 Db 7842 -----GAGGCTGTAG- 7853
 Qy 2301 rLeuAsnIleYsGluSerLeuSerSerThrLeuSerArgSerPheGluSerLeuGlu 2321
 Db 7854 -----GCCAAAGACAGAAATCTTAATGTAAGTCAAGTGAAGTCTTGAAGT 7897
 Qy 2321 rGluIleValYsLeuAsnThrGluLeuGluThrLeuLeuAsnYsPheYsValVal 2341
 Db 7898 TGAGAGAGCTCAGTGTCAAGAGCTTGAAGAGCCCAAAATATTAATTAATGTTTGA 7957
 Qy 2341 rArgThrAlaAlaValYsGluAspHisSerLeuIleYsAspYrGluYsAspLeuAl 2361
 Db 7958 ATCTTCACTG-----AATGGCTCATTAAGAAAGTGAAGATGCGCAACA 8002
 Qy 2361 aAlaGluGluYsArgHisAspGlu-----LeuArgLeuGluGluGluYsLeu 2378
 Db 8003 GAACTGAGAGAGAGAGTGAAGAAATCAGTGAAGTGAAGAAATCAATTAAGAGCAACA 8062
 Qy 2378 uGluIleGluYsArgYsPheSerAspSerAlaSerIleGluLeuYsPhe----- 2394
 Db 8063 GCAGCTTGTCTTAAGCTGTCCAGGTGAGAGAGACCAACATTTGAGAGAGCAAAA 8122

Oy	2395	CyegluileguluPheleuAenGluileuLeuPheyleysylalabanielleleGlnserVa	2414
Db	8123	CTTAAAGATCTGAGAAATCTGCACAGTGGAAATGGAGGAGAAAGATCCAAAGCTCTCAATTC	8162
Oy	2414	IGlnAapRaphPheSerGluValGlnValPheleuAenGlnValGlySerThrleuGlnG	2434
Db	8183	AAATGCCCTCTTGGCAGGACACATTGAAGTGTCTGACAGCTTCTTCAAGAACTTAGACA	8242
Oy	2434	UGluLeuGlu---HislyblysglyPheMetGlnTripleuGlnUGluUGluPhegly-----	2450
Db	8243	TGAGCTTGAATTGACAAATAATGACAAATATGCTTTGTTGAAAAAGTAAACAAAATGAC	8302
Oy	2451	-----AspleuHisValAspAlaIyslys-----Le	2455
Db	8303	TGCAAAAGAAACTGAGCTGCAGAGGGAATATCATATGATGCGACGAAAACACAGACACT	8362
Oy	2459	uSerGluUGluMetGlnGlnGluAenAArgIleAlaSerThrIleGlnleuLeuThly	2479
Db	8363	GCAAGAGAACTCACTGAGAGAGAAAAATAGGCTAGCTGAGAGATTGGCAGTTCCTTGG	8422
Oy	2479	sArgyleuysAlaValValGlnserlysIleGlnArgGluIleThrValTytleuAenG	2499
Db	8423	AGAAATAAAGAGC-----AGCAAAAGATCA-----	8447
Oy	2499	nPheGluAlaIybleuGlnGluIylyblysglnGlnAenlysgluLeuMetAArgAArgMetG	2519
Db	8448	-----TTGAAGGAGCTCACACTGAAATATGTAATGTAATGAAGG-----	8466
Oy	2519	uHisHleGlyProSerAlaSerValMetGlnGluGluAenAlaArgleuLeuGlyIle	2539
Db	8487	-----ACCTTAGATTGCTATCACAAAGACAGGTGAAAAAGAAAGG-----	8528
Oy	2539	uLySerThrValGlnAapGluSerLyblysglnGlnSerAArgIleuysMetleuGluAenG	2559
Db	8529	-----AAAGTAGAGAGGAAATAGCTGAATATCAGCTACGG-----	8564
Oy	2559	uLeuAenleuVallybAspAspAlaMetHislysglyGluys-----ValAlaIlele	2577
Db	8565	-----CTTCAATGAAGCTGAAAAAACAACAGCGCTTTGCT	8599
Oy	2577	UGlnAapRlyblyleuSerAArgAenAlaGlnAlaGluAenAenAlaMetGlnValIylyse	2597
Db	8600	TTTGGAC-----ACAAACAACAGTATGAATATAATTCAGACATATCCAGAGAGAAAT	8653
Oy	2597	uThrlyblysglnAapAenleuGlnAlaAlaMetlysgluileGluAenleuGlnlybme	2617
Db	8654	GACTTCTTAAAGAAGAATGCTCTCAGTTCACAGAGCTGGAGATGACCTTTAAAGTCTAG	8713
Oy	2617	tValAlaIysglyAlaValProTyrylysglnGluIleAapAen-----	2631
Db	8714	T-----AAAGAAGAGCTCAATATTCATTGAAAGTACTAC	8749
Oy	2632	-----leuLySerThrlybValIylybIleGluMetGluIylybIlelyTyT-----	2646
Db	8750	TCAGATTGAGAGATGAGAAACCAAGATGGACAATCTAAATAATGTAAATCAGTT	8809
Oy	2647	-----SerlybAlaThrAapGlnGluIleAlaTyryleuIylybSerlys-----	2660
Db	8810	GAAAGAGAAATGAACCTGCCCCAGGGGAAAAATGAAGTTCTTGATCAAAATCCTGTAAACA	8865
Oy	2661	-----leuGlnAapRlysglnGluIylyleuAArgyleuysgluGluLeuAArgAlaGlnAl	2680
Db	8870	GCTGGAAGAGGAAAAAGAGATATCTGCANAAAGAACTCTCAACTTCAAGCTGCACAGGA	8929
Oy	2680	AAspAenAapRlyThrThrValCysValProlybAapRlyGlnlybAlaSerThrPheProva	2700
Db	8930	GAAAGCAAAACA-----	8942
Oy	2700	lThrCysgllyGlySerGlyIleValGlnSerThrAlaMetleuValleuGlnserG	2720
Db	8943	-----GGTACTGTTATGATATCAAGGTGATGAATTTAAACAATCACTGA	8983
Oy	2720	u-----LybAlaAlaIleuGln-----AArgIleuSerThrIstTyrylybly	2733

Db	8964	GATCAAGAACTGAAAGAACTCTTGAAGAAAAAACAAGAGGCACTGAATTA	CTTGGCA	90433
Qy	2733	slvstytrhihiisleuserarghrhmetserseisergluasparglylvrhllyeal	27533	
Db	9044	TAAGTACTGTTCCCTG-----CTTAATAAGCCATGAAAGATTAGAAAGCTAAAGA	9094	
Qy	2733	alyaserapalahisersehiethrhllysersehis-----argel	2768	
Db	9095	GATGTATAGACACAAGTGGCCCACTGTGTTCACAGCAATTAACAGATCCCGAG	9154	
Qy	2768	ysereprohiislystrhgutntrlyarghielglyprovalthrprogluargserglume	2788	
Db	9155	GTCTTCCT-----TTGCTAGTCTCACTTTTCCAGGACCATCTCCAT	9156	
Qy	2768	lproserleu-----hisleuglyserprolyllysergluusererthlyvar	2805	
Db	9197	CCCTTCTGTACTGMAAAGAGTATTATCTTGGCCAAATTAAGCTTCAGGCAAGAGCA	9256	
Qy	2805	gvalvalser-----probanargsergluliety	2815	
Db	9257	AAGATCCAGTGGAATATGGAGAAATGGTGGAGACAACACCTCTCTACCCAGAGACTT	9316	
Qy	2815	rser-----gluleuvalmetser-----proglylvs-----	2824	
Db	9317	TTCTAAAAAAGCAAGAAAGCAGTCATGATGATTCACCTTCGACAGACAGGAAG	9376	
Qy	2824	-----	2824	
Db	9377	TACTGAGTTTGAGCCAGAGGAGCTTCCAGAGTTGTAAAGAAAGGTTTGTGCAATCC	9436	
Qy	2825	-Thrglymethiylvs-Hisile-----leuserproserl	2836	
Db	9437	GACAGGAAGAAGTACGCCCATATATCTCTCGAAGAACCAACATGGCAATCCGAGCCAGCC	9486	
Qy	2836	ysvalglyleuhiilylvslyvarglaleuserpro-----	2847	
Db	9497	CCGCTGCTCACAG-AAGTTAGGGCTATCCCACTGAGTCTGGCAAGAAATCTTG	9555	
Qy	2848	-----Aenargserglumetprothrlnhiysali	2858	
Db	9556	CAGAGTCTCCAAACCAACACAGCTGTGGCAGACATACAAAGGTCAAAATTCCTCAGC	9615	
Qy	2858	leserproglylvrthrgly-----leuhiilyasleuThrGluserThrleuphea	2876	
Db	9616	GGAGCCAGTGAATTACAGGCACCATCTCCGAGAACCCACCAAGAAATCCCTCCACATCA	9675	
Qy	2876	spasleuserseerprocylyselnglnlyvalglnghuanleuanserprolysg	2896	
Db	9676	ATAATCTTCTCGAAGAAATCCGACTGACACGCCCCAGAGAGGGCTGAGGGTCAAGCGAG	9735	
Qy	2896	lylvsleuphe-----Aapvallyserleusermetprotyrcypro	2911	
Db	9736	GCCGACTGTGCCCCAGCCCAAGCTGAGTCCAGAGCGCAGTGAAGACTGTAAAG	9755	
Qy	2911	ergin	2912	
Db	9796	TCCAG	9800	
RESULT 7				
US-10-084-817-361				
; Sequence 361, Application US/10084817				
; Publication No. US20030119009A1				
; GENERAL INFORMATION:				
; APPLICANT: Susan Stuart				
; APPLICANT: Jed G. Nuchtern				
; APPLICANT: Sharon E. Pion				
; APPLICANT: Jaeson M. Shohet				
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION				
; FILE REFERENCE: PA-0046 US				
; CURRENT APPLICATION NUMBER: US/10/084,817				
; CURRENT FILING DATE: 2002-02-25				
; PRIOR APPLICATION NUMBER: 60/270,784				

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; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 361
; LENGTH: 10281
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 026662.3
US-10-084-817-361

Alignment Scores:
Pred. No.: 2,86e-63 Length: 10281
Score: 1149.00 Matches: 706
Percent Similarity: 37.53% Conservative: 550
Best Local Similarity: 21.09% Mismatches: 1030
Query Match: 7,78% Indels: 1062
DB: 14 Gaps: 141

US-09-724-584-1 (1-2954) x US-10-084-817-361 (1-10281)
QY 333 ThrProHisValAsnGluValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGlu 352
DB 197 ACAAGAGCTCTTCAGAAAAATTCAGAGCTTGAAGCAGACCTTGACAACTGAAAGAA 256
QY 353 IleAspLeuLysGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGln 372
DB 257 AAGCAGCAAGGACAGTTTACAGCTTGACGCTCGAGCGCTCGAGAGCAAAACAG 316
QY 373 AlaMetAlaLysGluGlu-----HisThrGlnLeuLeuAla 384
DB 317 AAGGTGAAAAAGAAAAACCGAGGTACCAACCTGAAAAAGGAGAAATCAAGATTGATG 376
QY 385 GlnIleLysGlnLeuHisLysGlnArgGlnAspArgGlnLeuProHisLeuThrAsnIleVal 404
DB 377 GAAATATGGAAGCTCTGAGAAACTTAAGCAGAAAGATTCTCAT-----GAACCTCA 430
QY 405 ValAlaSerSerGlnLysSerGlnLysPhe-----GlnArg 416
DB 431 GTCAGAGAGCTCACAGTGAATTTCCAGAAAGCAACATGATTCAGCCAAAAACAAATA 490
QY 417 ValLysArgLysArgArgValThrTrpAlaProGlnLysIleGlnAsnSerLeuHisAla 436
DB 491 GAAAAAAGCTGGAACAGAACTTAAGAGGTAAATGAGCTTGAAGAAAGCAACAGAGCT 550
QY 437 SerGlnValSerAspPheAspMet-----Leu 445
DB 551 GGCAGAGCTGCGAGATGTCTCTGATCATCATGCAATACCACAAAAAATTTTACACT 610
QY 446 SerArgLeuProGlnAsnPheSerLysLysAlaLysPheSerAspPheProSer----- 463
DB 611 CCACCTAACCCCAAGCAATATATATAGTGTCCAAAGTATGAGATCTAAAGAAAAATAT 670
QY 464 PheProGlnLysAspAspSer-----ValCysThrGlnPheSer 476
DB 671 AATAAAGAGGTGGAAGCAAGAAAAAGATTAGAGCGAGAGTTAAAGCCTTGGAGCTTAA 730
QY 477 AspPheAspAspAlaLeuSerMetMetAspSerAsnGlnIleAspAlaGluTrpAsnLeu 496
DB 731 AAAGCAGCCAGACTCTTCCACAGCCACCATGAATCACCGGACATTGCCCGCATCAG 790
QY 497 AlaSerLysValThr-----HisArgGlnLysThrSerLeuHis----- 509
DB 791 GCTTCATCATCTGTGTCTCATGCGAGCAAGAGAAAGACCCCAAGCATCTTTCATCTAAT 850
QY 509 ----- 509
DB 851 TCTCAAGAACTCCATTAGAGAGATTTCTCTGCATCTTACTTTCTGGGAAACAAGAG 910
QY 510 -----GlnSerMetIleAspPheGlnLysIleSerAspSerValGlnPheHis 525
DB 911 GAGACTCCAAAGTCGATCACTTGCAGAAATAGGAAAAAGATGCTAATATGCGATTCTTT 970

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QY 526 AspSerSerLysGlnAsnGlnLeuGlnIleuGlnIleuProLysAspSerGlnAspMetAlaGlu 545
DB 971 GACATTTCTAGACAGTCTCATCTTTG-----GATCAATATTAAAA 1009
QY 546 CysArgLysAlaSerPheGlnLysGluIleThrSerLeuGlnGlnLeuGlnSerLys 565
DB 1010 GCGCAGAACTCAAGAGCTTAAGAAAAAGATTATAGTGAAGTTAGCGCTGCAGAGACAT 1069
QY 566 GlnGlnGlnLysLysGlnLeuValGlnSerPheGlnLeuLysIleAlaGlnLeuGlnGlu 585
DB 1070 GAAAAAGAAATGAAGAGCCCAAGTGAATGATTCA-----GAATCCAACTC 1117
QY 586 GlnLeuSerValLysAlaLys-----AsnLeuGlnMetValThrAsnSer-- 600
DB 1118 CAACCTGAGG---AAAGCAAAAGTGGAATTAATTGAAAAAGAAAGTTTGAACAATATGT 1174
QY 601 ArgGlnHisSerIleAsnAlaGluValGlnThrAspValGlnLysGlnValAlaArgLys 620
DB 1175 AAGGATGAACCTAGTGAACCAACAGCACAATACGAC----- 1210
QY 621 GlnMetSerValLeuGlnLysSerGlnLysAsnAlaSerAsnSerAspLeuGlnAspSer 640
DB 1211 -----CAGGCTCAACCAAGTATCTGATTTGAAACAAATACTGAAAAAATTG 1258
QY 641 SerValAspGlnLysArgLeuSerSerSerHisAspGlnCysIleGlnHisArgLysMet 660
DB 1259 ACGGAAAGAT-----TTGATGTTGACGACCAAAATGCAAAAGTCCAGATGTTCT 1309
QY 661 LeuGlnGlnLysIleValAspLeuGlu---GlnPheIleGlnAsnLeuAsnLysSer 679
DB 1310 CTGGAACAGAAATTAAGAAAAAGAAAGAGATTCAAGAGAGCTCTCCCGT----- 1363
QY 680 GlnAsnAspLysGlnLysSerSerGlnLysAspPheMetGlnSerIleGlnLeuCysGlu 699
DB 1364 -----CAACGCGTCTTCTCCAAACACTGAGCAGAGTGATTCAGATG----- 1408
QY 700 AlaIleMetAlaGluLysAlaAsnAlaLeuGlnGlnLeuAlaLeuMetArgAspAsnPhe 719
DB 1409 -----AAGCCAGACTCACCCAGAGGTACAGCAAGCCAG---AATATG 1450
QY 720 AspAsnIleIle-----LeuGlnAsn 726
DB 1451 CACAACGCTCGCAGGCTGAACCTGATTAACATCATCATGTAACCAACAGCTAGAAAAAC 1510
QY 727 -----GlnThrLeuLysArgGlnIleAlaAspLeuGlnArgSer----- 739
DB 1511 AATTGGAAGAGTTTAACCAAAAGTTGACAGAGCTGAACAGCGCTTCAGGCGAGTCAG 1570
QY 740 LeuLysGlnAsnGlnLysThrAsnGlnPheGlnIleLeuGlnLysGlnLysGln----- 757
DB 1571 ATCAAGGAGAAATGAGCTGAGAGAGAAAGCATGAGGAAATGAAGAAAGAAACAACCTCCT 1630
QY 758 LysGlnHisGlnAlaGlnLeuIleHisGlnIleGlnSerLeuLysLysLeuValGlnAsn 777
DB 1631 AAGAGCTCATCTGACCAAAAGCCAGAGAGTCTGCACTTGAGGCGCAAACTCAAGAAC 1690
QY 778 AlaGlnMet-----TyrAsnGlnAsnLeuGlnLysAspLeuGlnThrLysThrLys 794
DB 1691 ATCAAAAGCTGTTTAATACAGACAGAGATTTTGAGAGAAAGAAATGAAGCCAAAGAT--- 1747
QY 795 LeuLeuLysGlnGlnIleIleGlnLeuAlaGlnLeuAlaGlnLysArgAlaAspAsnLeuGln 814
DB 1748 -----ACCTCTCGAGAAACCATGTTAAGATCTTCAAGAAAAATTAATCAGCAAGAA 1801
QY 815 LysLysValArgAsnPheAspLeuSerValSerMetGlnAspSerGlnLysLeu----- 832
DB 1802 AACTCTTGACTTTAGAAAACTGAAGCTTCTGTGCTGATCTCGAAAAAGCAGCGAGAT 1861
QY 833 CysGlnGlu-----IlePheGlnLeuLysGlnSerLeu 843
DB 1862 TGTTCCTCAAGACCTTTTGAAGAAAAAGAGACATCATCATGTAACCAACTTAATGATTA 1921

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Db 3998 AGTCAAAAGCAGATGCACACCTTCCTCTCTGCAAAACAATGAAACAGCTGAAAT 4057
QY 1293 GUGUUGLYSGHLEUVALSPSErPhearGInGInLeuaspCyseValGlyle 1312
Db 4058 GAGCTAGAGAAAATATGTGAAATAGTACGAGCTGAAAGAAAGTAACTGTAAGTACGAGCTG 4117
QY 1313 SerSerProAsnHisAspAlaValAlaenGInGInLysValSer 1327
Db 4118 AATGATTTCAAGGTGCAAGATGATTCACAGCACTAGGAAATGCGAGAGAGTGGGAAA 4177
QY 1328 ---LeuGlyGlyValAsnSerLeu---GInSerGInMetLeuArgGlyGluArgAsp 1344
Db 4178 CTACCTAAATGAAGTAAATATTAATATGATGACAGTGTCTCTCCATGTGATGAGTAAAGT 4237
QY 1345 GIn----- 1345
Db 4238 GAAAGCATATCACAGAGTGAATTTGGTGAACAACAAATGAACAGACCCCTGTCTTTG 4297
QY 1345 ----- 1345
Db 4298 GCTCATTTGACAGAGATTAATTCACAGCACTTGCACTTGCAACAAGAGTTCAA 4357
QY 1346 -----LeuGInThSerCySylsAlaLeu 1353
Db 4358 ATGCACTTTGCCGAATTCAGAGAAATCTTATCTTTACAAAGTGAACACAAATTTTA 4417
QY 1354 -----ValSerGInLeuGInLeuArgAlaHisValLysSer 1366
Db 4418 CATGATCAGACTGTGAGATGAGCTTAAATGTCAGAGCTGACAGCTATGTGATCA 4477
QY 1367 ValGInGlyGlyAsnLeuGInLeuThryLysLeuAsnGlyLeuGInGInLysGInLeu 1386
Db 4478 TTAAGGCCGAAATTTGTCTGTTCACAGAACTGAGAACTTTCAAGTCACTTGGTGG 4537
QY 1387 GlyLysSerGIn-----GInSerGInValLeuLysSerMetLeuGInAsnLys 1403
Db 4538 AAGGAGATGCAGCTGGGCTTGAGAGGGGCTCCCTTCATCCCTGATCCTCTGTGTG 4597
QY 1404 GInAspAsnAsnLysLeuLysGInGInAlaGIn----- 1414
Db 4598 CCTGACAGCTTACCTTAGCAGTTTGGAGACTCTCTTTTACAGAGCTTTTACAA 4657
QY 1415 -----GlyLysSerSerLysGInAsnGInPhe 1423
Db 4658 CAGACAGAGATATCTCTTTTGAATTAATTAAGAGGGCTGTTACAGCAACAGATGC 4717
QY 1424 SerLeuGInGInValPhe----- 1429
Db 4718 AGTGAATGAAGTATTTTTCAGCAGCTGACAGAGAGAAATCTGACCGAAGAAACC 4777
QY 1430 ---SerGlySerGInLysLeuValAspGInLe-----GInValLeuLysAla 1444
Db 4778 CCTTGGGCCCCCAGCAAGGCTGTGAAGGCTTGAAGTCTCTGTGAGCTGTAACCGCAG 4837
QY 1445 GInLeuLysAlaAlaGInGInLysLeuGIn-----LysAspArgAspLys 1460
Db 4838 TCCTCTGAGAACTGAGAGAAATGAAAGTCAAGGATTAATGAATAATGAAGAAATT 4897
QY 1461 PheGInLeuValGInThryAlaAsnThryAsnLeuValGIn---GlyLysLeuGInThryPro 1479
Db 4898 CAAGAGCTGAGCACTTAATTAATCTGTAAGAGCAAGAGCTTGAAGCTTGAAGAGC 4957
QY 1480 LeuGInAlaAspHisGIn-----GInAspSerLysAspArgSerGInGInMetGIn 1497
Db 4958 TATTGTGAGAAATGAACAGTGCACAGAGCAAGAGCTGACCAAGCTACTCTGAGATGAG 5017
QY 1498 IleLysValLeuGlyGlyLysLeuGInLysArgAsnGInLysLeuGIn----- 1513
Db 5018 TCCTAAGTGGCGCGGAGAAAGAAACAGAGCAAGCAACTGCTCACTTGAAGTGAAGTGA 5077
QY 1514 ArgLeuGInGInGInLysLeuGInLysSerAsnLysLeuGInLysLeuGInLysGInMet 1533
Db 5078 CGACTCCAGCTTACAAAGCTGAGCTTAAGTCTCGG----- 5113

QY 1514 GInThrySerValLeuLysAspLysPheGInGInLysLeuGInSerLeuLysSerGIn 1553
Db 5114 -----TCCTTGTGGATCCACACAGAGTCAATTCAGGC----- 5152
QY 1554 AsnIleLeuLysGInAsnLysPheThryLysLysHisSerAspThryGInAla 1573
Db 5153 -----CGAATGAGAGCTGACATATCAAAAGAACATCTTCTGAAACTTCACAGA 5203
QY 1574 GInLeuGInLys-----ThryGInGInLysLeuGIn 1583
Db 5204 AGAACACCAAGCATGATGTTTCATCATGATTTGTGATAAAGATGCTCAGACAGACTCAAT 5263
QY 1584 Leu-----AlaLysAsnLeuAlaIleAlaAspAsnCyProIle 1598
Db 5264 CTAGACATGAGAAATTAATTAATGAGCTGTGATTAAGAACCCACAGAGAGTGTCTGGG 5323
QY 1599 ThryGInGInLysGInThry-----SerAla 1606
Db 5324 GACAGTCCCAAGATACCAATTAATGAGCTCCAGGGAAGATMAAACCCAGGCTTTCA 5383
QY 1607 AspCyValHisProLeu----- 1612
Db 5384 GAATGATTTGATGATGATTTTCTGCTTAATGCTTTGATGATGATTTCTCTG 5443
QY 1613 -----GInGInLysIleLeuLeuLysThryGInLysGInLysThryAsnGInGIn 1630
Db 5444 GGGAAATCGAGAAATATCATTAATCTTCAACTGGGGTAAAGAACATCAAAATGAGAT 5503
QY 1631 GInLysLeuLysHisGInLysAsnGInLysGInGInAlaGInValGInLysCySylu 1650
Db 5504 TTGATATTTCTCATGTGATGATGAGACCGTACACA-----AAA 5542
QY 1651 ValGInHisLeuMetLysSerMetIleGInSerLysSerLeuGInSerLeuGInHis 1670
Db 5543 GTTGAATGTTGCTAAATGAATGAAGAAATTAAGATCAAAATC----- 5587
QY 1671 GInLysHisAspThryGInGInLysLeuAla-----LeuLys 1683
Db 5588 -----CATTTACAGAGATGACCACTAATGACCAAAATTAAGATGATGAATGGAA 5641
QY 1684 GInGInMetGInValValThryGInGInLysGInLysGInGInThryHisGInLys 1703
Db 5642 AAAATAGTTGGGAATTAAGAAAGAAACACAGATTTAAATGAAAAATTTGAATATTTT 5701
QY 1704 ThryAlaGInValAspHisLeuLysGInAsnIleGInLeu-----GlyLeuAsnPheLys 1721
Db 5702 TCTGTGATCACAGAGATTAATCTCAGAGATGAAGAACTTGAAGGCTCAATTTCTGAT 5761
QY 1722 AsnGInLysGIn---GInLysThryLysGInGInLysGInLysLeuAsnGInLysLys--- 1739
Db 5762 TTAAGAAATGATGAGATTAATTAATCACTGTAAGATTAATGAGTGAAGGCTG 5821
QY 1740 -----GInLeuGInGInSerGInHisArgLeuGInLys 1750
Db 5822 AATGACAGCTGAAAGAGAGATTTCTTGATGTGAAAAATGAGCTGAGATGATGATGAG 5881
QY 1751 GIn-----IleGInLysLeuMetLysSerLys 1760
Db 5882 GAGAAAGCTAGCATGAGATGAAGCCCTTACTGAGGCTGAGCTTGAAGGATGATCA 5941
QY 1761 AspLysGInSerAlaLeuGInThryLysGInLysGInLysValIle---AsnLeu 1779
Db 5942 ACAGAGAACTATGATTTTGAAGAAAGACAAATTAATTAAGCAAGGTTATGTCTGCTT 6001
QY 1780 AsnGInGInMetGInMetValMetLeuGInMetGInLysLysAsnSerGInArgThry 1799
Db 6002 GAAGAAGACTCTGATGTGTACAAAGTGAAGAAACACAGCTTCTGAGATTAATGATCT 6061
QY 1800 ValIleAlaGInArg-----AspGInLeuGInAspAspLeuArgLysSerValGIn 1816
Db 6062 ATGCAAAAAAACCAGGAGCTGATCAGTTGTCTGAAAAAATGAAGAGAGAAAAACAA 6121

QY	1817	MetSerIleGluThr-----	-----	GlnAspSer	1824
Db	6122	--GAGCTTGAGTCTTCATCAAGATGAGTCTCCATTCGATTCAGGTGCAGGCGACAG	6178		
QY	1825	LeuArgLysAlaGlnGluAlaLeuGlnGlnGlnIleuAspLysValGlnIleuThrSer	1844		
Db	6179	GTCGAAGAAAAGACGGAACTCTTCAGACTTTGTCCTCTGATGTAGTGAAGCTGTTAAA	6238		
QY	1845	GlnIleSerValLeuGlnGlnIleuLysIleSerLeuLeuGlnAsnGlnMetLeuTyrAsnVal	1864		
Db	6239	GACAAAACTCATCTCCAGAGAAAAGCTGCAGAGTTTGAAAAGAGCATCACAGGACTGCT	6298		
QY	1865	AlaThrValLysGluThrLeuSerGluArgAspLeuAsnGlnSerLysGlnHisLeu	1884		
Db	6299	TTGACAAAATGTGACTGGAAATCCAAATTGCAACATCGAATTAAGAAAATTCCTT	6358		
QY	1885	PheserGluIleGluThrLeuSerLeuSerLeuLysGluLysGluPhe-----	1900		
Db	6359	GTCAGGAATCTGAAAGCTTCGAGGCCAGATCACTAGTGAATCAGATTATGAAAAGCTGAT	6418		
QY	1901	-----AlaLeuGlnGlnAlaGluLysAspLysAlaAspAlaValArgLysThrIle	1917		
Db	6419	GTCCTCAAGGCTTGAGAGCCGCACTGGTGTGAGAAAGTGAGTTCCGATTGAGGTGAC	6478		
QY	1918	AspIleThrGluLysIleSerAsnIle-----	1926		
Db	6479	TCAACACAGGAGGAAGTCCATCAGCTGAGAGAGCATCGAATACTGAGATTCCGACTT	6538		
QY	1927	-----GluGlnGlnLeuLeuGlnGlnIleAlaThrAsnLeuLysGluThrLeuTyrGlu	1943		
Db	6539	GAGCCGATGAAAGACAGCAGCTGCACATCGAGAGAAATCGAAAAGACCGACCGGAG	6598		
QY	1944	ArgGlnSerLeuIleGlnCysLysGlnLeuAlaLeuAsnThrGlnHisLeuArgGlu	1963		
Db	6599	AATGATTCACTT-----AAGATTAAGTTGAGAACCTTGAAGGAGATTCCAGACG	6649		
QY	1964	ThrLeuLysSerLysAspLeuAlaLeuGlnLysMetGlnGlnIleuArgAspGlnAlaIle	1983		
Db	6650	TCAGAAAGAAACACGAGGACTGATGACTT-----CTTGATGCCGGAATTCCAAAGCA--	6700		
QY	1984	AsnLysValIleAlaLeuThrGlnLysMetSerSerLeuGlnGlnIleAsnGlnAsn	2003		
Db	6701	-----GAACTGAGACTCTTAAACACAAATGAAAGAGTGC	6736		
QY	2004	ValThrThrLeuLysGluGluGlu-----	GluLysGluThr	2016	
Db	6737	GCCAGAGCCCTGAAAATTGTAANTATACCTTGACAGCTTAAGCTCGAAAAGAAAAT	6796		
QY	2017	PheTyrLeuGlnArgProSerLysGlnGlnSerSerSerGlnMetGlnIleuArgGlu	2036		
Db	6797	CTGACAAAACAAATACAAAGAAAACAAAGCTCAGTTGTCAGAACTACCAATCTCTCT	6856		
QY	2037	SerLeuLysThrLysAspLeuGlnLeuGlnGlnAlaGluLysGluIleSerGluAlaThr	2056		
Db	6857	TCATTTAAAACCTGTTAGAGAAAAGGAGACAGACAGATACGATCCAAAGAAATCT	6916		
QY	2057	-----AsnGlnIleLysAsnLeuThrAlaLysIleSerSer	2068		
Db	6917	AAAATCGACGTGAGATGCTTCAGAAATCAGTTAAAGAGCTTAATGAGCGCATGACGCC	6976		
QY	2069	Leu-----GluGlnGluIleLeuGln--AsnAlaSerIleLeuAsnGluAlaValSer	2085		
Db	6977	TTTGTTGGTGTGACAAAGAAATATTAGAGGCCACAGAAACAGAGTCTAGACCCACCAATGAG	7036		
QY	2086	GluArgGluAsnLeuArgHisSerLysGlnGlnIleuValSerGluLeuGlu-----	2102		
Db	7037	GAAAGCATCAGCTGAGAAATAGCATTTGAAAGCTGAGAGCCGCCCTTAAAGACTTAATGAA	7096		
QY	2103	-----GlnLeuSerLeuThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArg	2120		
Db	7097	AAGAAGCAGCTCTGTGCTTTCACAACTGAG-----GAAAGTGAGCAT	7141		
QY	2121	GluLysAspGluAlaValAsnLysIleAlaSerLeuAlaGlnGluIleLysIleLeuThr	2140		

Db	7142	CATGCAGATTTACTTAAGGTAAGTAGAGAACTTTGAAGAAGACTGAGATGACCAG	7201
Oy	2141	LysGluMetAsp-----GluPheArgAspSerLys-----GluSerLeu	2153
Db	7202	ACAAACCAAGACGATGCAGACTCTTGAGCAGACAGAAATTCAAAGAGAGAGTAGACACCTTA	7261
Oy	2154	GInGluGlnSerSerHisLeuSerGluGluLeuCyThrTyrTyrThrGluLeuGlnMet	2173
Db	7262	AAAGCAAAATAGAAAGAGTAGACCCAAAGCTGTGAGAGGCTGTGAATTGATGTTGGTACT	7321
Oy	2174	LeuLysGInGlnLysGluAspLLeuAsnMetLysLeuAlaGluLysValLysGluValAsp	2193
Db	7322	ATTAAGGTGAGAAAGAAAGATCTGCAATATGAATTACAAAGAGCAAGACGCAATATCT	7381
Oy	2194	GluLeuLeuGlnHisLeuSerSerLeuLysGluGlnLeuAspGlnIleGlnMetGluLeu	2213
Db	7382	GAATTA-----GAAATTA	7393
Oy	2214	ArgAsnGluLysLeuArgAsnTyrGluLeuCyGluLysMetAspIleMetGluLysGlu	2233
Db	7394	ATAATATTCATCATTTGAAAT-----	7414
Oy	2234	IleSerValLeuArgLeuMetGlnAsnGluProGlnGlnGluAspAspValAlaGlu	2253
Db	7415	-----ATTTTGCAGAAAGAAAGACCAAGCAAGATCAGATGAAGAAAGAAATTCAGACCT	7468
Oy	2254	ArgMetAspIleLeuGluSerArgAsnGlnIleGlnIleGlnLysMetGluLysIleSer	2273
Db	7469	GCCATGGAGATGCTTCACACA-----CAATTAAGAAGCTCAATGACAGAGTGCCA	7519
Oy	2274	AlaValTyrSerGluGlnHisThrLeuLeuSerSerLeuSerSerGluLeuGlnLysGlu	2293
Db	7520	GCCTGCATATATGACCA-----	7537
Oy	2294	ThrGluAlaHisLysValHisCysMetLeuAsnIleLysGluSerLeuSerThrLeuSer	2313
Db	7538	--GAAGGCTGTAG-----GCCAAAGACAGAAATCTTAGT	7570
Oy	2314	ArgSerPheGlySerLeuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeu	2333
Db	7571	AGTCAAGTAGACGTCTTGAACTTGAGAGAGCTCAGATGCTCAAGACCTTGATGAGGCC	7610
Oy	2334	LeuAsnLysPheLysValValTyrGArgThrAlaAlaValLysGluAspHisSerLeuIle	2353
Db	7631	AAAATATATGATTTGTTTGTGCATCTTCACTG-----AATGGCTCATTT	7675
Oy	2354	LysAspTyrGluLysAspLeuAlaAlaGluGlnLysArgHisAspGlu-----Leu	2370
Db	7676	CAAGAAAGTAGAAGATGGCAGACAGAAACTGAGCAAGAAAGATGAAGAAATCAGTAGACTG	7735
Oy	2371	ArgLeuGlnLeuGlnCysLysGlnGlnHisValLysArgLysTrpSerArgAspAlaSerGlu	2390
Db	7736	AAAAATCAATTTCAAGACCAAGACGACCTGTCTTAACTGTCTCCAGGTGGAAGAGAG	7795
Oy	2391	GluLeuLysPhe-----CysGlnIleGluPheLysAsnGlnLysLeuPheLys	2406
Db	7796	CACCAACTTTGGAAGAGCAAAACTTGAACTGAGAACTGACACGTGCAATTTGACAGAC	7855
Oy	2407	LysAlaAsnIleIleGlnSerValGlnAspAspPheSerGluValGlnValPheLeuAsn	2426
Db	7856	AAGATCCCAAGGTCAATCCAAAAAAGCCTCTTTCAGAGACACATTAGAAAGTCTCTCAG	7915
Oy	2427	GlnAlaGlySerThrLeuGlnGlnGluLysGlu-----HisLysLysValPheMetGlnTrp	2445
Db	7916	AGTTCTTACAAGAATCTTAGAGATGAGCTTGAAATTGACAAAAATGCAAAAAATGCTCTT	7975
Oy	2446	LeuGluGluLysPheGly-----AspLeuHisVal	2454
Db	7976	GTGAAAAAAGAAACAAATGACTGCAGAAAGAACTGACTGCAGAGCAAGAAATGCAAGAC	8035
Oy	2455	AspAlaLysLys-----LeuSerGluGluMetGlnGlnLysAsnArgGlnIleAla	2471

DB: 12 Gaps: 139
 US-09-724-584-1 (1-2954) x US-10-240-965-201 (1-10281)
 333 ThrProHisValAsnGluValLeuAspArgGluAlaLeuLeuLeuArgTyArgGlu 352
 197 ACAAGAGCTCTTCAAGAAATTCAGAGCTGAGAGCAGCTTGACAAATGAGAGAGAA 256
 353 IleLeuAspLeuLeuGluLeuGluLeuLeuGluLeuGluLeuGluLeuGluLeu 372
 257 AAGCAGCAAGGCGACCTTTCAGCTTGCAGCTGCGCTGCGAGAGAGCAAAACAG 316
 373 AlaMetAlaLeuGluGlu-----HisThrGluLeuLeuAla 384
 317 AAGGTGAAATGAAAAAAGCGAGGTACAACTGAAAAAGGAGATTAAGATTGATG 376
 385 GluIleLeuGluLeuHisLeuLeuLeuArgGluAspArgIleThrHisLeuThrAsnIleVal 404
 377 GAAATATGTGAAGCTCGAGAAACTAAGCAAGATTTTCAT-----GACTTCA 430
 405 ValAlaSerSerGluLeuSerGluGluLeuAsp-----GlnArg 416
 421 GTCAAGAGAGTCAAGAGTATTTCCAGAGAGACAACTGAATTGAGCAAAAAACAAATA 490
 417 ValLeuAspGlyArgArgValThrThrAlaProGlyLeuIleGluAsnSerLeuHisAla 436
 491 GAAAAAAGTGAACAGCACTTAAAGGTGAATCTGAGCTTGAAGAGCAACAGAGCT 550
 437 SerGlyValSerAspPheAspMet-----Leu 445
 551 GCGCAGTCTCGAGATCTCTCTGATTCATGCAATACACCAAAAAATTTTACAAT 610
 446 SerArgLeuProGlyAsnPheSerLeuLeuValAlaLeuPheSerAspMetProSer----- 463
 611 CCACATACACCAAGTCAATATATATAGTGCTCCAGATGATGAGATCTTAAAGAAAAATAT 670
 464 PheProGluIleAspAspSer-----ValCysThrGluLeuHis 476
 671 AATAAAGAGGTGAAGAAAGAAAAAGATTAGAGCAGAGTTAAAGCTTGAGAGCTAAA 730
 477 AspPheAspAlaLeuSerMetLeuAspSerAsnGlyIleAspAlaGluThrAsnLeu 496
 731 AAAGCAAGCCAGACTCTTCCACAGCCACCATGAATCACCAGCATTCGCCGATCAG 790
 497 AlaSerLeuValThr-----HisArgGluLeuThrSerLeuHis----- 509
 791 GCTTATCATCTGTCTTCATGCGACAGAGAAAGACCCCAAGCATCTTTTCATCTAT 850
 509 ----- 509
 851 TCTCAAGAACTCCAATTAGAGAGATTTCTGCACTTACTTTCTGGGGAACAAGAG 910
 510 -----GlnSerMetIleAspPheGluGlnIleSerAspSerValGlnPheHis 525
 911 GTGACTCCAAGTCGATCAACTTTGCAATAGGGAAGAAAGATGCTTATGCACTTTCTTT 970
 526 AspSerSerLeuGluAsnGluLeuGlnIleuProLeuAspSerGlyAspMetAlaGlu 545
 971 GACATTTTAGCAGATCCATCTTTTG-----GATCAATTAAAA 1009
 546 CysArgGlyAlaSerPheGluLeuGluIleThrSerLeuGlnGlnIleuGlnIleuGlnIleu 565
 1010 GCGCAGATTCAGAGACTTAAGAAACAAAGATTAATGAGTTGAACTACGCTGCAAGAGACAT 1069
 566 GluGluGluLeuLeuGluLeuValGlnSerPheGluLeuLeuIleAlaGluLeuGluGlu 585
 1070 GAAAAAGAAATGAAAGGCCCAAGTGAATTAAGTTCAA-----GACTCCCACTC 1117
 586 GlnLeuSerValLeuAlaLeu-----AsnLeuGluMetValThrAsnSer--- 600
 1118 CAACCTGAGG---AAAGCAAAAGTGAATTAATTAAGAAAAAGAGAAAGTTTGAACAAATGT 1174
 601 ArgGluHisSerIleAsnAlaGluValGlnThrAspValGluLeuValAlaArgLeu 620

DB 1175 AGGATGAACCTAGTGAAGAAACACAGCAATATCGAC----- 1210
 621 GluMetSerValLeuGluAspSerGlyTyArgAlaSerAsnSerAspLeuGlnAspSer 640
 1211 -----CAGGCTCAACCAAGATATATGATGGAACCAAAAACTGAAAAAATTG 1258
 641 SerValAspGlyValArgLeuSerSerSerHisAspGluCysIleGluHisArgLeuMet 660
 1259 ACGGAAGAT-----TTGAGTTGTACAGCAGCAAAATGCAGAAAGTCCAGATGTTT 1309
 661 LeuGluGlnLeuIleValAspLeuGlu-----GluPheIleGluAsnLeuAsnLeuSer 679
 1310 CTGGAACGAAAAATTAAGAAAAAGAAAGAGTTTCAAGAGAGACTCTCCCGT----- 1363
 680 GluAsnAspLeuGluLeuSerSerGluGluAspPheMetGluSerIleGluLeuCysGlu 699
 1364 -----CAACAGCTGTTCTTCCAAACACTGAGCAGCAGAGTGCATCCAGATG----- 1408
 700 AlaIleMetAlaGluLeuAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspPhe 719
 1409 -----AAGCCAGACTCACCCAGAGATTACAGAACCAAG---AATATG 1450
 720 AspAsnIleIle----- 1450
 1451 CACAACTCTCTGAGCTGAGCTGAACTGATTAATCATCATCATGATTAACCAACAGCTAGAAAAC 1510
 727 -----GluThrLeuLeuArgGluIleAlaAspLeuGluArgSer----- 739
 1511 AATTGGAAGAGTTTAACGAAAAAGTTTGACAGCTGAAACAGAGCTTCCAGCGAGTCAAG 1570
 740 LeuLeuGluAsnGlnGluThrAsnGluPheGluIleLeuGluLeuGluGluGluGluGlu 757
 1571 ATCAAGAGAAAGAGACTGAGAGAAAGCATGAGGAAATGAAGAAAGAAACAACTCTCT 1630
 758 LysGluHisGluAlaGluLeuIleHisGluIleGlySerLeuLeuLeuValGluAsn 777
 1631 AAGAGTCACTGAGCAAAAGCCAGAGAAAGTCTCCACTGAGCAGAGACTCAAGAAC 1690
 778 AlaGluMet-----TyrAsnGlnAsnLeuGluGluAspLeuGluThrArgThrLeu 794
 1691 ATCAAAAGCTGTTTAATACAGCCAGATTTTGCAAGAAAGAAATGAAGCGAAAGAT--- 1747
 795 LeuLeuLeuGluGlnGluIleGluLeuAlaGluLeuValArgValAlaAspAsnLeuGln 814
 1748 -----ACCTCTCAGAGAAACCATGTTAAGAGATCTTCAAGAAAAATTAATACAGCAAGAA 1801
 815 LysLeuValArgAsnPheAspLeuSerValSerMetGlyAspSerGluLeu----- 832
 1802 AACTCTTGACTTTAGAAAAAAGTGAAGCTTGCTGTGCTGATCTGGAAGAACAGCAGCAT 1861
 833 CysGluGlu-----IlePheGlnLeuLeuGlnSerLeu 843
 1862 TGTCTCAAGACCTTTGAAGAAAGAGAACATCATCATTTGAACCACTTAATGATTAAGTTA 1921
 844 SerAspAlaGluAlaValThrArgAspAlaGlnLeuGluCysSerPheLeuArgSerGlu 863
 1922 AGCAAGACAGAGAAAGAGTCCAAA---GCTTGTCTGAGTCTTTAGAGTTAAAAAAA 1978
 864 AsnLeuGluLeuLeuGluLeuMetCysAspThrSerAsnThrTyrAsnGlnLeuGluLeu 883
 1979 GAATATGAATTTGAAGAAAGAAACCTGTTTCTTTGTTTGAAGAAAGTGAAGAAAGAA 2038
 884 AlaAlaSerLeuPheGluLeuGlnLeuGluThrArgLeuSerAsn----- 898
 2039 CTTTAATCT-----CAGATGATATCAGAAAAAGAAACTTGACAGATTAATTT 2086
 899 -----TyrIleLysMet 902
 2087 AATCACTTGAACCTTGTCTGAGAGACAGCAAAATTAAGTCAATGATTAACAGAGAGA 2146
 903 GluAlaAspLeuGluLeuGluLeuGlnIlePheAsnGluIleAsnTyrLeuAsnGly 922

Db 2147 GTAAAGACCTGGAGATGACAGAGAAACCTAAGTGTGAGATCGAAGAACCTTCACAAAC 2206
 QY 923 LeuLeuAlaGlyLys-----ValProArgAspLeuLeuSerArgValGluLeuGlu 939
 Db 2207 GTGTTAGACAGATGACAGTGTGAGAGACCCAGAAACTAGCTTATATGAGCTACAG 2266
 QY 940 LysIleValSerGluPheSerLysGlnLeuGluLysAlaLeuGluLysAsnAlaLeu 959
 Db 2267 CAGAAA---GCTGAGTTCTCA-----GATCAAAACATCGAAG 2302
 QY 960 GluAsnGluValThrCysLeuSerGluIleLysPheLeuProAsnGluValGluCysLeu 979
 Db 2303 GAAATAGAAATATATGCTTTGAAGACTCTCAG---CTTACGGGCAATTTGAAGTCTA 2359
 QY 980 LysAsnGlnIleSerLysAlaSerGluIleMet----- 991
 Db 2360 GAACACAAAGCTCAGTTACTCTCAATGAATATATGACAAAGACCGGTGTACCAAGAC 2419
 QY 992 -----LeuLeuLysGlnGluLys----- 997
 Db 2420 TTGCATGCCGAATATGAGAGCCTCAGGATCTGCTAAATCCAAAGATCTTCTGTGTG 2479
 QY 998 -----GluHis 999
 Db 2480 ACAATGAGATCATCAGAGAAAGCTTTGGCTTTGATCAGCAGCTGCCATGATCAT 2539
 QY 1000 Ser---AlaSerIleIleSerLysGlnIleIle----- 1010
 Db 2540 TCCTTGCAAATATATATGAGAACAGAGACATCCTTCAGAGAGAGTGAATGTGCT 2599
 QY 1010 ----- 1010
 Db 2600 TTAGAGCAGACCAAGTCCGAAAAATTCGCCATCTCAAAATAGATTCATCTACT 2659
 QY 1011 -----MetGlnGlnIleSerGln 1017
 Db 2660 GAATTTTCATAGCTCAAAAAACAGATGAATCAGACCTGCAAAAGAGTGTGAAGG 2719
 QY 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnIleThrGluGln 1037
 Db 2720 TTGGTGCAATCATAGAGAAATAGAGAAATCTCATGAAGACAGAACAGATGATCA 2779
 QY 1038 GlnIleLeu-----GluMetLysLysMetHisAspAsp----- 1048
 Db 2780 AGTTTGTGGCTGAACAAGTCAGCGCATTAAGTTACAGAGACACTTCTGTCTAC 2839
 QY 1048 ----- 1048
 Db 2840 CAGATGTGTTGCTGAAACCTTAAGTGCCTTGAGAACAGAAAAAGCTGCAACTT 2899
 QY 1049 LeuPheGlnLysTyrIleArgAsnLysSerGlu----- 1059
 Db 2900 TTAATGATTAAGTGAAGAACTGAGCAGAGATTCAGAAATTAAGAAAGACAAACAT 2959
 QY 1060 ---AlaGluAspLeuLeuArgGluMetGluAsnLeuLysGlyThrMetGluSerValGlu 1078
 Db 2960 CTACTTGAAGACTCTTAAGAGACTTACAACTTTATCCGAAACCTTA---AGCTTGAG 3016
 QY 1079 ValLys-----IleAlaAspThrLysHisGlnLeuGlnGluThrIleArg 1093
 Db 3017 AAGAAAGAAATAGTTCATCTTCTCTAATTAAGAGAAATGAGAGCTGACCCAA 3076
 QY 1094 Asp-----LysGlu-----GlnLeuLeuHisGlnLysLysTyrPhePhe 1106
 Db 3077 GAGATGAGGACTCTTAAGGAATTAATGATCATCTTAATCAAGAGAAATGAACTTAATC 3136
 QY 1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
 Db 3137 CAGAAAGTAGAGTTTGGCAAACTATATATAGATGAAGAGAGAAAGCAATTCACAGTTA 3196
 QY 1119 SerAspSerLeuProSerLysLeuVal-----GluGlyAsn 1131
 Db 3197 JCTGTATCAGTACAGACGAGAAAACTTATTTTACTACAAAGATGTGAAGAAACCGGAAT 3256

QY 1132 SerGlnAspProIle----- 1136
 Db 3257 GCATATGAGGATCTTACTGCAAAAAATACAAAGCAGACAGAAAGAAATTCATAATTAGAA 3316
 QY 1136 ----- 1136
 Db 3317 TGCTTGCTAATGAATGACACTAGCTTTGTGAAAAATAGAAAAATGAGTTGGAACAGCTA 3376
 QY 1137 -----GluIleAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
 Db 3377 AAGAGAGATTTGCAAGAGAACCAAGAAATTTCTTAACAAATATGACATTTGCTGAGAA 3436
 QY 1151 ArgAsn---AsnIleMetValCysLeuGlnThr----- 1160
 Db 3437 AGAAATCAGAAATCTGATGCTAGAGTTGAGACAGTGCAGCAAGCTTGAGATCTGAGATG 3496
 QY 1160 ----- 1160
 Db 3497 ACAGATTAACCAAAACATTTCAAGAGCAGGCTGTGTTAAAGCAAGAAATCTGACT 3556
 QY 1161 -----GluArgAsnSerLeuLysGlnIleValIleAspLeu-----AsnThr 1174
 Db 3557 TTAAGAGAGAACAAACAAATGCAAAAGAGATTAATGACTTATTAACAGAGAAATGAA 3616
 QY 1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
 Db 3617 CAGCTGATGAAGTATATGAGACTTAACATGATGTCAAAATCTAAGATCGAACCAATT 3676
 QY 1185 GluLysSerAspLeuGln-----LysProLysGln 1194
 Db 3677 AGGAACCTGTGAAAGAGAGACAGTGCAGAGAAATCAATGATTTTAACTCAGATG 3736
 QY 1195 AspLeuGlnGluGluValLysLeu-----LeuLeuGluMetGlu 1208
 Db 3737 GATCTTGAAGTAAAGAAATTTCTAGATGTTATATGCGCAGTGTGCAATTAGAA 3796
 QY 1209 LeuLeuLysGlyHisLeuThrAspSerGlnLeuSerIleGluLysLeuGlnLeuGln 1228
 Db 3797 GCTATG-----CTAAGAAATTAAGAAATTAATACTTCGAGAAAGTGAAGAGAG 3847
 QY 1229 LeuGluValThrGluLysLeuGlnThrLeuGlnGlnGluMetLysAsnIleThrIleGlu 1248
 Db 3848 -----GAGTGCCTGCAGCCTGATTAACAGACAAT----- 3877
 QY 1249 ArgAsnGlnLeuGlnThr---AsnPheGluAspLeuLysAlaGluHisAspSer---Leu 1266
 Db 3878 AGAGGAGATCTTGAAGACAGAAATTTGCAAGACATGACAGTCAAGAAATTAAGTGCCTT 3937
 QY 1267 Lys-----GlnAspLeuSerGlu 1272
 Db 3938 AAAAGCTGTGAATAGATCGGAGAAAGATATATTCAGGGCCTCATGATTTGTCAACA 3997
 QY 1273 AsnIleGlnIleSerIleGlnThrGlnAspGlnLeuArgAlaIleGlnGluLeuArg 1292
 Db 3998 AGTCAAAAGCAATGACACACCTTCAGTCTCTGCAAAACAAATGAACAGCTGAAT 4057
 QY 1293 GluGlnIleGlnLeuValAspSerPheArgGlnIleLeuLeuAspCysSerValGlyIle 1312
 Db 4058 GAGCTAGAGAAATATATGTAATATCTGACAGCTGAAAGTGAACCTGTAACAGCTG 4117
 QY 1313 SerSerProAsnHisAspAlaValAlaAsnGlnGluLysValSer----- 1327
 Db 4118 AATGATTCAGAGTCAAGATGTATACACAGCAACTGAGAAAGAGGAGAGAGTAGGAGAA 4177
 QY 1328 ---LeuGlyGluValAsnSerLeu-----GlnSerGluMetLeuArgGlyGluArgAsp 1344
 Db 4178 CTACTAATTAAGATTAATATTTAAATGATACAGTGTCTTCTTCATGTGAGTATAGT 4237
 QY 1345 Glu----- 1345
 Db 4238 GAAGCATACAGAGAGGTGAATTTGTGTGAACCAACAAATGAACAGACCTGTGTCTTGT 4297

QY 1345 ----- 1345
 Db 4298 GGTCCATTGGAGAGATTAATTCCTACAGCACTTGCTACAGACAAAGATTCA 4357
 QY 1346 ----- 1346
 Db 4358 ATGACATTGGCCGAATTCGAAGAAATTTCTATCTTACAAAGTGCAACAAAATTTTA 4417
 QY 1354 ----- 1354
 Db 4418 CATGATCAGCACTGTCAGATGAGCTCTTAAATGTCAAGCTGCAGACCTATGTGACTCA 4477
 QY 1367 ValGluGluAsnLeuGluIleThrIlySlyAsnGlyLeuGluIlySlyLeu 1386
 Db 4478 TTTAAAGCCGAAATTTGGTCTTGTCACGAATCTGAGAACTTTCAGAGTACCTGGG 4537
 QY 1397 GlyIlySerGlu-----GluSerGluValLeuIlySerMetLeuGluAsnLeuIly 1403
 Db 4538 AAGGAGATGCAGCTGGCTGGAGAGGGGCTGTTCCATCCCTGTCATCTGTGTG 4597
 QY 1404 GluAspAsnIlyLeuIlySlyGluIlyValGlu----- 1414
 Db 4598 CCTGACACTTACCTTAGCAGTTTGGAGACTCCTCTTTACAGACTTTTGA 4657
 QY 1415 ----- 1415
 Db 4658 CAGACAGAGATATGCTCTTTGAGTAATTAAGAAAGGCTGTTTCAGCAACAGTGC 4717
 QY 1424 SerLeuGluIlyAlphe----- 1429
 Db 4718 AGTGAATGAAGTATTTTGCAGAGTGCAGAGAGAAATGACCAAGAAAGAAC 4777
 QY 1430 ---SerGlySerGluIlyLeuValIleGluIle-----GluValLeuIlySala 1444
 Db 4778 CCTTCGGCCCGCAGCAAGGCTTGAAGAGCTTGAAGCTTCTGAGGTGACCGGAG 4837
 QY 1445 GluLeuIlySalaIleGluIlyLeuIlyGlu-----IleIlyAspArgAspIly 1460
 Db 4838 TCCCTCGAAGACTTGAAGAAATGGAAGTCAAGGATTTATGAAAATGAAGAAATT 4897
 QY 1461 PheGluLeuValGlnThrAlaAsnThrAsnLeuValGlu---GlyIlyLeuIlyThrPro 1479
 Db 4898 CAAGAGCTCGAGCACTTAAAGTCTGAAGCAAGAGCTTGACTGCTTGAAGAGC 4957
 QY 1480 LeuGlnIleAspHISGlu-----GluAspSerIleAspArgAspSerGluIlyMetGlu 1497
 Db 4958 TATTGTGAGAAATGAACAGTGCACAGCAAGCTGACAAAGCTGACTCTGGAGATGAG 5017
 QY 1498 IleIlySalaIleGluIlyLeuIlyLeuIlyArgAsnGlnIlyIlyLeuGlu----- 1513
 Db 5018 TCCAAAGTGGCGGCGAAGAAAGAACAGCAAGCAAGCTGCACTTGAGCTGGAAGTACA 5077
 QY 1514 ArgLeuGlnIlyGluIlyLeuIlyLeuIlySerAsnIlySlyLeuIlyIleLeuGlnIlyMet 1533
 Db 5078 CGATCCCGAGTACAGAGCTGTGACTTAAGTCTCG----- 5113
 QY 1534 GluThrSerValLeuLeuIlyAspAspLeuGlnIlyIlyLeuGluSerLeuLeuSerGlu 1553
 Db 5114 -----TCTTGTCTGGCATCGACACAGAAAGTGTATTCAGGC----- 5152
 QY 1554 AsnIleIleLeuIlySlyGluAsnIleAspThrIlyLeuIlyIlyHisSerAspThrGlnIle 1573
 Db 5153 -----CGAATGAGAGCTGATCATATCAAAAGAACATATCTGAAACTACAGAA 5203
 QY 1574 GlnLeuGlnIly-----ThrGlnIlyGlnIly 1583
 Db 5204 AGAACAACAAGCATGATGTCATAGATTGCTGTAAGAGAGCTCCAGCAGAGACTCAAT 5263
 QY 1584 Leu-----AlaIlyAsnLeuAlaIleAlaIleSerAspAsnGlyProIle 1598
 Db 5264 CTAGACATTGAGAAATATAGAGAGCTGTGATGAAACCAACAGAGAGAGCTGTGG 5323
 QY 1599 ThrGlnIlyIlyGluThr-----SerAla 1606

Db 5324 GAACAGTCCCGCATACCAATTAATGAGCTCCAGGGGAAGATMAAACCCAGGCTTTCA 5383
 QY 1607 AspCysValHisProLeu----- 1612
 Db 5384 GAATCATTTCTGAATGTGCATTTTGTGCTCAATGCTTTGGTACCTATGATTTCTCG 5443
 QY 1613 -----GluGluIlyIleLeuLeuIlyThrGluGluIlyLeuHisGlnIlyThrAsnGluGln 1630
 Db 5444 GGGAAATCGAAGATATCATATGATTTCAACTGCGGGTAAAGACATCAATAGAAAT 5503
 QY 1631 GluIlySlyLeuHisGluIlySlyAsnGluGlnIlyValGlnIlyLeuIlySlyGlu 1650
 Db 5504 TTGACATTAATCTCATGTGATAGAGACCGTGACAA-----AAA 5542
 QY 1651 ValGluHisLeuMetIlySerMetIleGluSerIlySerSerLeuGluSerLeuGlnHis 1670
 Db 5543 GTTGAAGTTTGTCTTAAATGAATGAAGAAATTAGACTCAAAATC----- 5587
 QY 1671 GluIlyHisAspThrGluGlnIlyLeuIleAla-----LeuIly 1683
 Db 5588 -----CATTTACAGAGGTACCACTTAATGACCAAAATTAAGCATGCATGAATGGA 5641
 QY 1684 GlnGlnMetGlnValIlyThrGlnIlyIlySlyGluLeuGlnIlyThrHisGlnIlyLeu 1703
 Db 5642 AAATAGTTGGGAGATTAAGAAAGAAATCACTCAATTTAAGTAAAGAAATGGAATTTT 5701
 QY 1704 ThrAlaGluValAspHisLeuIlySlyGluIlyLeuIlyLeu-----GlyLeuAspHely 1721
 Db 5702 TCTTGATACACAGAGATTACTCCAGAGATGAAGAACTTGAAGGCTCAATCTGAT 5761
 QY 1722 AsnGluAlaGln---GlnIlyThrIlySlyGluIlyIlySlyLeuAsnIlySly--- 1739
 Db 5762 TTGAATGATGCATGAGATTAATCATCAGCTGAGATGATGAGATTAATGAGGCAAGTG 5821
 QY 1740 -----GluLeuGlnIlySerGlnHisAspLeuIlyIly 1750
 Db 5822 AATGACACTGAGAGAGATTTCTTGATGTGGAATGAAGTACAGTACATGCATCG 5881
 QY 1751 Glu-----IleGluIlyLeuMetIlySerLeuIly 1760
 Db 5882 GAGAAAGCTAGATGACATGAGACCTGCTACCTGAGGAGTACCTAGAGTACTCA 5941
 QY 1761 AspIlyGluSerAlaLeuGluIlyThrIlyLeuIlySlyGluIlyIlyValIle---AsnLeu 1779
 Db 5942 ACAGAGAACTATGTTTGAAGAAAGACATGAATGAAGCAAGATATGCTGCTG 6001
 QY 1780 AsnGlnIlyMetGluMetValMetLeuGluIlyMetGluIlyLeuIlyAsnSerGlnIlyThr 1799
 Db 6002 GAGAGAACTCTCAGTGTGTCAGAGTGAAGAAACAGCTTCGTGAGCAATTAGATCT 6061
 QY 1800 ValIleAlaGluArg-----AspIlyLeuGlnIleAspIlyLeuIlySerValGlu 1816
 Db 6062 ATGTCAAAAAAGACAGCGCATGTGATCATGTTCTGAAAAATGAAGAGAAAAACACA 6121
 QY 1817 MetSerIleGluThr-----GlnAspAsp 1824
 Db 6122 ---GAGCTTGATGCTCATCAAGTGAAGTGTCTCATTCATTCAGTGCAGAGCAAG 6178
 QY 1825 LeuArgIlySalaGlnIlyAlaLeuGlnIlyGlnIlyIlySlyAspIlyValGlnIlyThrSer 1844
 Db 6179 GTGAAGAAAGACGGAAGCTCTTCAAGCTTTGCTCTTGATGTGAGTGAAGCTGTTAAA 6238
 QY 1845 GlnIleSerValLeuGlnIlyIlyIleSerLeuLeuGlnIlyGlnIlyMetLeuIlyIlyVal 1864
 Db 6239 GACAAACTATCTCCAGAAAGAGCTGAGAGTTTGAAGAAAGACTCACAGCACTGTCT 6298
 QY 1865 AlaThrValIlySlyThrIlyLeuSerGluIlyArgAspIlyLeuAsnIlySerIlyGlnHisLeu 1884
 Db 6299 TTGACAAATGTGAGCTGGAAGAACCAATTGACAACTGAATTAAGAGAAAGATTTGCTT 6358
 QY 1885 PheSerGluIleGluThrLeuSerLeuSerLeuIlySlyGluIlyIlyPhe----- 1900

```
Db 6359 GTCAAGATCTGAAAGCTCAGGCCAGCTGATGATTAATGAAAGCTGAAT 6418
Qy 1901 -----AlaLeuGlnGlnAlaGlnLysAspLysAlaAspAlaAlaArgLysThrIle 1917
Db 6419 GTCTCAAGAGCGCTTGAGAGCGCACGTGGTGAGAAAGTAGTTCGATGAGGCTGAC 6478
Qy 1918 AspIleThrGlnLysIleSerAsnIle----- 1926
Db 6479 TCAACACAGAGAGAGTGCATCATGAGAAAGAGCATCGAAGAACTGAGAGTTCCGATT 6538
Qy 1927 -----GlnGlnGlnLeuGlnGlnAlaThrAsnLeuLysGlnThrLeuLysGln 1943
Db 6539 GAGCCGATGAAAAGAGAGAGCTGCACATGCGAGAACTGAAAAGAACCGAGCGGAG 6598
Qy 1944 ArgGlnSerLeuIleGlnCysLysGlnGlnLeuAlaLeuAsnThrGlnHisLeuArgGln 1963
Db 6599 AATGATTCACCT-----AAGATAAAGTTGAGAACTTGAAAAGGAAATTGCAAGAG 6649
Qy 1964 ThrLeuLysSerLysAspLeuAlaLeuGlyLysMetGlnGlnGlnArgAspGlnAlaIle 1983
Db 6650 TCAGAGAGAAACCGAGAGCTAGTGATT-----CTTGATGCCGAGAAATTCGAAAGCA-- 6700
Qy 1984 AsnLysValIleAlaLeuThrGlnLysMetSerSerLeuGlnGlnIleAsnGlnAsn 2003
Db 6701 -----GAAGTAGAGACTTAAACACAAATAGAAAGATG 6736
Qy 2004 ValThrThrLeuLysGlnGlnGln-----GlnLysGlnThr 2016
Db 6737 GCCAGAGGCTGAAAGCTTTTGAATAGACCTTGTCACCTTAAAGCTGTAAGAAAAGAAAT 6796
Qy 2017 PheThrLeuGlnArgProSerLysGlnGlnSerSerSerGlnMetGlnLeuLeuArgLys 2036
Db 6797 CTGACAAAACAATACAGAAAACAAGGTCAGTGTCCAGACTACACAAAGTACTCTCT 6856
Qy 2037 SerLeuLysThrLysAspLeuGlnGlnGlnAlaGlnLysGlnIleSerGlnAlaThr 2056
Db 6857 TCATTAAAGTCTGTAGAGAAAAGAGCAAGCAGATACAGTCAAAAGAAAGATCT 6916
Qy 2057 -----AsnGlnIleLysAsnLeuThrAlaLysIleSerSer 2068
Db 6917 AAAACGTCAGTGAGATGCTTACGAATCAGTTAAAGAGCTTAATGAGGACCTACAGCC 6976
Qy 2069 Leu-----GlnGlnGlnIleLeuGln--AsnAlaSerIleLeuAsnIleValSer 2085
Db 6977 TTGTGCTGACCAAGAAATTATGAGGCCACAGAACAGATCTAGACCCCAATAGAG 7036
Qy 2086 GlnArgGlnAsnLeuArgHisSerLysGlnGlnLeuValSerGlnLeuGln----- 2102
Db 7037 GAAAGACATCAGCTGAGAAATAGCATTTGAAAAGCTGAGAGCCGCTAGAAAGCTAATGAA 7096
Qy 2103 -----GlnLeuSerLeuThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArg 2120
Db 7097 AAGAGACGCTCTGTCTTACACAACTGAAG-----GAAAGTAGCAT 7141
Qy 2121 GlnLysAspGlnAlaValAlaAsnLysIleAlaSerLeuAlaGlnIleLysIleLeuThr 2140
Db 7142 CATGCAAGATTACTTAAGGGTAGAGTGAAGAACTTTGAAAGAGACTAGAGTGGCCAG 7201
Qy 2141 LysGlnMetAsp-----GlnPheArgAspSerLys-----GlnSerLeu 2153
Db 7202 ACAAAACAAGAGCATGAGCTCTTGAGGACAGAAATTTCCAAAGAGAGTGAAGAACCTTA 7261
Qy 2154 GlnGlnGlnSerSerHisLeuSerGlnLeuLysCysThrLysThrGlnLeuGlnMet 2173
Db 7262 AAAGCAAAATATGAAAGGATGACCCAAAGCTGAGAGGTCTGGAATTAAGATTGTTACT 7321
Qy 2174 LeuLysGlnGlnLysGlnAspIleAsnAsnLysLeuAlaGlnLysValLysGlnValAsp 2193
Db 7322 ATAAAGGTCAAGAAAAGAGATCTGCAAATGATTAACAAAAGAGCAAGAGCAATATCT 7381
Qy 2194 GlnLeuLeuGlnHisLeuSerSerLeuLysGlnLeuAspGlnIleGlnMetGlnLeu 2213
Db 7382-GAATTG-----GAAATA 7393

Qy 2214 ArgAsnGlnLysLeuLeuArgAsnThrGlnLeuLysCysGlnLysMetAspIleMetGlnLysGln 2233
Db 7394 ATAAATTCTCTTTGAAAT----- 7414
Qy 2234 IleSerValLeuArgLeuMetGlnAsnGlnProGlnGlnGlnLysAspValAlaGln 2253
Db 7415 -----ATTTCAGAAAAGAAAGACAGAGAAAGATGACAGTGAAGAAAATCAAGCACT 7468
Qy 2254 ArgMetAspIleLeuGlnSerLysArgAsnGlnGlnIleGlnGlnLysMetGlnLysIleSer 2273
Db 7469 GCCATGAGATGCTTCAACA-----CAATTAAAGAGCTCAATGAGAGAGTGGCA 7519
Qy 2274 AlaValLysSerGlnGlnHisThrLeuLeuSerSerSerGlnLeuGlnLysGln 2293
Db 7520 GCCCTGCATTAATGACCA----- 7537
Qy 2294 ThrGlnAlaHisLysHisCysMetLeuAsnIleLysGlnSerLeuSerThrLeuSer 2313
Db 7538 --GAGCCTGTAG-----GCCAAAGACAGAACTTAAGT 7570
Qy 2314 ArgSerPheGlnSerLeuGlnThrGlnHisValLysLeuAsnThrGlnLeuGlnThrLeu 2333
Db 7571 AGTCAAGTAGAGTCTTGAACCTTGAGAAAGCTCAGTTGTCACAGGCTTGATGAGGCC 7630
Qy 2334 LeuAsnLysPheLysValValLysArgThrAlaAlaValLysGlnAspHisSerLeuIle 2353
Db 7631 AAAATATATATATTGTTTTCATCTCAGT-----AATGGCTCATTT 7675
Qy 2354 LysAspThrGlnLysAspLeuAlaAlaGlnGlnLysArgHisAspGln-----Leu 2370
Db 7676 CAAGAAGTAGAAGATGCGCAAGCAAGAACTGAGAGAAAGATGAAAGAAATCAGTAGACTG 7735
Qy 2371 ArgLeuGlnLeuGlnCysLeuGlnGlnHisGlyArgLysThrPheArgAspSerAlaSerGln 2390
Db 7736 AAAAATCAAAATTCAGACCAAGACAGCTTGTCTTAACCTGTGCCAGTGAAGAGAG 7795
Qy 2391 GlnLeuLysPhe-----CysGlnIleGlnPheLeuAsnGlnLeuLeuPheLys 2406
Db 7796 CACCAACTTGGAGAGCAAGAACTTAGAAGCTGAGAAATGTGACAGTGAATGGAGCAG 7855
Qy 2407 LysAlaAsnIleIleGlnSerValGlnAspAspPheSerGlnValGlnValPheLeuAsn 2426
Db 7856 AAGATCCAAAGCTCAGATCAAAATATGCTTTTGACAGACACATTAAGAGTGTGCGAG 7915
Qy 2427 GlnValGlySerThrLysGlnGlnGlnLeuGln--HisLysLysGlnPheMetGlnThr 2445
Db 7916 AGTCTTACAAAGATCTAGAGAAATGAGCTTGAAATGACAAATAATGCAAAATGTCTCTT 7975
Qy 2446 LeuGlnGlnPheGly-----AspLeuHisVal 2454
Db 7976 GTTGAAAAGATTAACAAATAGCTGCMAAGAAAGTGAAGTGCAGAGGAAATGATCAGAG 8035
Qy 2455 AspAlaLysLys-----LeuSerGlnGlnMetGlnGlnGlnAsnArgArgIleAla 2471
Db 8036 ATGGCACAGAAAACAGCAGAGCTGCAGAAAGAACTCAGTGGAGAGAAAATAGGCTAGCT 8095
Qy 2472 SerThrIleGlnLeuLeuThrLysArgLeuLysAlaValAlaGlnSerLysIleGlnArg 2491
Db 8096 GAGAGTTGCAAGTTACTGTGGAAAGAAATAAAGAG-----AGCAAGATCA-- 8143
Qy 2492 GlnIleThrValLysLeuAsnGlnPheGlnAlaLysLeuGlnGlnLysLysGlnGlnAsn 2511
Db 8144 -----TTGAAAGAGCTCACTAGCAAAAT 8167
Qy 2512 LysGlnLeuMetArgArgMetGlnHisHisGlyProSerAlaSerValMetGlnGlnGln 2531
Db 8168 AGTGATTTAAGAG-----AGCTTGATTCATGACAAAGAGC 8206
Qy 2532 AsnAlaArgLeuLeuGlnLysLeuLysThrValGlnAspGlnSerLysLysLeuGlnSer 2551
Db 8207 CAGGTGAAAAGAGAGG-----AAAGTGAAGAGAGAAATAGCTGAATATCAGCTA 8257
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Oy	385	GlulileuysGlnleuhiVibysgluikrgGluabaprgLiletrPhisIeuthrYsnlIeVal	404
Db	292	GAATAATGTGAAAGTGTGGAGAAACTAAGCAGAAAGATTCTCAT	345
Oy	405	ValAlaSerSergIngluSergIngluAsp	416
Db	346	GTCAAGAGACTCCAAAGTGATTTTCCAGAGAAGCAACATGAATTCAGCCAAAGCAAAATTA	405
Oy	417	VallYsarGlyVsArGArGValThrTrpLaProGlyVsIleGlnAsnSerleuHiSala	436
Db	406	GAAAAAATCGSAGCAGAACTTAAAGAGTGTAAATCATCGACTTGAAGAAGCAACAAAGT	465
Oy	437	SergIValSerAspPheAspMet	445
Db	466	GGCGAGCTGCGAGAGATGCTCTCTGTAATCCATGCAATACCAACAAAAATTTTTCAACT	525
Oy	446	SerArGleuProGluYAsnPheserIySulAlaLysPheSerAspMetProSer	463
Db	526	CCACTAACCCCAAGCAATATATTATGTGGTTCCAAAGTATGAAGATCTAAAGAAAAATAT	585
Oy	464	PheProGluIleAspAspSer	476
Db	586	AATAAAGAGGTTCAGAGAAAGAAAAAGATTAGAGCAGAGCTTAAAGCCTTGGACAGCTAA	645
Oy	477	AspIleAspAspAlaLeuSerMetMetAspSerAsnGlyIleAspAlaGluTrpAsnleu	496
Db	646	AAAGCAGCCAGACCTTTTCCACAGCCACCACATGAATCACCGGACATTTGCCCGGACATAG	705
Oy	497	AlaSerIySValThr	509
Db	706	GCTTCATCATCTGTGTTTCATGAGCAGAAAGAAAGAACCCCAAGTCATCTTTCATCTAAT	765
Oy	509		509
Db	766	TCTCAAAAGACTCCAATTAGAGAGATTCTTCGATCTTACTTTTCTGGGAGCAAGAG	825
Oy	510	GlnSerMetIleAspPheGlyGlnIleSerAspSerValGlnPheHis	525
Db	826	GTGACTCCAAAGTCGATCAACTTTTGCAAATAGGAAAAAGAGATGCTAATAGCAGTTCTTT	885
Oy	526	AspSerSerIySgluAsnGlnleuGlnIyIleuProLysAspSergIyAspMetAlaGlu	545
Db	886	GACAAATTCAGAGCTTCATCTTTTG	924
Oy	546	CysArGlySAlaSerPheGluIySgluIleThrSerleuGlnGlnleuGlnIySerIyS	565
Db	925	GGCGAAGATCAAGACCTAAGAAACAGATTAATGAGTTGGAAGCTACGCTCGCAAGACAT	984
Oy	566	GluGluGluIyLysGlnleuValGlnSerPheGluIyLysIleAlaGluIyIyGlnleuGlu	585
Db	985	GAAAAAGAAATCAAAAGCCCAAGTGAATAAGTTCA	1034
Oy	586	GlnleuSerValIySAlaLys	600
Db	1033	CAACTGGAG--AAAGCAAAAGTGAATTAATTGAAAAAGAAAGATTTGAAACAAATGT	1089
Oy	601	ArgGluHisSerIleAsnAlaGluValGlnThrAspValGluIySgluValValArgLys	620
Db	1090	AGGAGTGAAGTACTAGTAGAACAACAGCACATACGAC	1122
Oy	621	GluMetSerValIyGluYAspSergIyTrpAsnAlaSerAsnSerAspIyGlnAspSer	640
Db	1126	-----CAGCGCTCAACCAAGTACTGCTGACTTGGACAAACAACTGAAAAAATTTG	1177
Oy	641	SerValAspGlyLysArgleuSerSerSerHisAspGluCysIleGluHisArgLysMet	660
Db	1174	ACCGAAGAT-----TTGAGTTGTGACGACCAACAAATGCAGAAAGTCCGAGATGTTCT	1224
Oy	661	LeuGluGlnLysIleValAspIyIyGluPheIleGluAsnleuAsnLysIySer	679
Db	1225	CTGGAAACGAAAAATTAAAGAAAAAGAAAGAGTTTCAAGAGACCTCTCCCGT-----	1276

QY	660	GIuaSenApLySgInuLysSerSergInuInAspPheMetGluSerTLeGInLeuYsgInu	699
Db	1279	-----CAACACGTTCTTTCCAAACACTGGACCAGAGATGCATCCAGTATG-----	1322
QY	700	AlaIleMetAlaGluLysAlaAsnAlaLeuGInGluLeuAlaLeuMetArgAspAsnPe	719
Db	1324	-----AAGCCGACATCACCCAGAGATTACAGCAAGCCAAAG---AATTATG	1367
QY	720	AspAnIleIle-----LeuGInuSn	726
Db	1366	CACACGCTCTGCAGGCTGAACCTGATAACTCATCATGATMAACACAGCTAGAGAAAC	1422
QY	727	-----GluThrLeuLysArgGluLLeAlaAspLeuGluuArgSer-----	739
Db	1426	AATTGGAGAGCTTTAAGCCAAAGTTGGCAGACAGCTGAACAGGCTTCCAGCCGAGTCAG	1487
QY	740	LeuYsgInuAsnGInuLuthrAsnGluPheGluIleLeuGluLysGluLuthrGIn-----	757
Db	1466	ATCAAGGAGATGAGCTGAGGAGAACATGAGAAATGAAAGAAAGAAACAACTCCTT	1541
QY	758	LysGInuHISgInuAlaGInLeuLLeHISgInuIleGlySerLeuLysLeuValGluAsn	777
Db	1546	AAGAGTCACTCTGACCAAAAGCCAGAGAGCTCCACCTGGAGGCAAGAACTCAAGAAC	1608
QY	778	AlaGluMet-----TyrAsnGInuSnLeuGInuLysAspLeuGluLuthrLysThrLys	794
Db	1606	ATCAACACAGCTTTAATCAAGAGCCAGAAATTTGCAGAGAAATGAAAGCCGAAGAT---	1667
QY	795	LeuLeuLysGluGInuGluIleGInLeuAlaGluLeuArgLysArgAlaAspAsnLeuGIn	814
Db	1663	-----ACCTCTCAGGAAACCCTGTTAAGAGATCTTCAAGAAATAAATATGACAGAA	1711
QY	815	LysLysValArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeu-----	832
Db	1717	AACCTCTGACTTTGAAAAAAGTGAAGCTTGCTGCTGCTGATCTCGAAAAAGCAGCAGAT	1776
QY	833	CysGluGlu-----IlePheGInLeuLysGInSerLeu	843
Db	1777	TGTTCTCAAGACCTTTGAAGAAAGACAATCATCATTTGAACAATTATGATAGTAA	1833
QY	844	SerAspAlaGluAlaValThrArgAspAlaGInuLysGluCysSerPheLeuArgSerGlu	863
Db	1837	AGCAAGACAGAGAAAGAGTCCAAA---GCCTTGCTGAGTGCCTTTAGAGTTAAAAAGAA	1897
QY	864	AsnLeuGInuLeuLysGluLysMetGluAspThrSerAsnTyrPyrAsnGInuLysGluLys	883
Db	1894	GAATATGATTAATGAAAGAGAGAAACTGCTTTCTCTTGAGAAAGTCAAAACGAAAAA	1955
QY	884	AlaAlaSerLeuPheGluLysGInLeuGluLuthrGluLysSerAsn-----	898
Db	1954	CTTTAACT-----CAGATGAMTTCGAAAAAGAAAACCTTCAGAGTAAATT	2007
QY	899	-----TyrLysLysMet	902
Db	2002	AATCACTTGAAAATTGCTGTGAGACACACGCAATAAAAAGTCATGATCAACAGAGAGA	2067
QY	903	GIuaLAspLeuGInuLysGluLeuGInSerAlaPheAsnGluLLeAsnTyrLeuAsnGly	922
Db	2062	GTAAGAACGCTGGAGATGACACAGAAACCTAATGTGCAGATCAGAAACCTTCACAAAC	2122
QY	923	LeuLeuAlaGlyLys-----ValProArgAspLeuLeuSerArgValGluLeuGlu	939
Db	2122	GTGTTAGACAGTAAGTCACTGAGGTGAGTACAGCCCGAAACTGATTATGAGAGCTACAG	2188
QY	940	LysLysValSerGluPheSerLysGInLeuGluLysAlaLeuGluGInuLysAsnAlaLeu	959
Db	2182	CAGAAA---GCTGAATTCGA-----GATCAGAAACATCAGAAG	2211
QY	960	GIuaSenGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeu	979
Db	2218	GAAATAGAAATATCTGTTTGAAGACTTCTCAG---CTTACTGGCGCAAGTTGAAGATCTA	2277
QY	980	LysAsnGInuLLeSerLysAlaSerGluGluLLeMet-----	991

Db 2275 GAACCAAGCTTCACTTACTGTAATGAAATTAATGACAAAGACCGGTGTTACCAAGC 2334
Oy 992 -----LeuLeuLyvGlnGluLy----- 997
Db 2335 TTGCATGCCGAATATGAGAGCTTCAGGGATCTGTAATAATCCAAGATCTTCTGGTG 2394
Oy 998 -----GluHis 999
Db 2395 ACAAAATGAATCATCAGAGAACTTTTGGCTTTTATCAGCAGCCTGGCATGCATCAT 2454
Oy 1000 Ser--AlaSerIleIleSerLyvGlnGluIle----- 1010
Db 2455 TCCTTGCATAATATATTGAGACACAGAGACATGCCCTTCAGAGAGAGTGAATGCTGT 2514
Oy 1010 ----- 1010
Db 2515 TTAGACGACAGCAAAAGTCCGAAATAATCTGCCATCTTACAAATAGAGTTGATTCACCT 2574
Oy 1011 -----MetGlnGlnGlnSerGlnGln 1017
Db 2575 GAATTTTCATTAGAGTCTCAAAAACAGATGAATCTCAGACCTGCMAAGCAGTGTGAAGAG 2634
Oy 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLyvAlaGlnGlnThrGluGlu 1037
Db 2635 TTGGTCGAATTCAAAGAGAAATAGAGAAATTCATGAAAGCAAGACAGATGCATCAA 2694
Oy 1038 GlnTyLeu-----GluMetLyvSmetHisAspAsp----- 1048
Db 2695 AGTTTGTGGGTGAACAAGTCAGCGCATTTAGTAAGTTACAGAGACACTTCTGCTCAC 2754
Oy 1048 ----- 1048
Db 2755 CAGATGTTGTGCTGAAACCTTAAGTCCCTTGAGAACMAAGAAAGAGCTGCACTT 2814
Oy 1049 LeuPheGlnLyvTyIleArgAsnLyvSerGlu----- 1059
Db 2815 TTAAATGATTAAGTGAAGTAAGTACGACGACAGAGATTCAGAATTTAAAAAGCAACCAT 2874
Oy 1060 ---AlaGluAspLeuLeuArgGluMetGluAsnLeuLyvGlyThrMetGluSerValGlu 1078
Db 2875 CTACTTGAAGACTCTTAAGAGAGCTACAACTTTATCGAAACCTTA---AGCTTGGAG 2931
Oy 1079 ValLyv-----IleAlaAspThrLyvHisGluLeuGlnGluThrIleArg 1093
Db 2932 AAGAAAGAAATGAGTTCATCTCTTAATTAAGGAAATGAGAGAGCTGACCAA 2991
Oy 1094 Asp-----LyvGlu-----GlnLeuLeuHisGluLyvLyvSerPhePhe 1106
Db 2992 GAGAAATGGGACTCTTAAGGAAATTAATGATCTTAAATCAAGAGAGATGAACCTTAATC 3051
Oy 1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
Db 3052 CAGAAAAAGTGAAGAGTTTGCAAAACTATATAGTGAAGGAGAAAGCAATTCACAGTTTA 3111
Oy 1119 SerAspSerLeuProProSerLyvLeuVal-----GluGlyAsn 1131
Db 3112 TCTGTCTAGTACAGCAAGAAAACTTATTACTACAAAGATGTGAAGAAACCGGAAT 3171
Oy 1132 SerGlnAspProIle----- 1136
Db 3172 GCATGTGAGATCTTAGTCAAAAAATACAAAGCAGACAGAAAGAAATTTAAATTAGAA 3231
Oy 1136 ----- 1136
Db 3232 TGCTTCTTAATGATGACTAGTCTTTGTGAAAATAGAAAATAGAGTTGGAACAGCTA 3291
Oy 1137 -----GluIleAsnAspTyHisAsnLeuIleAlaLeuAlaThrGlu 1150
Db 3292 AAGGAAGCATTTGCAAGAGACACCAAGAAATCTTAACAAAAATTAGCAATTTGCTGAAGAA 3351
Oy 1151 ArgAsn---AsnIleMetValCysLeuGlnThr----- 1160

Db 3352 AGAAATCAGAAATCTGATGCTAGAGTTGGAGACAGTCAGCAAGCTGTGAGATCTGAGATG 3411
Oy 1160 ----- 1160
Db 3412 ACAGATAACAAACAAATTTTAAGAGCGAGGCTGTGGTTTAAAGCAAGAAATCATGACT 3471
Oy 1161 -----GluArgAsnSerLeuLyvGlnGluValIleAspLeu-----AsnThr 1174
Db 3472 TTAAGGAAGAACAAACAAATATGCAAAAGAGATTAATGACTTTTACAGAGAAATGAA 3531
Oy 1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
Db 3532 CAGCTGATGAAGATTAATGAGACTTAACATGATATGCAAAATCTGAAGTCAAGCAAAAT 3591
Oy 1185 GluLyvSerAspLeuGln-----LyvProLyvGln 1194
Db 3592 AGGAATCTGTGAAAGAAAGAGAGAGTGAAGAAATCAATGTAATTTTAACTCTGATG 3651
Oy 1195 AspLeuGlnGlnGluGluValLyvLeu-----LeuLeuGlnMetGlu 1208
Db 3652 GATCTTGAAGTTAAAGAAATTTCTTAATAGTATTATGCGCACTGTGCTGAATTAAGA 3711
Oy 1209 LeuLeuLyvGlyHisLeuThrAspSerGlnLeuSerIleGluLyvLeuGlnLeuGlnAsn 1228
Db 3712 GCTATG-----CTAAGAAATGAAGAAATTAACCTTCAGAAAGTGAAGAGAGAAAG 3762
Oy 1229 LeuGluValThrGluLyvLeuGlnThrLeuGlnGlnGluMetLyvAsnIleThrIleGlu 1248
Db 3763 -----GAGTGCCTGCAGCATGAATTAACACAAAT----- 3792
Oy 1249 ArgAsnGlnLeuGlnThr---AsnPheGlnAspLeuLyvAlaGlnHisAspSer---Leu 1266
Db 3793 AGAGAGATCTTGAACCAAGCAATTTGCAAGACATGCAGTCAAGAAATTAAGTGGCTT 3852
Oy 1267 Lys-----GlnAspLeuSerGlu 1272
Db 3853 AAAGCTGTAAGATGATGCGGAAGAAAGATATATTACAGGGCTCATGAGTTGTCAACA 3912
Oy 1273 AsnIleGlnGlnSerIleGlnThrGlnAspGluLeuAlaAlaGlnGlnGluLeuArg 1292
Db 3913 AGTCAAAAGCAAAATGACACACCTTCAGTCTCTGCAAAACAAATGAACAAAGCTGAAT 3972
Oy 1293 GlnGlnLyvGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerValGlyIle 1312
Db 3973 GAGCTAGGAAATATGTGAATTAATGATGACAGTGTCTTCCATGATGTGAGTTAGTG 4032
Oy 1313 SerSerProAsnHisAspAlaValAlaAsnGlnLyvAlaSer----- 1327
Db 4033 AATGATTAAGGTCAAGATGATATCACAGCACTAGAAATAGGCAAGAGGTAGAGAA 4092
Oy 1328 ---LeuGlyGluValAsnSerLeu-----GlnSerGluMetLeuArgGlyGluArgAsp 1344
Db 4093 CTACTAATGAAGTTAAATATTAATGATGACAGTGTCTTCCATGATGTGAGTTAGTG 4152
Oy 1345 Glu----- 1345
Db 4153 GAAACATACAGAGAGTGAATTTGGTGAACAACCAATGAACAGCACCCTGTGCTTTTG 4212
Oy 1345 ----- 1345
Db 4213 GCTCATGAGAGAGATTAATCTTAAGAGCACTTGACATTTGTGACAGAAAGTCA 4272
Oy 1346 -----LeuGlnThrSerCysLyvAlaLeu 1353
Db 4273 ATGCATTTGCCGAATTCAGAGAAATTTCTTAATCTTAACAAAGTGAACACAAATTTTA 4332
Oy 1354 -----ValSerGluLeuGlnLeuLeuArgAlaHisValLyvSer 1366
Db 4333 CATGATCAGCACTGTCAATGAGCTTAAATATGTCAGAGCTGCGACCTATGTGACTCA 4392
Oy 1367 ValGlnGlyGluAsnLeuGluIleThrLyvLyvLeuAsnGlyLeuGlnLyvGluIleLeu 1386
Db 4393 TTAAGGCCGAAATATTTGCTGTGTGCACGAATCTGAAGAACTTTCAAGGTGACTGTGGT 4452

OY	1387	GlYlySerGlu-----	GluserGluValLeuLySerMetLeuGluAsnLeuLyS	1403
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Db	4453	AAGGAGATGCACTGGCGGCTTGAGAGAGGCGCTGTTTCATCCCTGTCATCCCTTTGTGTG		4512
OY	1404	GlUAAspAsnAsnLyLeuLySgluGlnIaGlu-----		1414
		: :::: :::: :::: :::: ::::		
Db	4513	CCTGACACTCTAGCTTACAGCAGTGTGGAGAGACTCCTCTTTACAGAGCTTTTGAA		4572
OY	1415	-----	-----GluYrSerSerLySgluaSnglnPhe	1423
		: :::: :::: :::: :::: ::::		
Db	4573	CAGACAGAGATATGCTCTTTTGAGTATTATAGAAAGGCGCTGTTTCAGCAAAACCAAGTGC		4632
OY	1424	SerLeuGluGluValPhe-----		1429
		: :::: :::: :::: :::: ::::		
Db	4633	AGTGTAGATGAAGTATTTTGGCAGCAGCTGTCAGAGAGAAATTCGACGAGAAAGAAACC		4692
OY	1430	---SerGlySerGlnLyLeuValaSpGluIle-----	-----GluValLeuLySglua	1444
		: :::: :::: :::: :::: ::::		
Db	4633	CCTTGCGGCCCGAGCGAAGGGTGTTAAGAACGCTAGTGTCCCTGTGAGAGTTACCGGAG		4752
OY	1445	GlnLeuLySgluaIaIaGluGlnUArgLeuGlu-----	-----IleLySAspArgSpTyx	1460
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Db	4753	TCCCTCGAAGAGCTGAAGAGAAATGAGAAAGTCAAGGATTTATGAAATAAGAAATAT		4812
OY	1461	PheGluLeuValaGlnThrAlaAsnThrLySsnLeuValGlu---GlyLyLeuGluThrPro		1479
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Db	4813	CAGAGCTCGAGCACTTTATTAAGTCTTGAAAGCAGAGCTTGACTGCTTACGAGAGACAG		4872
OY	1480	LeuGlnAlaAspHisGlu-----	-----GluAspSerIleAspArgArgSerGluGluMetGlu	1497
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Db	4873	TATTTGTCAGAAATATGAACAGTGGCAACAGAACCTGACACAGCGTGAACCTCGAGATGGAG		4932
OY	1498	IleLyValLeuGluGluLySLeuGluArgAsnGlnTyrLeuLeuGlu-----		1513
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Db	4933	TCCAAAGTTGGCGCGAGAAAGAAACAGACGGAACAACCTGACCTTGAGACTGGAAGTAGCA		4992
OY	1514	ArgLeuGlnGluGluLySLeuGluLeuSerAsnLySLeuGluIleLeuGlnLySgluMet		1533
		: :::: :::: :::: :::: ::::		
Db	4993	CGACTCCAGCTACAGAGCTGTGGACTTAAGTTCTCGG-----		5028
OY	1534	GluThrSerValLeuLeuLySAspAspLeuGlnGlnLySLeuGluSerLeuLeuSerGlu		1553
		: :::: :::: :::: :::: ::::		
Db	5029	-----TCCTTGCTGGCATGCACAGACAGATGCTATTCAAGGC-----		5067
OY	1554	AsnIleIleLeuLySgluAsnIleAspThrThrLeuLySHisSerAspThrGlnAla		1573
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Db	5068	-----CGAATGAGAGCTGTACATATCAAAAGAACATACTTCGAAGATCAAGAA		5118
OY	1574	GlnLeuGlnLyS-----	-----ThrGlnGlnLeuGln	1583
		: :::: :::: :::: :::: ::::		
Db	5119	AGAACACCAACAGCATGATGTTTCATAGATTTGTGTATAAAGATGCTCAGACAGACTCAAT		5178
OY	1584	Leu-----	-----AlaLySAsnLeuAlaIleAlaAspAsnCySProIle	1598
		: :::: :::: :::: :::: ::::		
Db	5179	CTAGACATTGAGAAATATACAGACTGTGTGATTGAACCAACAGAGAGTGTCTGGG		5238
OY	1599	ThrGlnGluLySgluThr-----	-----SerAla	1606
		: :::: :::: :::: :::: ::::		
Db	5239	GAAACGTCCTCCAGATACCAATTTATGAGCTCCAGGGGAAAGATAAACCAAGGCTCTTCA		5298
OY	1607	AspCyValHisProLeu-----		1612
		: :::: :::: :::: :::: ::::		
Db	5299	GAAATCATTTTCGAATTTGTCAATTTTCTGTGTCTTAATGCTTTGGTACCTATGGAATTTCTGT		5358
OY	1613	-----GluGlnLySgluLeuLeuLeuThrGlnGluLeuHisGlnLySThrAsnGlnGln		1630
		: :::: :::: :::: :::: ::::		
Db	5359	GGGAATCAGGAAGATATCCATATCTTCAACTGCGGGTAAAGAGACATCAATGAAGAT		5418
OY	1631	GluLySLeuLeuHisGlnLySAsnGlnLeuGlnGlnAlaGlnValGlnLeuLySgln		1650
		: :::: :::: :::: :::: ::::		
Db	5419	TTGAATTAATTCATGTATAGAGGACGCTGACAGA-----AAA		5457

QY	1651	alGlnHisLeuMetCysSerMetIleGluSerCysSerSerLeuGluSerLeuGlnHis	1670
Db	5458	GTGAAAGCTTTGGCPAAATGAAATATAAAGAAATTGACATCAAAATC-----	5502
QY	1671	GluYshIAspThrGlnGlnGlnLeuLeuAla-----	LeuLys 1683
Db	5503	-----CATTTACAGAGAGCTACCACTAATGACSCAAATTTGAAGCATATGAATTGGAA	5556
QY	1684	GlnGlnMetGlnAlaValThrGlnCyluYsLeuGluGlnGlnInthrHisGlnHisLeu	1703
Db	5557	AAATAGATTGGGAACTTAAGAAAGAAAACTCACATTTTAAGTGAAAAATGGAATATTTT	5616
QY	1704	ThrAlaGluValAspHisLeuLysGlnAsnIleGluLeu-----GlyLeuAspPheLys	1721
Db	5617	TCTTGATGATCACAGAGATTACTCCAGAGATGAAACTTCTGAAGGCTCTCAATTGAT	5676
QY	1722	AsnGluAlaGln---GlnYsThrThreGlnGlnCysLeuLeuAsnGluAsnLys---	1739
Db	5677	TTAGAAATGCTGCAGATAAATCATCTACGCTGAATATTTGGAGATTAATGGGCCAAAGCTG	5736
QY	1740	-----GluLeuGlnInserGlnHisArgLeuGlnCys	1750
Db	5737	AATGACAGCTGGAAGAGAGATTTCTTGATGTGAAATAGCATGAGATGATCAGATCG	5796
QY	1751	GluY-----IleGlnCyluMetLysSerLeuLys	1760
Db	5797	GAGAAAGCTAGCATGAGATGAAGCCCTTACCTGAGGCTGACTTAAGAGTAGTTCTCA	5856
QY	1761	AspYsgIuSerAlaLeuGlnThrLeuLysGlnSerGlnCyluYsValIle---AsnLeu	1779
Db	5857	ACAGAGAAAGCTATGTTTGAAGAAAAGACAATGAAATTAAGACAAAGTTATTGTCTGCTT	5916
QY	1780	AsnGlnCyluMetGlnMetValMetLeuGluMetGlnCyluLeuYsaAsnSerGlnArgThr	1799
Db	5917	GAAAGAAAGCTCTCAGTGGTACAAAGTGAAGAAACCAAGCTTCGTGAGATTAAGATTA	5976
QY	1800	ValIleAlaGluArg-----AspGlnLeuGlnAspAspLeuArgGluSerValGlu	1816
Db	5977	ATGTCMAAAAAAACCCAGCGACTGGATCAGTTGCTGTCAAAAAAAGAGAGAAAAACA	6036
QY	1817	MetSerIleGluThr-----GlnAspAsp	1824
Db	6037	---GAGCTTGAGTCTCATCAAGTAGAGTGTCTCATTTGACATTCAGGTGGCAGAGCCAG	6093
QY	1825	LeuArgYsaIaGlnGlnAlaLeuGlnGlnGlnLysAspYsaValGlnCyluLeuThrSer	1844
Db	6094	GTGAAGGAAAGACGGAAGCTCTTCACAGCTTTCCTCTGATGTGAAGTAGCTGTAAA	6153
QY	1845	GlnIleSerValLeuGlnGlnLysIleSerLeuLeuGlnGlnMetLeuTryAsnVal	1864
Db	6154	GACAAAATCTCTCCAGGAAAGCTCAGAGTTTGGAAAAGGACCTCACAGGCACTGTCT	6213
QY	1865	AlaThrValLysGlnThrLeuSerCyluYsAspAspLeuAsnGlnSerLysGlnHisLeu	1884
Db	6214	TTGCAAAATGTAGCTGGAAACCAATTTGCACACATCGAATTAAGAGAAAGAAATTCCT	6273
QY	1885	PheSerGlnIleGlnThrLeuSerLeuSerLeuLysGlnLysGluPhe-----	1900
Db	6274	GTCAAGGAATGTGAAGCTTCACAGCCAGACAGCTGATGATCAAGTATTAAGAAAAGCTGA	6333
QY	1901	-----AlaLeuGlnGlnAlaGlnLysAspYsaIAspAlaAlaArgLysThrIle	1917
Db	6334	GTCTCCAAAGGCTTTGGAGCGCGACTGTGTGAGAAAGTAGTGTGCAATTGAGGCTGAGC	6393
QY	1918	AspIleThrGluYsIleSerAsnIle-----	1926
Db	6394	TCAACACAGGAGGAGTGTCATCAGCTGAAGAAAGAGCATCGAAGAACTGAAGATTCCGATT	6453
QY	1927	-----GlnGlnGlnLeuLeuGlnGlnAlaThrAsnLeuLysGlnThrLeuYsGlu	1943
Db	6454	GAGGCCGATGAAGAAAGACAGCTTCACATCGCAGAGAAACTGAAAGAAACCCGAGCGGAG	6513
QY	1944	ArgGluSerLeuIleGlnCyluYsGlnCyluLeuAlaLeuAsnThrGlnHisLeuArgGlu	1963

[illegible]

Db	7435	GGCCCTGCATATGACCA-----	7452
Qy	2294	ThrgLualahIeLVyNHISyMeLeuabnIlelyegIuserLeuserSerThrluser	2311
Db	7453	---GAAGCCTTAAG-----	7489
Qy	2314	ArgserPheglYserLeuGlnThrGlnHisValyLeuabnThrgIleuGlnThrlreu	2333
Db	7486	AGTCAAGTAGAGTGTCTTGAACTTGAGAGGCTCAGTTGACAAAGCCTTGATGAGGCC	7545
Qy	2334	LeuabnLyPheLyValValTyArgThrlaIaValyGluabnHiserLeulle	2353
Db	7546	AAAAATATATATATTTGTTTGGCAATCTTCAGT-----AAAGCCTCAATT	7590
Qy	2354	LyAsPtrygIuLyAsPLeuLaIaIaGluGlnLyAsArgHisAsPglu-----Leu	2370
Db	7591	CAGAAGATAGAAGATGGCAAGACAGAACTGGAGAAAGAAAGATGATGAAATCAGTAGACTG	7650
Qy	2371	ArgLeuGlnLeuGlnCyLeuGlnGlnHisGlyArgLytrPserAsPserLaserGlu	2390
Db	7651	AAAAATCAAAATTCAGACCAAGACAGCTTGTCTTAAACSTGTCCACAGTGAAGAGACG	7710
Qy	2391	GluLeuLyPhe-----CysgluIleGluPheLeuabnGluLeuLeuPheLy	2406
Db	7711	CACCACTTTGGAAAGAGCAAAACTTGAACSTGAAATCTGACAGTGGAAATTGGACAG	7770
Qy	2407	LySaLaabnIleIleGlnSerValGlnAsPserPheSerGluValGlnValPheLeuabn	2426
Db	7771	AAGATCCAAAGCTCAATCCAAATAATGCCCTTGGCAGACACTTAGAAGTCTGACG	7830
Qy	2427	GlnValGlySerThrlLeuGlnGluGlu---HisLybLyGlyPheMetGlnTrp	2445
Db	7831	AGTTCTTCAAGAAATCTGAGAGATGAGCTTGAATTGACMAAAATGGAACMAATGCTCTT	7890
Qy	2446	LeuGluGluPheGly-----AsPLeuHisVal	2454
Db	7891	GTTGAAAAAGTAAACAAATACTGTCAGAAAGAACTGACCTGCAGAGGAAATGCAATGAG	7950
Qy	2455	AsPaLaLybLyS-----LeuserGluLyMetGlnGlnLeuabnArgArgIleLa	2471
Db	7951	ATGCGACACGAACACGACGACTGCCAGAAACAATCTGAGTGGAGAAATAAGCTAGCT	8010
Qy	2472	SerThrlleGlnLeuLeuThrlYAsArgLeuLySaLaValValGlnSerLySleGlnArg	2491
Db	8011	GGAGAGTGTGCACTTACTGTTGAAAGAAATAAGAC-----ACCAAAAGATCAAA--	8058
Qy	2492	GluIleThrlValTyrlLeuabnGlnPheGluLaLyLeuGlnGluLybLyGluGlnabn	2511
Db	8059	-----TTGAAGGAGCTCACACTGAATAAT	8082
Qy	2512	LyegIleuMetArgArgMetGluHisIleGlyProSerIaSerValImetGluGlu	2531
Db	8083	AGTGAATTTGAAGAAAG-----AGCCTAAGTTGCAITCACAAACAC	8121
Qy	2532	AsnaIaArgLeuLeuGlyIleLeuLyThrlValGlnAsPgluserLybLyLeuGlnSer	2551
Db	8122	CAGGTGAGAAAGAAAGG-----AAAGTAGAGAGGAAATAGCTGAATATCAGCTA	8172
Qy	2552	ArgIleLybMetLeuGluabnGluLeuabnLeuValyAsPaPalaIaMetHisLybGly	2571
Db	8173	CGG-----CTTCAAGAAAGCT	8187
Qy	2572	GluLybS-----ValaIaIleLeuGlnAsPrybLeuuserArgnaIaGluLaIaGlu	2589
Db	8188	GAAAAGAAACCCAGGCTTGTCTTTGGAC-----ACAAACAAACAGTATGAAGTAGAA	8211
Qy	2590	LeuabnIaMetGlnValLyLeuThrlYbLySleGlnAsPserbnLeuGlnaIaIaMetLyb	2609
Db	8242	ATCCAGACATATCGAGAGAAATATGACTTTAAAGAAAGATGCTCAGTTACAGAGCTG	8301
Qy	2610	GluIleGluabnLeuGlnLybMetValaIaLybGlyLaIaValProTyrlYbGluGluIle	2629
Db	8302	GAGGTAGACCTTTTAAAGCTTAGT-----AAAGAAAGACTC	8337

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QY 2630 Aspaen-----LeuysThrlvsValValylleGlumetGlu 2642
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QY 2643 LyslleLysTyr-----SerLysAlaThrAspIngluile 2654
      :::::
      8398 AATCTAAATATGTAATCATGTTGAAGAAAGAAATGAACGTGCCAGGGGAAATGAAG 8457
QY 2655 AlaTyrLeuLysSerCys-----LeuGluAspLysGluGluGlyLeuArgArgLeuLys 2672
      :::::
      8458 TTGTGATCAAAATCCGTGAACAGCGTGAAGAGAAAGAAAGACTCTGAGAAAGAACCTC 8517
QY 2673 GluGluLeuArgArgAlaGlnAlaAspAsnAspThrThlValCysValProLysAspTyr 2692
      :::::
      8518 TCTCAACTCAAGCTGCACAGAGAAAGCAAAACA----- 8553
QY 2693 GluLysAlaSerThrPheProValThrCysGlyGlyGlySerGlyTleValGlnSerThr 2712
      :::::
      8554 -----GGTACTGTATGATAC 8571
QY 2713 AlaMetLeuValLeuGlnSerGlu-----LysAlaAlaLeuGlu----- 2725
      :::::
      8572 AAGTCGATGATTAACAACACTGAGATCAAGAAGCTGAAGAAAGAACTTGAAGAAAGAAAC 8631
QY 2726 ArgGluLeuSerHisTyrLysLysLysTyrHisHisLeuSerArgThrMetSerSer 2745
      :::::
      8632 AAGGAGCGCATGATTAAGTCTGATTAAGTCTGCTCTG-----CTTATAAGCCAT 8682
QY 2746 GluAspArgLysLysThrLysAlaLysSerAspAlaHisSerSerHisThrLysSer 2765
      :::::
      8663 GAAGAAGTGAAGAAAGCTTAAGAGATGTTAGAGACAAAGTGGCCATGTGTTTACAG 8742
QY 2766 His-----ArgLysSerProHisLysThrGluThrTyrArgHisGlyPro 2780
      :::::
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QY 2781 ValThrProGluArgSerGluMetProSerLeu-----HisLeuLysSerProLys 2797
      :::::
      8785 GTTGTTCGAGCACTTCCTCAATCCCTTCTGTTACTGAAGAGAGTTATCATCTGCGCA 8844
QY 2798 LysSerGluSerSerThrLysArgValAlaSer----- 2808
      :::::
      8845 AATAAAGCTTCAGAGAGCAAGAGATCCAGTGAATGCGAGAGTGTGAGAGACCA 8904
QY 2809 ---ProAsnArgSerGluLysTyrSer-----GlnLeuValMetSer----- 2821
      :::::
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QY 2822 ---ProGlyLys----- 2824
      :::::
      8965 CACCTGCAAGAGACAGAGAGTACTAGTTGAGCCAGAGAGACTTCCAGAAATTGTA 9024
QY 2825 -----ThrGlyMetHisLys-HisIle----- 2831
      :::::
      9025 AAGAAAGGTTTCTGCACATCCCAAGAGAAAGACTAGCCCAATATATCTCTCGAAGACA 9084
QY 2832 -----LeuSerProSerLysValGlyLeuHisLysLysArgAlaLeuSerPro-- 2847
      :::::
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QY 2848 ----- 2850
      :::::
      9144 GAGTCTCGCAAGAAATCTTCAGAGAGTCTCAAAACCAAGCTGTGTGAGAGAGATC 9203
QY 2850 rGluMetProThrGlnHisValIleSerProGlyLysThrGly-----LeuHisLysAs 2868
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QY 2868 nLeuThrGluSerThrLeuPheAspAsnLeuSerSerProCysLysGlnGlnLysValIle 2888
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RESULT 10
US-09-954-456-1153
; Sequence 1153, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1153
; LENGTH: 10211
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1153
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Pred. No.: 1,236-62 Length: 10211
Score: 1139.00 Matches: 703
Percent Similarity: 37.36% Conservative: 556
Best Local Similarity: 20.86% Mismatches: 1052
Query Match: 7.71% Indels: 1060
DB: 10 Gaps: 139
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      112 ACAAGAGCTCTCAAGAAATTCAGAGAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 171
QY 353 lLeuAspLeuLysLysGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGlnLeu 372
      :::::
      172 AAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231
QY 373 AlaMetAlaLysGluGlu-----HisThrGlnLeuLeuAla 384
      :::::
      232 AAGGTGAATATGAAGAAACCGAGGGTGAACAACCTGAAGAGAGAGAGATCAAGATTGATG 291
QY 385 GluLysGlnLeuHisLysLysGluArgGluAspArgLysArgLysLeuThrAsnIleVal 404
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      292 GAATATGTGAAGAGTCTGAGAGAAAGTAAGCAAGAAATTTCTCAT-----GAATTCGA 345

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Db 2335 TTGCATGCCGAATATAGAGCCTCAGGATCTCTAAATCCAAAGATGCTTCTGTG 2394
 QY 998 -----GluHis 999
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 QY 1000 Ser---AlaSerIleIleSerIleGlnIlele----- 1010
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 QY 1010 ----- 1010
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 QY 1011 -----MetGlnGlnSerGlnGln 1017
 Db 2575 GAATTTTCATTAGAGTCTCAAAAACAGATGAAGTCAAGCTCCAAAAGAGTGAAG 2634
 QY 1018 IleGlnIleuThrAspGlnValThrHisThrGlnSerIleValGlnIleThrGln 1037
 Db 2635 TTGGTCAAAATCAAGAGAAATAGAGAAATCTCATGAAGCAGAACAGATGCATCA 2694
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 QY 1048 ----- 1048
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 Db 2992 GAGATGGAGACTCTTAAGAGAAATTAATGATCATCTTAATCAAGAGAGTGAATTAATC 3051
 QY 1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProIleu 1118
 Db 3052 CAGAAAGTGAAGAGTTTGCAAACTATATAGATGAAGAGAGAAAGCATTTCAAGATT 3111
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 Db 3112 TCTGATCATCAAGCAAGAAATTAATTAATCAAGAGATGCAAGAAACCGGAAT 3171
 QY 1132 SerGlnAspProIle----- 1136
 Db 3172 GCATATGAGGATCTTAGTCAAAAATCAAGACAGACAGAGAAAGATTTAAATTAGA 3231
 QY 1136 ----- 1136
 Db 3232 TGCTTGCTAAATGAATGACCTAGTCTTTGTGAATAATAGAAAAATGAGTTGAAACGCT 3291
 QY 1137 -----GluIleAsnAspIleuHisAsnIleuIleAlaIleuAlaThrGln 1150
 Db 3292 AAGGAGCATTTGCAAAAGAACACCAAGAAATCTTAACAAATTAAGCATTTGCTGAAGA 3351
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 QY 1160 ----- 1160
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QY 1161 -----GluArgAsnSerIleuGlnIleuValIleAspIleu-----AsnThr 1174
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 Db 3532 CAGCTGATGAAGGTAATGAAGACCTTAACATGATATGTAATAATCTTAAGATCGAACCAATT 3591
 QY 1185 GluIleuSerAspIleuGln-----LysProIleGln 1194
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 Db 3652 GATCTTGAAGTGAAGAAATTTCTGTAGATTAGTATAATGCGAGCTGTGCTCAATTGA 3711
 QY 1209 LeuIleuIleuGlnHisIleuThrAspSerGlnIleuSerIleGlnIleuGlnIleuAsn 1228
 Db 3712 GCTATG-----CTAAGAAATTAAGAAATTAATACTTCAGAAAGTGAAGAGAGAG 3762
 QY 1229 LeuGlnValThrGlnIleuGlnIleuGlnIleuMetIleuMetIleuThrIleGln 1248
 Db 3763 -----GAGTGCCTGCAGCATGAATTAACAGCAATT----- 3792
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 Db 3793 AGAGAGATCTTGAAGACAGCAATTTGCAAGACATGACATGACACAAATTAATGAGCCTT 3852
 QY 1267 Lys-----GlnAspIleuSerGln----- 1272
 Db 3853 AAGAGCTGTAATAGATCCGAAAGAAAGTATTTTCAGGCGCTCATGAGTTGTCAACA 3912
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 1607 AspCysValHisProLeu----- 1612
 5299 GAATGCAATTTGCAATTTCTGCTGCTAATGCTTGGTACATGATTTCTCG 5358
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 5458 GTTGAAGTGTCTGAATGAATGAAGATTAAGACTCAAACTC----- 5502
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5503 -----CATTTACAGAGGTAACTAATGACCAAAATTGAAGCATGATAGATTGGAA 5556
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 1722 AsnGlnAlaGln-----GlnValThrValGlnGlnCysLeuLeuAsnGlnValSer 1739
 5677 TTGAAGAAATGATGACAGATTAATCATCAGCTGAAGATTTGAGATTAATGCGCAAGCTG 5736
 1740 -----GluLeuGlnGlnSerGlnHisArgLeuGlnCys 1750
 5737 AATGACAGCTGGAAGAGAGATTTCTTGATGTGAAGAAATGAGCTGATGATGATGATG 5796
 1751 Glu-----IleGlnGlnLeuMetLeuSerLeuVal 1760
 5797 GAGAAAGCTAGCATGACATGAGACCTCTTACCTGAGAGCTGACTTGAAGGTAGTCA 5856
 1761 AspValGlnSerAlaLeuGlnThrLeuValSerGlnGlnValValIle--AsnLeu 1779
 5857 ACAAGAAAGCTATGTTTGAAGAAACATGAATGAAGCAGAGATTTTGTCTGCTT 5916
 1780 AsnGlnGlnMetGlnMetValMetLeuGlnMetGlnGlnLeuValAsnSerGlnArgThr 1799
 5917 GAAGAAAGAACTCTGAGTGTCAAGTGAAGAAACCAAGCTTGGTGAAGATTAATGAT 5976
 1800 ValIleAlaGluArg-----AspGlnLeuGlnAspAspLeuValGlnSerValGlu 1816
 5977 ATGTCAAAAGAAACACAGGCACTGATGATGATGATGATGATGATGATGATGATGATG 6036
 1817 MetSerIleGluThr-----GlnAspArg 1824
 6037 ---GAGCTTGAAGTCTCAATCAAGTGAAGTCTCCATTCGATTCAGTGGCAGAGCAGAG 6093
 1825 LeuArgValAlaGlnValAlaLeuGlnGlnGlnValAspValGlnGlnLeuThrSer 1844
 6094 GTGAAGAAAGAAAGCAAGCACTCTTCAAGCTTGTCTGATGATGATGATGATGATGAT 6153
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 1865 AlaThrValValGlnThrLeuSerGlnValArgAspLeuAsnGlnSerLeuHisLeu 1884
 6214 TTGACAAATGATGAGCTGGAAGAAACCAATTGCACAACTGAAATGAAGAAATTCCT 6273
 1885 PheSerGlnIleGlnThrLeuSerLeuSerLeuValGlnValPhe----- 1900
 6274 GTCAAGAAATGCAAGAGCTGAGGCGCAGCTGATGATGATGATGATGATGATGATGAT 6333
 1901 -----AlaLeuGlnGlnAlaGlnValAspValAspAlaAlaArgValThrIle 1917
 6334 GTCTCAAGGCTTGAAGGCGCAGCTGATGATGATGATGATGATGATGATGATGATGAT 6393
 1918 AspIleThrGlnValIleSerAsnIle----- 1926
 6394 TCACACAGAGAGAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 6453
 1927 -----GlnGlnGlnLeuGlnGlnAlaThrAsnLeuValGlnThrLeuTyrGln 1943
 6454 GAGCGGATGAAGAAAGAGAGCTGACATCCAGAGAACTGAAGAAAGCGGAGGAG 6513
 1944 ArgGlnSerLeuIleGlnCysValSerGlnGlnLeuAlaLeuAsnThrGlnHisLeuArgGln 1963
 6514 AATGATTCATCT-----AAGATTAAGTGAAGCTTGAAGAGAAATTCAGAGATG 6564
 1964 ThrLeuValSerValAspLeuAlaLeuGlnValMetGlnGlnGlnValArgAspGlnAla 1983

Db 6565 TCAGAGAAACAGGAGCTAGTACT-----CTTGATCCGAGATTCACAAAGA---- 6615
 QY 1984 AsnLysValIleAlaLeuThrGluLysMetSerSerLeuGluGlnIleAsnGluAsn 2003
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 QY 2057 -----AsnGluIleLysAsnLeuThrAlaLysIleSerSer 2068
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 QY 2089 Leu-----GluGluGluIleLeuGln--AsnAlaSerIleLeuAsnGluAlaValSer 2085
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 QY 2086 GluArgGluAsnLeuArgHisSerLysGlnIleValSerGluLeuGlu----- 2102
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 QY 2103 -----GlnLeuSerLeuThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArg 2120
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 Db 7309 ATTAATTCATCATTTGAAAT----- 7329
 QY 2234 IleSerValLeuArgLeuMetGlnAsnGluProGlnGlnGluAspArgValAlaGlu 2253
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 QY 2294 ThrGluAlaHisLysHisCysMetLeuAsnIleLysGluSerLeuSerSerThrLeuSer 2313
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 QY 2334 LeuAsnLysPheLysValValTyrArgThrAlaAlaValLysGluAspHisSerLeuIle 2353
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 QY 2354 LysAspTyrGluLysAspLeuAlaAlaGluGlnLysArgHisAspGlu-----Leu 2370
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 QY 2512 LysGluLeuMetArgArgMetGluHisIleGlyProSerAlaSerValMetGluGluGlu 2531
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 QY 2532 AsnAlaArgLeuLeuGlyIleLeuLysThrValGlnAspGluSerLysLysLeuGlnSer 2551
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 QY 2552 ArgIleLysMetLeuGluAsnGluLeuAsnLeuValLysAspAspAlaMetHisLysGly 2571
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 QY 2572 GluLys-----ValAlaIleLeuGlnAspLysLeuLeuSerArgAsnAlaGluAlaGlu 2589
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 QY 2630 AspAsn-----LeuLysThrLysValValLysIleGlnMetGlu 2642
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2643 LysIleLysTyr-----SerLysAlaThrAspGlnIle 2654
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8518 TCTCAACTTCAAGCTGCACAGAGAAAGCAAGAAACA----- 8553
2693 GlnLysAlaSerThrPheProValThrCysGlnGlyGlySerGlyValGlnSerThr 2712
8554 -----GGTACTGTTATGATAC 8571
2713 AlaMetLeuValLeuGlnSerGlu-----LysAlaAlaLeuGlu----- 2725
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2766 His-----ArgLysSerProHisLysThrGluThrTyrArgHisGlyPro 2780
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2781 ValThrProGluArgSerGluMetProSerLeu-----HisLeuGlySerProLys 2797
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2809 ---ProAsnArgSerGluLysSer-----GlnLeuValMetSer----- 2821
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8965 CACCTGCAAGAAAGACAGGAAGTACTAGTTAGCCAGAGGACTTCAGAAAGTTGA 9024
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2848 -----AsnArgSe 2850
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9264 CACCGCAAAATCGTCCAGTCAATATATCTTCTGAGACAAGTCCGACTGAAGCCCCAG 9323
2888 nGluAsnLeuAsnSerProLysGlyLysLeuPhe-----AspValLysSe 2903
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Db 9384 CAAGGCGAGTGAAGACTGTAAGTTCAG 9411
RESULT 11
US-09-967-768A-186
Sequence 186, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 186
LENGTH: 10211
TYPE: DNA
ORGANISM: Homo sapiens
US-09-967-768A-186
Alignment Scores:
Pred. No.: 1,236-62 Length: 10211
Score: 1139.00 Matches: 703
Percent Similarity: 37.36% Conservative: 556
Best Local Similarity: 20.86% Mismatches: 1052
Query Match: 7,71% Indels: 1060
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QY 353 IleLeuAspLysLysLysGlnLeuGlnLysLeuGlnLysSerSerSerGluThrLysAlaGln 372
172 AAGCAGAAAGGCAAGTTCAGCTTGACGTTCAGAGCTTCGAGGCTGCGCTCAGAGACAGCAG 231
QY 373 AlaMetAlaLysGlnGlu-----HisThrGlnLeuLeuAla 384
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Db 232 AAGGTGAATGAAGAAACCAAGGCTACAAACSTGAAGAGGAGAAATCAAGATTCAGATG 291
QY 385 GluIleLysGlnLeuHisLysGlnLysArgGluLysAspArgGlnIleThrHisLeuThrAsnIleVal 404
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Db 292 GAATATATGTAAGAGTGTGAGAAACTGAAGCAGAGATTTCTCAT-----GAACTTCA 345
QY 405 ValAlaSerSerGlnLysSerGlnLysPhe-----GlnArg 416
346 GTCAAGAGTCAAGATTTCCAGAGAGACAACTGAATTCAGGCAAGAAACCAATA 405
417 ValLysAspLysValArgValThrThrAlaProGlyLysValGlnAsnSerLeuHisAla 436
406 GAAGAACTGGAAGCAAGAACTTAAAGGTGTAAATGTGACGTTGAAGAAAGCAAGAGT 465
437 SerGluValSerAspPheAspMet-----Leu 445
466 GCGAGCTGCGAGATGCTCTGTAATCATGCAATACACCAAGAAATTTTACAACT 525
QY 446 SerArgLeuProGluLysAspHisSerLysLysAlaLysPheSerAspMetProSer----- 463
526 CCATTAACACCAAGTCAATATTAATGATGCTTCAAGTATGAAGATCTAAGAAAGAAATAT 585
464 PheProGluIleAspAspSer-----ValLysThrGluPheSer 476
586 AATAAGAGCTTGAAGAAAGAAAGATTAAGAGCAGAGTTAAAGCCTTGACAGCTAA 645

Oy	477	Asp	He	Asp	Ala	Leu	Ser	Met	Met	Asp	Ser	Asn	Gly	I	Leu	Asp	Ala	Glu	Thr	Asp	Leu	496	
Db	646	AAAGCAAGCCAGACTCTTCCAAAGCCACCACTGAATCACCGCGACATTGCCCGCATCAG	705	
Oy	497	Ala	Ser	Leu	Val	Thr	-----	His	Arg	Glu	Leu	Ser	Leu	His	-----	-----	-----	-----	-----	-----	-----	509	
Db	706	GCTTCATCATCTGTGTCTCATGGCAGCAAGAAAGAACCCCAAGTCATCTTTCATCTAAT	765	
Oy	509	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	509	
Db	766	TCTCAAGAACTCCAAATTAGAGAGATTCTCTCGCATCTTACTTTCTGGGAAACAAAG	825	
Oy	510	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	525	
Db	826	GTCAGTCGAATGCATCAACTTGTGCAATATAGGAAAAAGATGCAATATAGCAGTTCTTT	885	
Oy	526	Asp	Ser	Ser	Leu	Ser	Glu	Asn	Glu	Leu	Gln	Leu	Pro	Leu	Phe	Asp	Ser	Gly	Asp	Met	Ala	Glu	545
Db	886	GACAAATTCACAGCTCCATCTTTTGTG	924	
Oy	546	Cys	Arg	Gly	Ala	Ser	Phe	Glu	Leu	Ser	Glu	Leu	Leu	Thr	Ser	Leu	Gln	Gln	Leu	Gln	Ser	Leu	565
Db	925	GCGCGAAATCAAGACCTAAGAAACAGATTAATGATGTTGAACTACGCTCCAAAGCAT	984	
Oy	566	Glu	Glu	Glu	Leu	Ser	Glu	Leu	Val	Gln	Ser	Phe	Glu	Leu	Ser	Leu	Ala	Glu	Leu	Glu	Leu	585	
Db	985	GAAAGAAATGAAAGGCCCAAGTGAATGATTTCA	1032	
Oy	586	Glu	Leu	Ser	Ser	Val	Leu	Ala	Leu	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	600	
Db	1033	CAACTGAGG--AAAGCAAAAGTGGAATTAATTGAAAAGAAAGTTTGTGAACAAATGT	1089	
Oy	601	Arg	Glu	His	Ser	Leu	Asn	Ala	Glu	Val	Gln	Thr	Asp	Val	Glu	Leu	Val	Val	Arg	Leu	520		
Db	1090	AGGATGAACAGTAGTGAAGAAACAACACATATACGC	1125		
Oy	621	Glu	Met	Ser	Val	Leu	Gly	Asp	Ser	Gly	Thr	Asn	Ala	Ser	Asn	Ser	Asp	Leu	Gln	Asp	Ser	640	
Db	1126	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	1173	
Oy	641	Ser	Val	Asp	Gly	Leu	Val	Arg	Leu	Ser	Ser	Ser	His	Asp	Gly	Cys	I	Leu	His	Arg	Leu	Met	660
Db	1174	ACGGAAGAT-----TTGAGTTGTACGCGACCAAAATGCAGAAAGTCCAGATGTTCT	1224	
Oy	661	Leu	Glu	Glu	Leu	Ser	I	Leu	Val	Asp	Leu	Gln	-----	-----	-----	-----	-----	-----	-----	-----	-----	679	
Db	1225	CTGGAACAGAAATTAAGGAAAAAGAGGATTTCAAGAGGAGCTCTCCCGT-----	1278	
Oy	680	Glu	Asn	Asp	Leu	Ser	Gln	Leu	Ser	Ser	Glu	His	Asp	Met	Glu	Ser	I	Leu	Gln	Leu	Cys	Glu	699
Db	1279	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	1323	
Oy	700	Ala	I	Met	Met	Ala	Glu	Leu	Ala	Asn	Ala	Leu	Glu	Leu	Glu	Leu							

QY	778	AlaGlnuIet-----	TyrAsnGlnAsnLeuGluValAspLeuGluThrIleStryrHis	794
Db	1606	ATCAACAAGCTGTTTAATCAAGCCAGCAATTTTGAGAGAAATGAATGAACCGAAGAT---		1666
QY	795	LeuLeuYsGluGluGluIleGlnLeuValaGluLeuArgLySargAlaAspAsnLeuGln		814
Db	1663	-----ACCTCTCAGGAACCATGTTAAGAGATCTTTCAAGAAAAATTAATCAAGCAAGA		1716
QY	815	LysIlySValArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeu-----		832
Db	1717	AACCTCCTTGACTTTAGAAAAAAGTAAAGCTGCTGCTGGCTGATCTGGAAAAAGCAGAGAT		1776
QY	833	CysGluGluIu-----		843
Db	1777	TGTTCTCAAGACCTTTTGAAGAAAAAGAACATCACTATGAACAACTTAATGATTAAGTTA		1833
QY	844	SerAspAlaGluAlaValThrArgAspAlaGlnYsGluCysSerPheLeuArgSerGlu		863
Db	1837	AGCAAGACAGAGAAAGAGATCCAAA---GCCTTGCTGAGTGGCTTTAGATTAATAAAAAA		1899
QY	864	AsnLeuGluLeuLeuYsGluLysMetClnAspThrSerAsnTrpTyrAsnGlnYsGluYs		883
Db	1894	GAATATGATTTGAAGAAAGAGAAAAAAGCTGTTTCTTTGTTGGAAAAAGTAAAAACGAAAAA		1953
QY	884	AlaAlaSerLeuPheGluLysGlnLeuGlnIuThrGluLysSerAsn-----		898
Db	1954	CTTTTAAGT-----		2001
QY	899	-----		902
Db	2002	AATCACTTGGAAACCTGTCTGAAGACACAGCAAAATAAAAAGTCATGAATATACACAGAGA		2066
QY	903	GluValaAspLeuGlnYsGluLeuGlnSerAlaPheAsnGluIleAsnTrpLeuAsnGly		922
Db	2062	GTAAGAAAGCGTGGAGATGAGACAGAGAAACCTAAGTGCAGATCAGAAACCTTACAAAC		2122
QY	923	LeuLeuValaGlyLys-----		939
Db	2122	GTTTGAACAGTAACTCACTGAGGTAGAGACCCAGAAACTTATGCTTAATGAGCTACAG		2188
QY	940	LysIlySValSerGluPheSerLysGlnLeuGlnYsAlaLeuGluGlnLysAsnAlaLeu		959
Db	2182	CAGAAA---GCTGAAGTTCTA-----		2211
QY	960	GluAsnGluValThrCysLeuSerGluTrpLysPheLeuProAsnGluValGluCysLeu		979
Db	2218	GAATAAGAAATATATGTTTGAAGACTTCTCAG---CTTACTGGCAAGTTGAAGATCTA		2277
QY	980	LysAsnGlnIleSerLysAlaSerGluGluIleMet-----		991
Db	2275	GAACCAAGCTTCACTTAAGTCAATGAATGAATGAACAAAGCCGCTTATCCAGAAC		2333
QY	992	-----		997
Db	2335	TTGCATGCCGAATATGAGAGCCTCAGGAGATCGCTAAATATCAAAAGATGCTTCTCGTGC		2399
QY	998	-----		999
Db	2395	ACAAATGAAGATCATCAGAGAAGTCTTTTGCTTTTGATCAGACAGCCTGCCATGATCAT		2455
QY	1000	Ser---AlaSerIleIleSerLysGlnIleIle-----		1011
Db	2455	TGCTTTGCAAAATATATATGAGAAACAGAACATGCTTTCAGAGAGAGTAATGTCTGT		2511
QY	1010	-----		1011
Db	2515	TTAGAGACAGACCAAAAGTCCGAAAAATTTCTGCCATCTTACAAATAAGAGTTATTCACCT		2577
QY	1011	-----		1011
Db	2575	GAATTTTCATTAGAGTCTCAAAAAACAGATGAACCTCAGACCTGCAAAAGCAGTGTGAAGAG		2633
QY	1018	IleLeuGlnLeuThrAspGluValIleThrIsthrGlnSerLysValGlnGlnIuThrGluGlu		1033

Db	2635	TTGGTGCAAATCAAAAGCAAAATAGACAAAATTCATGAAAGCCAAACAGATGCATCA	2694
Qy	1038	GlntYrLeu-----GlumetYsYmeChIAspAsp-----	1048
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Qy	1048	-----	1048
Db	2755	CAGAAATGTTGTCTGAAACCTTAAGTCCCTTGAAACAAAGAAAAAGCTGCACCTT	2814
Qy	1049	LeuPheGluYsYrYlIeArgAsnYsSerGlu-----	1055
Db	2815	TTAAATGATTAAGGTAGAACTGAGGACGACGATTTCAAGATTAATAAAGCAACCAT	2874
Qy	1060	---AlaGluAspLeuLeuArgGluYmeGluAsnLeuYsGluThiMetGluSerValGlu	1078
Db	2875	CTACTTGAAGACTCTCTTAAGAGAGCTACACTTTATCCGAACCTTA---AGCTTGAG	2931
Qy	1079	ValYs-----IleAlaaspThiYsHISgluLeuGluGluThiIeArg	1093
Db	2992	AAGAAAGAAATGATGTTCCATCTCATCTTCTCTAAATAAAGGAAATTGAAGAGCTGACCCA	3050
Qy	1094	Asp-----LysGlu-----GlnLeuLeuHISgluYsLysYrPhe	1106
Db	2992	GAGAAATGGACTCTTAAGGAAATTAATGCATCTTAATAACAGAAATGACCTTAATC	3051
Qy	1107	GlnIleMetGlnThiIePhe-----ProIleThiProLeu	1118
Db	3052	CAGAAAGTGAAGAGTTTGCACAACTATATAGTGAAGAGCAAAAGCATTTCAAGATTA	3111
Qy	1119	SerAspSerLeuProProSerLysLeuVal-----GluGluYAsn	1131
Db	3112	TCTGATCAGTACAGCAGAAAGAACTTATTTTACTACAAAGTGTGAAGAAACCGGAAT	3171
Qy	1132	SerGlnAspProIle-----	1136
Db	3172	GCATGTGAGATCTTAGTCAAAATAACAAGCAGACAGAAAGAAATTTAAATTAGAA	3231
Qy	1136	-----	1136
Db	3232	TGCTTGTCAATGAATGCATAGTCTTTGTGAAAATAGCAAAAATGAGTTGGACAGCTA	3291
Qy	1137	-----GluIleAsnAspThiYsAsnLeuIleAlaLeuAlaThiGlu	1150
Db	3292	AAGCAAGCATTTGCCAAGAGACACCAAGATTTCTTAACAAAATATGCACTTTCGTGAAGA	3351
Qy	1151	ArgAsn---AsnIleMetValCysLeuGluThi-----	1160
Db	3352	AGAAATCAGAAATCTGATGCTGAGTTGGAGACAGTGCAGCAAGCTGTGAGATCTGAGATG	3411
Qy	1160	-----	1160
Db	3412	ACAGATTAACAAACAAATTTCTAGACGAGCTGTGTTTAAACAAATACTGACT	3471
Qy	1161	-----GluArgAsnSerLeuYsGluGlnValIleAspLeu-----AsnThi	1174
Db	3472	TTAAAGCAAGAACAAACAAATATGCAAAAGAAAGTATTAATGCTTATTCACAGAGATTA	3531
Qy	1175	GlnLeu-----GlnSerLeuGlnAlaGlnSerIle	1184
Db	3532	CAGCTGATGAAGTATGAGACTAAACATGATGCTCAAAATCTGAAATCTCAACAACT	3591
Qy	1185	GluYsSerAspLeuGln-----LysProYsGln	1194
Db	3592	AGCAATCTGTGAAGAAAGACAGAGTGAAGAAATCAATGATTAATTTTAACTTCAAGT	3651
Qy	1195	AspLeuGluGlnGluGluValYsLeu-----LeuLeuGluYmeGlu	1208
Db	3652	GATCTTGAAGTTAAAGAAATTTCTGTAGTATGTTAATGGCGAGTTGGTGCATTTAA	3711
Qy	1209	LeuLeuYsGluHISLeuThiAspSerGlnLeuSerIleGluYsLeuGlnLeuGluAsn	1228

Db	3712	GCTATG-----CTAAGAAATTAAGAAATTAABACTTCAGGAAAGTGCAGAGAGAG	3762
Qy	1229	LeuGIuValThrGIuLysLeuGIuThrLeuGIuGIuLueLysAsnIleThrIleGIu	1248
Db	3763	-----GAGTGCCTGCAGCATGATTAACAGACAAATTT-----	3792
Qy	1249	ArgAsnGIuLeuGIuThr--AspPheGIuAspLeuLysValAsnIleAspSer--Leu	1266
Db	3793	AGAGAGATCTTGAAGCCAGCAATTTGTCMAAGACATGCACACAAAGAAATTAAGGCCTT	3852
Qy	1267	Lys-----GlnAspLeuSerGIu	1272
Db	3853	AAAGACTGTGAATAGATGCGGAGAAAGAAAGTAATTTTCAGGGCCTCATGACTTCAACA	3912
Qy	1273	AsnIleGIuGIuInserIleGIuThrGlnAspGIuLeuArgAlaIaGIuGIuLeuArg	1292
Db	3913	AGTCAAAAGCAATATGCACACCTTCAGTGCCTCTGCACAAACCAATATGAACACTCAAT	3972
Qy	1293	GIuGIuLysGIuLeuValAspSerPheArgGIuGIuLeuAspCysSerValGIuIle	1312
Db	3973	GAGCTAGGAAATAATGTGAATACTCAGCGCTTAAAGATATGAATCTGTAACTGACCTG	4032
Qy	1313	SerSerProAsnHISAspAlaValAlaAsnGIuLysValSer-----	1327
Db	4033	AATGATTTAAGCTCAGATGTATATACAGCAACTAGAAATATGCGAAGAGAGTAGGAAA	4092
Qy	1328	--LeuGIuGIuValAsnSerLeu-----GlnSerGIuLeuValArgGIuIuArgAsp	1344
Db	4093	CTACTAAATGAAGTTAAATTTAAATGATGACAGTGTCTCTCCATGGTGAATTAGTG	4152
Qy	1345	GIu-----	1345
Db	4153	GAAGACATACCGAGAGGTGAATTTGTGAACCAACCAATGACACACCCTGTCTTTTG	4212
Qy	1345	-----	1345
Db	4213	GCTCCATTGACGAGAGTAATTTCTACAGACATTGACATTGTGCACAAAGAAATTTCAA	4272
Qy	1346	-----LeuGIuThrSerCysLysAlaLeu	1353
Db	4273	ATGCACCTTGGCCGATTCGCAAGAAATTTCTTATCTTTACAAAGTGAACCAAAATTTTA	4332
Qy	1354	-----ValSerGIuLeuGIuLeuLeuArgAlaHISValLysSer	1366
Db	4333	CATGATCAGCACTGTCAAGTACGCTTAAATATGCAGAGCTGACAGCTTATGTGATCTCA	4392
Qy	1367	ValGIuGIuGIuAsnLeuGIuIleThrLysLysLeuAsnGIuLeuGIuLysGIuIleLeu	1386
Db	4393	TTAAAGCCGCAAAATTTGTGCTTGTCTTCAACGAATTTGAGAAACTTTCAAGGTGATGGTG	4452
Qy	1387	GIuLysSerGIu-----GlnSerGIuValLeuLysSerMetLeuGIuAsnLeuLys	1403
Db	4453	AAGAGATAGCAGCTGGGCTTGAGAGAGGGGCTGTTCAATCCCTGTATCCTCTTGTGTG	4512
Qy	1404	GIuAspAsnAsnLysLeuLysGIuGIuAlaGIu-----	1414
Db	4513	CCTGACAGCTTACGCTTAGCAGATTGGAGACCTCTCTTTACAGAGCTTTTAGAA	4572
Qy	1415	-----GluLysSerSerLysGIuAsnGIuPhe	1423
Db	4573	CAGACAGAGATATGTCTTTTGAATTAATTTAGAAAGGGCTGTTTCAGCAAAACAGATGC	4632
Qy	1424	SerLeuGIuGIuValPhe-----	1429
Db	4633	AGGTGATAGTAAGTAATTTTTCAGACAGCTGCAGAGAGAGAAATCTGACACAGAAAGAAC	4692
Qy	1430	--SerGIuSerGIuLysLeuValAspGIuIle-----GluValLeuLysAla	1444
Db	4693	CCTTCGGCCCGAGGAAAGGGGTGTGAAGAGCTTGAGTCCCTGTGTGAGGTGACCGGCAG	4752
Qy	1445	GlnLeuLysAlaIaGIuGIuArgLeuGIu-----IleLysAspArgAspTyr	1460
Db	4753	TTCCTCGAGAGCTTAGAAGAAATTAAGAAATCAAGGATTAAGAAATTAAGAAATTTAAGAAATTT	4812

Db	6832	AAACTGCAATGGAGATGCTTCAGATACAGTTAAAGAGACCTAAATGAGGCACTGACACCC	6891
Qy	2069	Leu-----GluGluGluIleLeuGln---AsnIleSerIleLeuAsnGluAlaValSer	2085
Db	6892	TTGTGTGGTGACCAAGAAATTTATGAAGCCCAAGAACAGACTGTAGACCCCAATATAG	6951
Qy	2086	GluArgGluAsnLeuArgHisSerIleGlnGluValSerGluLeuGln-----	2102
Db	6952	GAAGAGCATCAGCTGAGAAATATGCAATGAAAGCTGAGAGACCCGCTGAAGCTGATGA	7011
Qy	2103	-----GlnLeuSerLeuThrIleuLeuSerArgAspHisAlaPheAlaGlnSerIleArg	2120
Db	7012	AAGAAGCAGCTGTGTCTTACAAACACTGAAAG-----GAAAGTGACGAT	7056
Qy	2121	GluIlyAspArgGluAlaValAsnIlyIleAsnLeuAlaGluIleIleValIleLeuThr	2140
Db	7057	CATGCAAGATTTACTTAAGGGTAAAGTGAAGAACCTTGAAAGAGAGCTGAGATAGCCAG	7116
Qy	2141	LysGluMetAsp-----GluPheArgAspSerIly-----GlnSerLeu	2153
Db	7117	ACAAACCAAGAGCATGCAAGCTCTTGAGGCAAGATTCCAAGAGAGAGTGAAGACCTTA	7176
Qy	2154	GlnGluGlnSerSerHisIleuSerGlnGluLeuCysThrTyrIlyThrGluLeuGlnMet	2173
Db	7177	AAAGCAAAAATAGAAAGGATGACCCAAAGCTGCAAGAGCTGCAATTAAGATGTTGTTACT	7236
Qy	2174	LeuIlySerGlnIlyGluAspIleAsnIlyIleAsnIlyValIleGluValAsp	2193
Db	7237	ATAAAGTCAGAAAAGAAATATGTCAAATGAATTAACAAAAGACCAAGAGCAATATCT	7296
Qy	2194	GluLeuLeuGlnHisIleuSerSerLeuIlySerGlnIleuAspGlnIleGlnMetGluLeu	2213
Db	7297	GAATTA-----GAAATA	7308
Qy	2214	ArgAsnGluIlyIleuArgAsnTyrGluLeuCysGluIlySmetAspIleMetGluIlySer	2233
Db	7309	ATAAATTCATCATTTGAAAT-----	7329
Qy	2234	IleSerValIleuArgLeuMetGlnAsnGluProGlnGlnIlyGluAspValAlaGlu	2253
Db	7330	-----ATTTGGCAAGAAAAGAGCCAAAGAAAGTACAGATGAAGAAAATCAAGCACT	7383
Qy	2254	ArgMetAspIleIleuGlnSerArgAsnGlnIlyIleGlnIlyLeuMetGluIlyIleSer	2273
Db	7384	GCCTATGAGATCGCTTCAACA-----CAATTAAAGAGCTCAATGAGAGAGCTGCA	7434
Qy	2274	AlaValTyrSerGlnGlnHisThrIleuLeuSerSerIleuSerSerGluLeuGlnIlySer	2293
Db	7435	GCCTCGCATATGACCAA-----	7452
Qy	2294	ThrGluAlaHisIlyIlyHisCysMetLeuAsnIleuIlyGlnSerLeuSerSerThrLeuSer	2313
Db	7453	--GAAGCTGTAAAG-----GCCAAAGACAGAAATCTTAAT	7485
Qy	2314	ArgSerPheGlnSerIleGlnThrGlnHisValIlySleuAsnThrGlnLeuGlnThrLeu	2333
Db	7486	AGTCAAGTAGAGCTGCTTGAACCTTGAAGAGCTCAGTTCCTCAAGAGCCTTGATGAGGCC	7545
Qy	2334	LeuAsnIlyPheIlyValIleValTyrArgThrAlaAlaValIlyGluAspHisSerIleIle	2353
Db	7546	AAAATAATATTTATGTTGTTTGCATCTTCAGAG-----AATGGCTCATTT	7590
Qy	2354	LysAspTyrGluIlyAspLeuAlaAlaGluIlyValGlnHisAspGlu-----Leu	2370
Db	7591	CAGCAAGTAGAAGATGGCAACAGAACTGAGAGAAAGATGAAGAAATCAGTAGACTG	7650
Qy	2371	ArgIleuGlnLeuGlnCysLeuGlnGlnHisGlyArgIlyIlyPheSerAspSerAlaSerGlu	2390
Db	7651	AAAATCAATTCAGAGCCAAAGAGAGCTGTGCTCTTAACGTCTCCAGAGTGAAGAGAGAG	7710
Qy	2391	GluLeuIlyPhe-----CysGlnIleGluPheLeuAsnGluLeuLeuPheIlyS	2406

Db	7711	CACCACTTTGGAAAGAGCAAAACTTAGACTGAGAAATCGACAGTGGAAATTGGACAG	7770
Qy	2407	LYSALAENILEIIEGINSERVALGNAAPAPHESERGLUVALGINVALPHELEUASN	2426
Db	7771	AAGATCCAAAGTGTACATTCATAAAATGCGCTTTGGACGACACATTAGAAAGTGTGCAG	7830
Qy	2427	GLNVALGYSERTHLEUNGINGLUINGLU---HILEYSLYSGLYPHIMERICINTPR	2445
Db	7831	AGTTCTTCAAGAACTTAGAGAAATGAGCTTGAAATTGACAAATAATGACAAATAATCTCTT	7890
Qy	2446	LEUNGILUPHESLY-----APLEUHNILEVAL	2454
Db	7891	GTTGAAAAAGTGAACAAATAATGACTGCAAGAAACTGAGCTGCAGAGGAAATTCATGAG	7950
Qy	2455	ASPALALYSLY-----LEUSERGLUYMETGNGINGLUENANARGARILEALA	2471
Db	7951	ATGCGACAGAAAAACGACGAGCTCGAAGAACTAGTGAGAGAAATAATAGCTAGCT	8010
Qy	2472	SEETHRIIEGLINLEUTHLYEARGLEULYALAVAILGINSELYSILEGINARG	2491
Db	8011	GGAGAGTTGCACTTACTGTTGGAAAGAAATAAAGAC-----ACCAAAAGATCAA---	8058
Qy	2492	GLUIETHRVALYRLEUASNINPHEGLUALAYSLLEUNGINGLUYSLYBGLUGLNASN	2511
Db	8059	-----TTGAAGGAGCTCACACTAGAAAT	8082
Qy	2512	LYEGULEUMETARGARGMETGLUHHIEGLYPROSERALASERVALMETGLUGLU	2531
Db	8083	AGTGAATTGAAGAAG-----AGCCTAGATTGCTCATGCCAAAGAC	8121
Qy	2532	ASNALARGLEULEUGLYILELEULERTHVALGINAPGUSERLYBLYLEUGLINSE	2551
Db	8122	CAGGTGCAAAAGCAAGGG-----AAAGTGACAGAGGAAATAGCTGAATATCACACTA	8172
Qy	2552	ARGILEUSMECLEUGLUAENGLULEUASNLEUVALYASAPAPALAMEHNILEYGLY	2571
Db	8173	CGG-----CTTCATGAGCT	8187
Qy	2572	GLUYYS-----VALAIAILEUGLINAPRYLEULEUSERARGENALAGLUVALGLU	2589
Db	8188	GAAGAAGAAACCCAGGCTTCTTTGGAC-----ACAAACAAACGATGAAAGTGA	8211
Qy	2590	LEUASNALAMEGINVALYSLLEUTHLYSLYSGINAPASNLEUGINALALAMELYS	2609
Db	8242	ATCCAGACATACCGAGAGAAATTAGCTCTTAAGAGAAATGTCTCAGTTCACAGAACTG	8301
Qy	2610	GLUILEGUANLEUGLNUYMECVALLALAYSLYALAVAIPLYRPLYBGLUGLUILE	2629
Db	8302	GAGATAGACCTTTAAAGTCTAGT-----AAAGAAAGACTC	8337
Qy	2630	ASAPSN-----LEULERTHLYSVALYSLYLEGLUMERGLU	2642
Db	8338	AATAATTCATTGAAGACTACTACTCAGATTTTGGAGAAATTGAAGAAACCAAGATGAC	8397
Qy	2643	LYSLILEYSLY-----SERYSALATHRAEPGINGLUILE	2654
Db	8398	AATCAAAATATGTAAATCACTGTGAAGAGAAATAGACGTGCCAGGGGAAAAATGAG	8457
Qy	2655	ALATRYLEULYSESY-----LEUGLUSPLYSGLUGLUGLYLEUARGARGLEULYS	2672
Db	8458	TTGTGTGATCAATCTCTGTAAACAGCTGGAAGAGCAAAAGATATCTGCAGAAAGAACTC	8517
Qy	2673	GLUGLUEUARGARGALAGINALAASAPASAPRTHRVALCYSVAILPROLYSAPPTYR	2692
Db	8518	TCTCAACTTCAAGCTGCACGAGACAGACAGAAAAACA-----	8553
Qy	2693	GLNYSALASERTHREPROVALTHRCYSGLYCYLYSERGLYLEVALGINSETRH	2712
Db	8554	-----GSTACTGTTATGATGATCC	8571
Qy	2713	ALAMECLEUVALLEUGLINSEGLU-----LYSALALALEUGLU-----	2725
Db	8572	AAGGTGATGATTAATTAACACTGAGATCAAGAACTGAAAGAACTCTTTGAAGAAAGAAACC	8631

QY 546 CysArgLysAlaSerPheGluLysGluLeuThrSerLeuGlnGlnLeuGlnSerLys 565
 Db 925 GCGCAGATCAAGACTAAGAAACAAGATTAAATGAGTTCGAACTACGCTGCAAGACAT 984
 QY 566 GluGluGluLysLysGluLeuValGlnSerPheGluLeuLysLeuAlaGluLeuGlu 585
 Db 985 GAAAGAAAGATGAAAGCCCAAGTGAATAGTTCAA-----GAACTCCAACTC 1032
 QY 586 GlnLeuSerValLysAlaLys-----AsnLeuGlnMetValThrAsnSer--- 600
 Db 1033 CAACTGAG---AAAGCAAAAGTGAATTAAATGAAAAAGAAAGTTTGAACAAATGT 1089
 QY 601 ArgGlnHisSerIleAsnAlaGluValGlnThrAspValGluLysValValArgLys 620
 Db 1090 AGGGATGAACTAGTACAGAACACACACAAATACGC----- 1125
 QY 621 GluMetSerValLeuGluAspSerGlyTyrAsnAlaSerAsnSerAspLeuGlnAspSer 640
 Db 1126 -----CAGCGCTCAACCAAGTATACCTGATTGAAACAAAACTGAAAAAATTG 1173
 QY 641 SerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGluHisArgLysMet 660
 Db 1174 ACGGAAGAT-----TTGAGTGTACAGCCACAAATGCAAAAGTCCAGATGTTCT 1224
 QY 661 LeuGluGlnLysIleValAspLeuGlu---GluPheIleGluAsnLeuAsnLysSer 679
 Db 1225 CTGGACAGAAATTAAGAAAGAAAGAAAGAGTTTCAAGAGAGACTCTCCCT----- 1278
 QY 680 GluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeuCysGlu 699
 Db 1279 -----CAACGCGTCTTCCAAACACTGCAGCCAGAGTGATCAGATG----- 1323
 QY 700 AlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgHisPhe 719
 Db 1324 -----AAGCCAGACTCACCCAGAGATTACAGCAAGCAAG---AATATG 1365
 QY 720 AsparnIlelle----- 1365
 Db 1366 CACAAACGCTCTGACGCTGAACCTGATTAACCTACATACATGAAACAAACAGCTAGAAAAC 1425
 QY 727 -----GluThrLeuLysArgGluIleAlaAspLeuGluArgSer----- 739
 Db 1426 AATTGGAAAGATTAAACCAAAAGTTGTGCAGAGCTGAACAGCCTTCCAGCCAGTCAAG 1485
 QY 740 LeuLysGluAsnGlnLysThrAsnGluPheGluIleLeuGluLysGluThrGln----- 757
 Db 1486 ATCAAGAGGATGAGCTGAGAGAGCATGAGAAATGAAGAAAGAAACAACTCCTT 1545
 QY 758 LysGluHisGluValGlnLeuIleHisGluIleGlySerLeuLysLeuValGluAsn 777
 Db 1546 AAGGCTCCTCTGACCAAAAGCCAGAGAGCTCCACCTGAGCAGAACTTCAAGAAC 1605
 QY 778 AlaGluMet-----TyrAsnGlnAsnLeuGlnGluAspLeuGlnThrLysThrLys 794
 Db 1606 ATCAACAGCTGTTTAAATCAAGACCAAAATTTTGCAGAAAGAAATGAAGCCAGAAAT--- 1662
 QY 795 LeuLeuLysGluGlnLysIleGlnLeuAlaGluLeuArgLysArgAlaAspAsnLeuGln 814
 Db 1663 -----ACCTCTCAGGAACCAACATGTTAAGAGATCTTCAAGAAAAAATTAATCAGCAAGAA 1716
 QY 815 LysLysValArgAsnPheAspLeuSerValSerMetGlyAspSerGluLysLeu----- 832
 Db 1717 AACTCCTTGAAGTAAAGAACTGAAGCTTGTGCTGAGTGAAGTGAAGAAAGCAGAGAT 1776
 QY 833 CysGluGlu-----IlePheGlnLeuIleGlnSerLeu 843
 Db 1777 TGTTCACAGACCTTTGAAGAAAGAGAACATCACTTGAACCACTTAATGATATAGTTA 1836
 QY 844 SerAspAlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGlu 863
 Db 1837 AGCAAGACAGAGAAAGATCCAA---GCCTTGCTGAGAGCTTTAGAGTTAAAAAAGAAA 1893

QY 864 AsnLeuGluLeuLysGluLysMetGluAsnThrSerAsnTyrTyrAsnGlnLysGluLys 883
 Db 1894 GAATATGATTAAGAAAGAAAGAAAGAACTCTGTTTCTTGTGAAAAAGCAAAAGAA 1953
 QY 884 AlaAlaSerLeuPheGluLysGlnLeuGlnThrGluLysSerAsn----- 898
 Db 1954 CTTTAACT-----CAGATGGAATCAGAAAAAGAAACTTCAGAGTAAATT 2001
 QY 899 -----TyrLysLysMet 902
 Db 2002 AATCCTTGAACCTTGTCTGAAGACACAGCAAAATAAAGTCAATATACACAGAGAA 2061
 QY 903 GluAlaAspLeuGlnLysGluLeuGlnSerAlaPheAsnGluIleAsnTyrLeuAsnGly 922
 Db 2062 GTAAGAACGCTGGAGATGACAGAGAAACCTAAGTGTGAGATCAGAAACCTTCACAAAC 2121
 QY 923 LeuLeuAlaGlyLys-----ValProArgAspLeuLeuSerArgValGluLeuGlu 939
 Db 2122 GTGTTAGACAGTAAAGTCAAGTGGAGGTAGAGACCCAGAAACTAGCTTATATGAGCTACAG 2181
 QY 940 LysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGluLysAsnAlaLeu 959
 Db 2182 CAGAAA---GCTGAGTCTCA-----GATCAGAAACATCAGAAAG 2217
 QY 960 GluAsnGluValThrCysLeuSerGluTyrLysPheLeuProAsnGluValGluCysLeu 979
 Db 2218 GAAATAGAAATATATGCTGTTTGAAGCTTCTCAG---CTTACGCGCAAGTTGAATATCTA 2274
 QY 980 LysAsnGlnIleSerLysAlaSerGluGluIleMet----- 991
 Db 2275 GAACACAGACTTCAAGTACTCTCAATATGAATATGCAAAAGACCGGTGTACCAAGAC 2334
 QY 992 -----LeuLeuLysGlnGluLys----- 997
 Db 2335 TTGATGCCGAATATGAGAGCCTCAGGAGCTGCTAAATCCAAAGATCTTCTGTG 2394
 QY 998 -----GluHis 999
 Db 2395 ACAATGAAGATCATCAGAGAAAGTCTTGGCTTTGATCAGACCTGCCATGATCAT 2454
 QY 1000 Ser---AlaSerIleIleSerLysGlnIlelle----- 1010
 Db 2455 TCCTTGCAATATATATTGAGAACAGAAAGACATGCTTCAGAGAGAGTGAATGTCTG 2514
 QY 1010 ----- 1010
 Db 2515 TTAGAGCAGACCAAAAGTCCGAAAAATTCCTCAATCTTCAAAATAGATGATTACATT 2574
 QY 1011 -----MetGlnGluGlnSerGluGln 1017
 Db 2575 GAATTTTATTAGAGTCTCAAAAAACAGATGAATCAGACCTGCAAAACAGATGTGAAG 2634
 QY 1018 IleLeuGlnLeuThrAspGluValThrHisThrGlnSerLysValGlnGlnThrGluGlu 1037
 Db 2635 TTGGTGCAATCAAAAGAGAAATAGAGAAATATCATGAAAGCAAGACAGATGATCAAA 2694
 QY 1038 GlnTyrLeu-----GluMetLysLysMetHisAspAsp----- 1048
 Db 2695 AGTTTGTGCTGAACAAGTCAGCGCATTTAGTATGACAGAAACATCTTGCTGAC 2754
 QY 1048 ----- 1048
 Db 2755 CAGAAATGTTGCTGAAACCTTAAGTCCCTTGAAGAAACAAAGAAAGAGCTGCACTT 2814
 QY 1049 LeuPheGluLysTyrIleArgAsnLysSerGlu----- 1059
 Db 2815 TTAATATGATTAAGTAAAGATCAGAGCAGAGATTCAGAAATTAAGAAAGCAACCAT 2874
 QY 1060 ---AlaGluAspLeuLeuArgGluMetGluAsnLeuLysGlyThrMetGluSerValGlu 1078
 Db 2875 CTACTTGAAGACTCTCTAAAGAGCTACAACTTTATCCGAAACCTTA---AGCTTGGAG 2931
 QY 1079 ValLys-----IleAlaAspThrLysHisGluLeuGluGluThrLysLeu 1093

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Db      2932 AAGAAAGAAATGAGTTCATCATCTTCTTAAATTAAGGAAATGAGAGCTGACCCAA 2991
Qy      Asp-----LysGlu-----GlnLeuLeuHisGluLysLysPhePhe 1106
Db      2992 GAGAAATGGAGCTCTTAAGAAATTAATGATCTTAAATCAAGAAATGAGTAACTATC 3051
Qy      1107 GlnAlaMetGlnThrIlePhe-----ProIleThrProLeu 1118
Db      3052 CAGAAAGTGAAGCTTTGCAAACTATATAGATGAAGGAGAAAGCATTTTCAGAGTTA 3111
Qy      1119 SerAspSerLeuProSerLeuLysLeuVal-----GlnGluAsn 1131
Db      3112 TCTGATCAGTACACAAAGAAAACTTATTTTACTAACAAGATGTAAGAAACCGGAAT 3171
Qy      1132 SerGlnAspProIle----- 1136
Db      3172 GCATGTGAGATCTTACGTCMAAAATACAAAGCAGACAGAAAGAAATTTCTAAATTAGA 3231
Qy      1136 ----- 1136
Db      3232 TGCTGTAATGAATGACACTAGTCTTTGTGAAAATAGGAAAATGAGTTGGAAAGCTA 3291
Qy      1137 -----GlnLeuAsnAspTyrHisAsnLeuIleAlaLeuAlaThrGlu 1150
Db      3292 AAGGAGCATTTGCAAAAGAACACCAAGAAATTTTAAACAAATTTAGCATTTGTGAGAA 3351
Qy      1151 ArgAsn-----AsnIleMetValCysLeuGluThr----- 1160
Db      3352 AGAAATCGAATCTGATCTGATAGTTGAGACAGCAGCAAGCTCTGAGTCTGAGATG 3411
Qy      1160 ----- 1160
Db      3412 ACAGATAACCAAAACATTTCTAAGACGAGCTGGTGTAAAGCAAGAAATCATGACT 3471
Qy      1161 -----GluArgAsnSerLeuLysGluGlnValIleAspLeu-----AsnThr 1174
Db      3472 TTAAGAGAAACAAACAAATGCAAAAGAGAAATTAATGACTTTTACAGAGATGAA 3531
Qy      1175 GlnLeu-----GlnSerLeuGlnAlaGlnSerIle 1184
Db      3532 CAGCTGATGAAGATTAAGACTTAACATGATGTCMAAAATCTGAATCAGAACCAATT 3591
Qy      1185 GlnLysSerAspLeuGln-----LysProLysGln 1194
Db      3592 AGGAACTCTGTGAAGAAAGAGAGAGTGAAGAAATCATGTAATTTTAAACCTCAGATG 3651
Qy      1195 AspLeuGlnGluGlnValLysLeu-----LeuLeuGlnMetGlu 1208
Db      3652 GATCTTGAAGATTAAAGAAATTTCTAGATAGTTAATGTCGCACTGGTGCATTTAGAA 3711
Qy      1209 LeuLeuLysGlnHisLeuThrAspSerGlnLeuSerIleGlnLysLeuGlnLeuLysn 1228
Db      3712 GCTATG-----CTAAGAAATAAGAAATTTAAACTTCAGAAAGTGAAGAGAAAG 3762
Qy      1229 LeuGlnValThrGlnLysLeuGlnThrLeuGlnGlnMetLysAsnIleThrIleGlu 1248
Db      3763 -----GAGTGCCTGCAGCATGAATTACAGACAATT----- 3792
Qy      1249 ArgAsnGlnLeuGlnThr-----AsnPheGlnAspLeuLysAlaGlnHisAspSer-----Leu 1266
Db      3793 AGAGGAGATCTTGAAGAACGCAATTTTGCMAAGCATGCACTCAAGAAATTTGTGACCTT 3852
Qy      1267 Lys-----GlnAspLeuSerGlu 1272
Db      3853 AAAGCTGTGAATGATGCGGAAGAAAGTATATTTCAGGCGCTCATGAGTGTCTCAACA 3912
Qy      1273 AsnIleGlnGlnSerIleGlnThrGlnAspGlnLeuArgAlaIleGlnGlnLysArg 1292
Db      3913 AGTCAAAAGCAACATGACACCTTCAGTCTCTCTGCAAAACAACATGAACAAGCTGAAT 3972
Qy      1293 GlnGlnLysGlnLeuValAspSerPheArgGlnGlnLeuLeuAspCysSerValGlyIle 1312

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Db      3973 GAGCTAGAGAAATATGTGAATTAATCTGACGCTGAAAAGATATGAACCTGTAACCTGAGCTG 4032
Qy      1313 SerSerProAsnHisAspAlaValAlaAsnGlnGluLysValSer----- 1327
Db      4033 AATGATTCAGAGCTGAGATGATATCAGCAACTAGAGAAATGCGAAGAGGTAGGAAA 4092
Qy      1328 -----LeuGlnGlnValAsnSerLeu-----GlnSerGlnMetLeuArgGlnLysArgAsp 1344
Db      4093 CTACTAAATGAAGTTAAATTAATTAATGATGACAGTGTCTTCTCCATGAGTGAAGTGTG 4152
Qy      1345 Gln----- 1345
Db      4153 GAAGACATACCAGAGAGGTAATTGTGTAACAACCAATGAAAGACACCTGTGTCTTGG 4212
Qy      1345 ----- 1345
Db      4213 GCTCATTTGACGAGAGTAATCTTACAGACCTTGACATTGTGACAAAGAAATTCAA 4272
Qy      1346 -----LeuGlnThrSerCysLysAlaLeu 1353
Db      4273 ATGACCTTTGCCGAATTGCAAGAGAAATTTCTTATCTTTACAAAGTGAACACAAATTTTA 4332
Qy      1354 -----ValSerGlnLeuGlnLeuLeuValAsnValIleValSer 1366
Db      4333 CATGATCAGCAGCTGCTGAGATGAGCTTAATAATGTCAGAGCTGACAGCTTATGTTGACTCA 4392
Qy      1367 ValGlnGlnGlnAsnLeuGlnIleThrLysLysLeuAsnGlnLysGlnLysGlnIleLeu 1386
Db      4393 TTAAGGCCGCAAAATTTGCTGTCTGCAACGAATCTGAAACCTTCAAGGATGCTGTGTG 4452
Qy      1387 GlyLysSerGlu-----GlnSerGlnValLeuLysSerMetLeuGlnAsnLeuLys 1403
Db      4453 AAGAGATGACGCTGGGCTTGAGAGAGGCTGCTTCATCTCTGATCTCTTGTGTG 4512
Qy      1404 GluAspAsnAsnLysLeuLysGlnGlnAlaGlu----- 1414
Db      4513 CTTGACAGCTCTAGCTTACAGAGTTTGGAGACCTCTCTTACAGAGCTTTTGAAG 4572
Qy      1415 -----GluTyrSerSerLysGlnAsnGlnPhe 1423
Db      4573 CAGACAGAGATATGCTCTTTGAGTAATTTAAGAAAGGCTGTGTTACAGAAACACAGTGC 4632
Qy      1424 SerLeuGlnGlnValPhe----- 1429
Db      4633 AGGTAGATGAAGATTTTTCAGACAGTCTGCAAGAGAGAAATCTGCACCAAGAAACACC 4692
Qy      1430 -----SerGlnSerGlnLysLeuValAspGlnIle-----GluValLeuLysAla 1444
Db      4693 CTTTCGGCCCGCAGGAGAGGCTTGAAGAGCTTGAAGTCCCTCTGTGAGGTGTAACCGGAG 4752
Qy      1445 GlnLeuLysAlaAlaGlnGlnLysArgLeu-----IleLysAspArgAspTyr 1460
Db      4753 TCCCTCGAAGCTGAGAAAGAAATGAAAGTCAAGAGATTAAGAAATTAAGAAATTT 4812
Qy      1461 PheGlnLeuValGlnThrAlaAsnThrAsnLeuValGln-----GlyLysLeuGlnThrPro 1479
Db      4813 CAAGAGCTCGACGCTTAATTAAGTTCTGAAGAGCAAGAGCTTGACCTGCTTAAGCAAGAG 4872
Qy      1480 LeuGlnAlaAspHisGln-----GluAspSerIleAspArgArgSerGlnGlnMetGlu 1497
Db      4873 TATTTGTCAGAAATGAACATGTCGCAACAGAGTGAACACGCGATCTGTGAGATGAG 4932
Qy      1498 IleLysValLeuGlnGlnLysLeuGlnLysArgAsnGlnTyrLeuLeuGln----- 1513
Db      4933 TCCAAGTGGCGCGCAAGAAAGAAACAGACGCAAGAACATGTCATCTGAGCTGGAATGACA 4992
Qy      1514 ArgLeuGlnGlnGlnLysLeuGlnLeuSerAsnLysLeuGlnIleLeuGlnLysGlnMet 1533
Db      4993 CGACTCCAGCTCAACAGCTGTGACTTAAGTCTCGG----- 5028
Qy      1534 GluThrSerValLeuLeuLysAspAspLeuGlnGlnLysLeuGlnSerLeuLeuSerGlu 1553
Db      5029 -----TCTTTCCTTGGCATCGACACAGAAAGATGCTATTCAGAGC----- 5067

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QY 1554 AsnIleIleuLygIuAenIleAspThrThreuleYsHIseserAspThrGlnAla 1573
Db 5068 -----CGAATGAGAGCTGTGACATATCAAAAGAACCTACTTACAAAGCTACAGAA 5118
QY 1574 GlnIeuGlnLyS-----ThrgInGlnIeuGln 1583
Db 5119 AGAACAACCAAGCATGATGTTGATTCAGATTTGATAAGATGCTGACAGAGACTCAAT 5178
QY 1584 Leu-----AlaLySAsnLeuAlaIleAlaIleAserAspAsnCySProIle 1598
Db 5179 CTGACACTTGAGAAATACAGACTGTGATGCAATTGAAACCAAGAGAGAGTCTGTGG 5238
QY 1599 ThrGlnGlnLygIuThr-----SerAla 1606
Db 5239 GAACAGTCCCCAGATACCAATTATGAGCTCCAGGGAGATAAACCCAGGGCTTTCA 5298
QY 1607 AspCySValHisProLeu----- 1612
Db 5299 GAATGCAATTCGATGTCATTTTCGTGCTAATGCTTTGGTACCTATGATTCCTG 5358
QY 1613 -----GlnGlnLySIIleuLeuLeuThrGlnGlnLeuHisGlnLySThrAsnGln 1630
Db 5359 GGGAAATCAGAGATATCCATTAATCTTCACTGGGGTAAAGAGACATCAAAATGAGAAAT 5418
QY 1631 GlnLyLeuLeuHisGlnLySAsnGlnLeuGlnIleAlaGlnIleuLySAsnGln 1650
Db 5419 TTGAGATTTACTTATGATGATGATGAGAGACCTGACAGA-----AAA 5457
QY 1651 ValGlnHisIleuLeuLeuSerMetIleGlnSerLySAsnGlnSerLeuGlnHis 1670
Db 5458 GTTGAAGATTGCTGAATGAAATGAAAGATTTAGACTCAAACTC----- 5502
QY 1671 GlnLyHisIleAspThrGlnGlnIleuLeuAla-----LeuLyS 1683
Db 5503 -----CATTTACAGAGGTACCACTAATGACCAAAATGACATGATGATGAGAA 5556
QY 1684 GlnGlnMetGlnIleValThrGlnGlnLySLeuGlnGlnIleHisGlnIleu 1703
Db 5557 AAAATAGTTGGGAACTTAAGAAAGAAACTCAGATTTAAGTAAATGGAATATTTT 5616
QY 1704 ThrAlaGlnValAspHisIleuLySLeuAenIleGlnLeu-----GlyLeuAsnPheLyS 1721
Db 5617 TCTTGATGATCACAGAGATTACTCCAGAGGTAGAAACTTGTGAAGCTCTCAATTTCTGAT 5676
QY 1722 AsnGlnValaGln-----GlnLySThrThrLySLeuGlnCysLeuLeuAsnGlnLyS 1739
Db 5677 TTGAAATGATCATCAGATTAATCATCATCAGTGAAGATTTGAGATTAATGTGCCAAGGTG 5736
QY 1740 -----GlnLeuGlnIleSerGlnHisAlaGlnGlnCys 1750
Db 5737 AATGACAGCTGAGAGAGATTTCTTGATGTGAAATGAGCTGATGATGATGATGCTG 5796
QY 1751 Gln-----IleGlnIleuLeuLeuSerLeuLyS 1760
Db 5797 GAGAAAGCTAGCATTTGAGCATGAAGCCCTTACTGAGGCTGATGAGGTAGTTCA 5856
QY 1761 AspLySLeuSerAlaLeuGlnIleuThrLeuLySLeuGlnGlnLySValIle-----AsnLeu 1779
Db 5857 ACAGAGAGAGCTATGTTTAAAGAAAGAACATGAATTAAGCAGAAAGTTATGTCTGCTT 5916
QY 1780 AsnGlnGlnMetCysValMetLeuGlnMetGlnGlnIleuLySAsnSerGlnIleuThr 1799
Db 5917 GAAGAGAACTCTCAGCTGTGTCACAGTGAAGAAACCACTGTGTGAGATTAATGATACT 5976
QY 1800 ValIleAlaGlnLyS-----AspGlnLeuGlnAspAspLeuAspGlnSerValGln 1816
Db 5977 ATGTCAAAAAAACAAGCAGCTGATCAGTGTCTGTAATAAATGAAGGAAACACAA 6036
QY 1817 MetSerIleGlnThr-----GlnAspAsp 1824
Db 6037 ---GACCTTGTGCTCATCAAAAGTGAATGTCTCATTTGATCAGGTGAGAGGAGAG 6093

QY 1825 LeuArgLySAlaGlnIleuAlaLeuGlnGlnIleuLySAspLySValGlnIleuThrSer 1844
Db 6094 GTGAGAGAAAGACGGAATCCCTTACAGACTTTTCTCTGATGTAGTGAAGCTTTAA 6153
QY 1845 GlnHisSerValLeuGlnGlnLySIIleuLeuLeuThrGlnAsnGlnMetLeuThrAsnVal 1864
Db 6154 GACAAACATCATCTCCAGGAAAGAGCTGACAGATTTGAAAGAGACTCACAGCAGCTGTCT 6213
QY 1865 AlaThrVallyGlnIleuSerGlnArgAspAspLeuAsnGlnSerLySAsnIleu 1884
Db 6214 TTGACAAATGTGATGAGCTGAGAAACCAATTTGCACAACTGAATTAAGAGAAAGATTTGCTT 6273
QY 1885 PheSerGlnIleGlnIleuThrLeuSerLeuSerLeuLySLeuGlnPhe----- 1900
Db 6274 GTCAAGAAATCTAAAGAGCTGACAGCCAGACTAGTGAATCAGATTAATGAAAGCTGAAT 6333
QY 1901 -----AlaLeuGlnIleAlaGlnLySAspLySAlaAspAlaAlaArgLySThrIle 1917
Db 6334 GTCTCCAGGCTTGTGAGGCGGCAGCTGTGAGAGAAAGTGAATTCATTTGAGAGCTGAGC 6393
QY 1918 AspIleThrGlnLySIIleuSerAsnIle----- 1926
Db 6394 TCAACACAGAGAGAAAGTGCATGCTGAGAGAGAGCATGAGAACTGAGAGATTCCCAT 6453
QY 1927 -----GlnGlnGlnIleuLeuGlnIleAlaThrAsnLeuLySLeuThrLySLeu 1943
Db 6454 GAGCCGATGAAAGAAAGACAGCTGCACATGCGAGAGAACTGAAGAACCCGAGCGGAG 6513
QY 1944 ArgGlnSerLeuIleGlnCysLySLeuGlnIleuAlaLeuAsnThrGlnHisIleuArgLyS 1963
Db 6514 AATGATTTCACTT-----AAGATTAAGTGAAGAACTTGAAGGAAATTTGAGATG 6564
QY 1964 ThrLeuLySAspLeuAlaLeuGlnLySLeuMetGlnGlnIleuArgAspGlnAlaIle 1983
Db 6565 TCAGAAAGAAACCAAGAGCTAGTGAAT-----CTTGATGCCAGAAATTTCCAAAGCA 6615
QY 1984 AsnLySValIleAlaLeuThrGlnLySAsnSerLeuGlnGlnIleuAsnGln 2003
Db 6616 -----GAAATGAGACTTTAAACACAAATGAAGAGATG 6651
QY 2004 ValThrThrLeuLySLeuGlnLyS-----GlyLySLeuGlnThr 2016
Db 6652 GCCAGAGAGCTGAAAGCTTTTGAATTAAGACCTTGTACAGTTAAGCTGAAAGAAAT 6711
QY 2017 PheThrLeuGlnArgProSerLySLeuGlnIleuSerSerGlnMetGlnIleuArgLyS 2036
Db 6712 CTGACAAACCAATATCAAGAAAGAAAGCTGAGTGTCTGAGAACTGACAAATTAATCTCTCT 6771
QY 2037 SerLeuLySThrLySAspLeuGlnGlnIleuAlaGlnLySLeuGlnIleuSerGlnIleuThr 2056
Db 6772 TCATTTAAAGTCTGTAGAGAAAGAGCAAGCAAGATTCAGATTCAAAGAAATCT 6831
QY 2057 -----AsnGlnIleLySAsnLeuThrAlaLySIIleuSer 2068
Db 6832 AAAACGTGAGAGATGCTTACGATTCAGATTAAGAGACTTAATGAGCAGATGAGCAGCC 6891
QY 2069 Leu-----GlnGlnIleuLeuGln-----AsnAlaSerIleuAsnGlnAlaValSer 2085
Db 6892 TTGTGTGTGATCCCAAGAAATTTAAGAGGCCACAGAACAGAGTCTGAGAACCCACCAATAGAG 6951
QY 2086 GlnArgGlnAsnLeuArgHisSerLySLeuGlnIleuValSerGlnLeuGln----- 2102
Db 6952 GAAGAGCATCAGCTGAGATGATGATGATTAAGAGCTTGAAGCCGCTGAGAGCTGATGAA 7011
QY 2103 -----GlnLeuSerLeuThrLySAspLeuSerAlaAspHisAlaPheAlaGlnIleuThr 2120
Db 7012 AAGAACACTCTGTCTCTTACAAACAGAG-----GAAAGTGAAGCAT 7056
QY 2121 GlnLySAspGlnAlaValAsnLySIIleuSerLeuAlaGlnGlnIleuLySIIleuThr 2140
Db 7057 CATGCAAGATTTACTTAAGGTAGAGAGTGAAGAACTTTGAAGAGAGCTTGAAGAGCAGAG 7116
QY 2141 LySLeuMetAsp-----GlnPheArgAspSerLyS-----GlnSerLeu 2153

Db 7117 ACAACCAAGACAGCTCTTGAAGAGAAATCCAAAGAGAGTAGAGACCTTA 7176
 Qy 2154 GlnGlnGlnSerSerHisLeuSerGlnGlnGlnCysThrTyLeuThrGlnLeuGlnMet 2173
 Db 7177 AAGCAAAAATGATGAGGATGACCCAAAGCTGGAAGAGCTGGAAATTTGATGTTTACT 7236
 Qy 2174 LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2193
 Db 7237 ATAAGCTGCAAGAAAAGAAATCTGCAAAATGAAATTAACAAAAGACAGAGGAAATATCT 7296
 Qy 2194 GlnLeuLeuGlnHisLeuSerSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2213
 Db 7297 GAATTA-----GAAATA 7308
 Qy 2214 ArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2233
 Db 7309 ATAAATTCATCATTTGAAAT----- 7329
 Qy 2234 ILeuSerValLeuArgLeuMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2253
 Db 7330 -----ATTTCAGAAAAGAAAAGACAGAAAGATGAAAGAAAATCAAGACT 7383
 Qy 2254 ArgMetAspIleLeuGlnSerArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2273
 Db 7384 GCCATGGAGATGCTTCAACA-----CAATTAAGAGCTCAATGAGAGCTGCA 7434
 Qy 2274 AlaValTySerGlnGlnHisThrLeuLeuSerSerLeuSerGlnGlnGlnGlnGlnGln 2293
 Db 7435 GCCCTGATATATGACCA----- 7452
 Qy 2294 ThrGlnAlaHisTyrHisCysMetLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2313
 Db 7453 -----GAGGCTGTAG-----GCCAAAGACAGAAATCTTACT 7485
 Qy 2314 ArgSerPheGlnSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2333
 Db 7486 AGTCAGATAGAGTCTTGAACCTTGAGAGAGCTGCTGCTACAGGCTTGTATGAGGCC 7545
 Qy 2334 LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2353
 Db 7546 AAAAATATATATATTTGTTTGAATCTTCACTG-----ATGCGCTCAT 7590
 Qy 2354 LysAspTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2370
 Db 7591 CAAAGATGATGAGATGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 7650
 Qy 2371 ArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2390
 Db 7651 AAAAATCAAAATTCMAAGCAAGCAAGCAAGCTGTCTTAACTGTCCAGGTGGAAGAGAG 7710
 Qy 2391 GlnLeuGlnPhe-----CysGlnIleGlnPheLeuGlnGlnGlnGlnGlnGlnGln 2406
 Db 7711 CACCAACTTGGAAAGACAAAATTAGAACTGAAATTCAGCACTGAAATGAGGCGAG 7770
 Qy 2407 LysAlaAsnIleIleGlnSerValGlnAspSerPheSerGlnValGlnValPheLeuGln 2426
 Db 7771 AAGATCCAGATGCTACAAATCAAAATGCTCTTTCAGAGACACATTAAGTCTGCGAG 7830
 Qy 2427 GlnValGlnSerThrLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2445
 Db 7831 AGTTCTTACAGAAATCTAGAGATGAGCTTGAATTCACAAAATGACAAATGTCCTTT 7890
 Qy 2446 LeuGlnGlnPheGln-----AspLeuHisVal 2454
 Db 7891 GTTGAAGAAAGTAAACAAAATGACTGCAAGAAAGAACTGCAAGAGAAATGATGATAG 7950
 Qy 2455 AspAlaLysLys-----LeuSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2471
 Db 7951 ATGAGCAGAGAAAACAGCAGAGCTGCAAGAAATTCAGTCAAGCAAGAAATAGCTTACT 8010
 Qy 2472 SerThrIleGlnLeuThrTyrArgLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2491

Db 8011 GGAAGTTGAGTTACTGTTGAAAGAAATTAAGAC-----AGCAAAATCA--- 8058
 Qy 2492 GlnIleThrValTyrLeuGlnGlnPheGlnAlaLysLeuGlnGlnGlnGlnGlnGlnGln 2511
 Db 8059 -----TTGAAGAGCTCACACTAGAAAT 8082
 Qy 2512 LysGlnLeuMetArgArgMetGlnHisIleGlnProSerAlaSerValMetGlnGlnGln 2531
 Db 8083 AGCGAATTTGAAGAG-----AGCTGAGTTGATGACCAAAAGAC 8121
 Qy 2532 AsnAlaArgLeuLeuGlnIleLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2551
 Db 8122 CAGGTGAAAAGAGAGG-----AAAGTCAAGAGAGAAATGCTGAATATACGCTA 8172
 Qy 2552 ArgIleLysMetLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2571
 Db 8173 CGG-----CTTCATGAGCT 8187
 Qy 2572 GlnLys-----ValAlaIleLeuGlnAspLysLeuLeuSerArgAsnAlaGlnGlnGln 2589
 Db 8188 GAAAAGAAACACAGGCTTGTGTTTGAC-----ACAAACAAACAGTATGAGTAGA 8241
 Qy 2590 LeuAsnAlaMetGlnValLysLeuThrTyrLysGlnAspAsnLeuGlnAlaLametyls 2609
 Db 8242 ATCCAGACATACCAGAGAAATTCCTTAAGAAAGATGCTCAGTTACAGAAAGCTG 8301
 Qy 2610 GlnIleGlnAsnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2629
 Db 8302 GAGATAGACCTTTTAAAGTCTAGT-----AAAGAAAGCTC 8337
 Qy 2630 AspAsn-----LeuGlnThrLysValValLysIleGlnMetGln 2642
 Db 8338 AATTAATTCATTAAGAGTACTACTCAGATTTTGAAGATTTGAAGAAACCAAGATGAC 8397
 Qy 2643 LysIleLysTyr-----SerLysAlaThrAspGlnGlnIle 2654
 Db 8398 AATCAAAATATATATATCACTGTAAGAAAGAAATGAACTGCGCCAGGAGAAATGAAAG 8457
 Qy 2655 AlaTyrLeuLysSerCys-----LeuGlnAspLysGlnGlnGlnGlnGlnGlnGlnGln 2672
 Db 8458 TTGCTGATCAAAATCTCTGAACAGCTGGAAGAGAAAGAGAAATCTGCAAGAAAGAACTC 8517
 Qy 2673 GlnGlnLeuArgArgAlaGlnAlaAspAsnAspThrThrValCysValProLysAspTyr 2692
 Db 8518 TCTCAACTTCAAGCTGCACAGAGAGAGCAAGAAACA----- 8553
 Qy 2693 GlnLysAlaSerThrPheProValThrCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 2712
 Db 8554 -----GGTACTGTTATGATACC 8571
 Qy 2713 AlaMetLeuValLeuGlnSerGln-----LysAlaAlaLeuGln----- 2725
 Db 8572 AAGTTCAGATATTAACACTGAGATCAAGAACTGAAAGAACTCTTGAAGAAAGAAACC 8631
 Qy 2726 ArgGlnLeuSerHisTyrLysLysLysTyrHisIleuSerArgThrMetSerSer 2745
 Db 8632 AAGAGGCAAGATGAATCTTGATTAAGTACTGTTCTTGT-----CTTAAGAGCAT 8682
 Qy 2746 GlnAspArgLysLysThrLysAlaLysSerAspAlaHisSerSerHisThrGlnGlnSer 2765
 Db 8683 GAAAGCTTAAGAGAAAGCTAAAGAGATGTAGAGACACAACTGGCCATCTGTGTTACAG 8742
 Qy 2766 His-----ArgLysSerProHisLysThrGlnThrTyrArgHisGlnPro 2780
 Db 8743 CAATCTAAACAGATTCACGAGGTCCT-----TTCGTAAGTCCA 8784
 Qy 2781 ValThrProGlnArgSerGlnMetProSerLeu-----HisLeuGlnSerProLys 2797
 Db 8785 GTTCTTCAGAGCAACATCTCCATCCCTCTGTTACTGAAAAGAGTTATCATCTGCGCAA 8844
 Qy 2798 LysSerGlnSerSerThrLysArgValLysSer----- 2808
 Db 8845 AATTAAGCTTCAGAGCAAGAGCAAGATCCAGTGCATAATGGAGAAATGCTGAGAGACA 8904

QY 2809 ---ProAnargSerGluIleTyrSer-----GlnLeuValMetSer----- 2821
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 Db 8905 ACACCTGCTACCCCAAGAGCTTTTCTTAAAAAAGCAGAAAGCAGTCAAGTGTATT 8964
 QY 2822 ---ProGlyLys----- 2824
 |||||
 Db 8965 CACCTTGCAAGAGACAGGAGTACTGAGTTGAGCCAGAGGACTTCAGAACTGTGA 9024
 QY 2825 -----ThrglyMetHisLys-HisIle----- 2831
 |||||
 Db 9025 AAGAAAGGTTTGTGACATCCCGACAGGAAAGACTAGCCCATATATCTCTGGAAGACA 9084
 QY 2832 -----LeuserProSerLysValGlyLeuHisLysLysArgAlaLeuserPro-- 2847
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 Db 9085 ACCATGGCAACTCGGACGAGCCCGCGCTGGCTGACAG-AGTTAGCGCTATCCCACT 9143
 QY 2848 -----AsnArgSer 2850
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 Db 9144 GAGTCTCGCAAGAAATCTTGCAAGTCTCCAAACCAACAGCGTGGGAGCAGATC 9203
 QY 2850 rGluMetProThrGlnHisValIleSerProGlyLysThrGly-----LeuHisLysArg 2868
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 Db 9204 ACAAAGGTCAAGTGTCTCAGCGAGCCCACTAGATTCAAGCACCATCTCCGAGAAC 9263
 QY 2868 nLeuThrGluSerThrLeuPheAspAsnLeuserSerProGlyLysGlnHisValGlu 2888
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 Db 9284 CACCCGGAATCCGCTCCAGTCAATATATCTCTGAGAGAACTCCGACTGACAGCCCCC 9323
 QY 2888 nGluAsnLeuAsnSerProLysGlyLysLeuPhe-----AspValLysSer 2903
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 Db 9324 AGAGGCGCTGAGGCTCAAGCGAGCGGCGACTTGTCCCAAGCCCCAAAGCTGAGTGCAGTC 9383
 QY 2903 rLysSerMetProTyrCysProSerGln 2912
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 Db 9384 CAAGGCGAGTGAAGACTGTAAAGTCCAG 9411
 RESULT 13
 US-10-146-473-81
 ; Sequence 81, Application US/10146473
 ; Publication No. US20030108888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scanlan, Matthew
 ; APPLICANT: Gout, Ivan
 ; APPLICANT: Stockert, Elisabeth
 ; APPLICANT: Gure, Ali
 ; APPLICANT: Chen, Yao-Tseng
 ; APPLICANT: Old, Lloyd
 ; TITLE OF INVENTION: Breast Cancer Antigens
 ; FILE REFERENCE: L00461/70130(GRV)
 ; CURRENT APPLICATION NUMBER: US/10/146,473
 ; CURRENT FILING DATE: 2002-05-15
 ; PRIOR APPLICATION NUMBER: US 60/291,150
 ; PRIOR FILING DATE: 2001-05-15
 ; NUMBER OF SEQ ID NOS: 82
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 81
 ; LENGTH: 4775
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-146-473-81
 Alignment Scores:
 Pred. No.: 2,316-57 Length: 4775
 Score: 1050.00 Matches: 417
 Percent Similarity: 42.28% Conservative: 303
 Best Local Similarity: 24.49% Mismatches: 549
 Query Match: 7.11% Indels: 434
 DB: 14 Gaps: 60
 US-09-724-584-1 (1-2954) x US-10-146-473-81 (1-4775)
 QY 2 SerGluGlyAspAlaValLysValCysValArgValArgProLeuIleGlnArgGlu--- 20

Db 137 AATGAAGGTGATGCCATCAAGTTTGTGGCAATTGCGTCTGCAGAAAGATCTGGC 196
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 QY 21 -----GlnGlyAspGlnAlaAsnLeuGlnTrrpLysAlaGlyAsnAsnThrIleSerGln 38
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 Db 197 TCAGCTGATGAGAGACAG---AACTTAAGCTTATCTGTGCTCTCCACGAGTCTCCG 253
 QY 39 ValAspGlyThr-----LysSerPheAsnPheAspArgValPheAsnSerHisGlu 55
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 Db 254 CTGCATCTCAACCTCGAGCCCAAGACCTTCACGTTTGATCATGTTCAGATGTGATACC 313
 QY 56 SerThrSerGlnIleTyrGlnGluIleAlaValProIleIleArgSerAlaLeuGlnGly 75
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 Db 314 ACTCAGAAATGCTGATTTGCAACTGAGCTGAAGACATGTGAGACTTCGATGAGCGGT 373
 QY 76 TyrAsnGlyThrIlePheAlaTyrGlyGlnThrSerSerGlyLysThrTyrThrMetC 95
 |||||
 Db 374 TATAATGGTATCATCTTTCATATGACAGCACTGCTCGGGAACATTTACTATGATG 433
 QY 96 Gly-----ThrProAsnSerLeuGlyIleIleProGlnAlaIle 108
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 QY 109 GlnGluValPheLysIleIleGlnGluIle-----ProAsnArgGluPhe 123
 |||||
 Db 494 GAATATTTGTTTCTTATATGATGCTGAAAAAAGAGCTGAGCTGAAAGAGTTTC 553
 QY 124 LeuLeuArgValSerTyrMetGluIleTyrAsnGluThrValLysAspLeuLeuCysAsp 143
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 Db 554 CTTTGTATGCTTCTTATGTAATCAACAGAGCAAGATATATGATCTACTG----- 607
 QY 144 AspArgArgLysLysProLeuGluIleArgGluAspPheAsnArgAsnValTyrValAla 163
 |||||
 Db 608 GACTTGCACTCGGCTGAGCTGACTTACTTAAAGGAGCATTCAGAGAGGAGACTTTGTGTT 667
 QY 164 AspLeuThrGluGluLeuValMetValProGlnHisValIleGlnTrrpLysLysGly 183
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 Db 668 GGTGGCGTGGAGCAGGTGTATCTCAGCTGTGAAGCCTATCAGTGTGCTGGAGGA 727
 QY 184 GlyLysAsnArgHisTyrGlyGluThrLysMetAsnAspHisSerSerArgSerHisThr 203
 |||||
 Db 728 TGGAGGAATAGACGCTGTGCATCAACATGAAGACAGAGAAATCGTGTGCTCATGCC 787
 QY 204 IlePheArgMetIleValGluSerArgAspArg---AsnAspProThrAsnSerGluAsn 222
 |||||
 Db 788 GCTTTACATTACATAGATGAGTCAATGGAGAAAGTAAATGAATGTGCAAT----- 838
 QY 223 CysAspGlyAlaValMetValSerHisLeuAsnLeuValAspLeuAlaGlySerGluArg 242
 |||||
 Db 839 -----ATACGAGACCTCCCTACTCAACCTGTGTGATTTGACAGATCTGAAGC 886
 QY 243 AlaSerGlnThrGlyAlaGluGlyValArgLeuLysGluGlyCysAsnIleAsnArgSer 262
 |||||
 Db 887 CAAAAAGATCCCATGACAGAGAGGATGAGATTGAAGAGAACAGCTTAATATGCATCA 946
 QY 263 LeuPheIleLeuGlyGlnValIleLysLysLeuSerAspGlyGlnAlaGly-----Gly 280
 |||||
 Db 947 TTGACCTCGCTGGGCAAGTGAATTACAGCACTTGTGACGTGGGTAAATGAAGAACAGACA 1006
 QY 281 PheIleAsnTyrArgAspSerLysLeuThrArgIleLeuGlnAsnSerLeuGlyLysAsn 300
 |||||
 Db 1007 CATGTTTGCTACAGAGACTCCAACTTACCTTCTTACTAGCGGATTCCTTGAGAGTAT 1066
 QY 301 AlaLysThrValIleIleCysThrIleThrProValSer-----PheAspGluThrLeu 318
 |||||
 Db 1067 GCCAAAGCAGCATATATGCAATGTCATCTGATCCAGAGTGTTTGGGAAACCCCTTA 1126
 QY 319 SerThrLeuGlnPheAlaSerThrAlaLysHisValArgAsnThrProHisValGlnGlu 338
 |||||
 Db 1127 TCACACTTAACCTTGTCCAAAGAGCCAGCTGATTAACAAAGCAGCTAATTAATGAA 1186
 QY 339 ValLeuAspAspGluAlaLeuLeuLysArgTyrArgLysGluIleLeuAspLeuLysLys 358
 |||||

Db 1187 -----GACACCCAGGAATGTGAGCCAGCTCCAAAGTGAAGAGCTCAAGAA 1240
 QY GlnLeuGluAsnLeuGluSerSerSerGluThrLysAlaGlnAlaMetAlaLysGluGlu 378
 Db 1241 CAACCTGGCGAGCTTCCTTCAGAGACAGACACCAAGAAAGCTTCCTGACCGAGACAA 1300
 QY HisThrGlnLeuLeuAlaGluLysGlnLeuHisLysGluLysGluLysArgLysIlePhe 398
 Db 1301 AAGAACTAACTAATATGAGATTTCCAG-----GAAACCAATGTTATTC 1345
 QY HisLeuThrAsnIleValValAlaSerSerGlnLysSerGlnLysAsnLysValLys 418
 Db 1346 TTT-----AGAAATCTGACAGGAAAGAAAG----- 1372
 QY ArgLysArgArgValThrTrpAlaProGluLysIleGlnAsnSerLeuHisLalaSerGly 438
 Db 1372 ----- 1372
 QY ValSerAspPheAspMetLeuSerArgLeuProGluLysAsnPheSerLysLysAlaLysPhe 458
 Db 1373 --TCTCTGATAGAAAAGTTACCCCAATTAGAAGACCTCAACCTCAAGAAAGAAATTT 1429
 QY SerAspMetProSerPheProGluLysLeuAspSerValCysThrGluPheSerAspPhe 478
 Db 1429 ----- 1429
 QY AspaAspAlaLeuSerMetCysAspSerAsnGlyIleAspAlaGluThrAsnLeuAlaSer 498
 Db 1430 -----ATTCAATCTAATAATAATGATTTGAAATTCGCA--GAGCAT 1468
 QY LysValIleThrHisArgGluLysThrSerLeuHisGlnSerMetLysAspPheGluGlnIle 518
 Db 1469 CAATAATAATACGCTTGGAAG--CTCCAC----- 1495
 QY SerAspSerValGlnPheHisAspSerSerLysGluAsnGlnLeuGlnIleuProLys 538
 Db 1496 -----MAGAAATCCCGGAGAGTTTCTGCGCTGAG 1525
 QY AspSerGlyAspMetAlaGluCysArgLysAlaSerPheGluLysGluLysIleThrSerLeu 558
 Db 1526 GAGCAGCATCTTGTCTC-----TCAGAAATTAGAAATGAGATTCMAACTCTG 1573
 QY GlnGlnGlnLeuGlnSerLysGlnGluGluLysGluLeuValGlnSerPheGluLeu 578
 Db 1574 CGAGAACCAATAGAGACACCAACCCAGAGTTGCAAGATATCTATGCAAAATATCTCCCTC 1633
 QY LysIleAlaGluLeuGlnGluLysLeuSerValLysAlaLysAsnLeuGluMetValThr 598
 Db 1634 AGG-----GAGGAGAAATGAGAACTGAGATT-----TTAGAGCTGTGAAA 1675
 QY AsnSerArgGlnHisSerIleAsnAlaGluValGlnThrAspValGluLysGluValVal 618
 Db 1676 AGAGCTCAAGAA----- 1687
 QY ArgLysGluMetSerValLeuGluLysAspSerGlyTyraAsnAlaSerAsnSerAspLeuGln 638
 Db 1687 ----- 1687
 QY AspSerSerValAspGlyLysArgLeuSerSerSerHisAspGluCysIleGlnHisArg 658
 Db 1687 ----- 1687
 QY LysMetLeuGluGlnLysIleValAspLeuGlnGluPheIleGlnAsnLeuAsnLysLys 678
 Db 1688 --ATGAGATGCCCAACCATTCGCAAAAGCTTTCTCTGCAATTAAGTGCATG 1744
 QY SerGluAsnAspLysGlnLysSerSerGluGlnAspPheMetGluSerIleGlnLeuLys 698
 Db 1745 GAGAAAGGTGACAA-----AATCGCAAGATTTTCACTTAAGCTCAAGAAAGAG 1795
 QY GlnAlaIleMetAlaGluLysAlaAsnAlaLeuGluGluLeuAlaLeuMetArgAspAsn 718
 Db 1796 CCATCTTTCTTGCA----- 1810

QY PheAspAsnIleIleLeuGluAsnGluThrLeuLysArgGluIleAlaAspLeuGluArg 738
 Db 1811 -----AACCTAGAAAGTTAAAAAGCAACCACTCTCGAAATTCAGACA 1852
 QY SerLeuLysGluAsn-----GlnGluThrAsnGlnPheGluIleLeuGluLysGluThrGln 757
 Db 1853 GAGCTGAATTAATCAACCAAGAAATATGAGAAATTC-----AAAGACTTACT 1900
 QY LysGluHisGluAlaGlnLeuIleHisGluIleGlySerLeuLysLysLeuValGluAsn 777
 Db 1901 AGCAAAAGCAGCTGAATTTGGAATCAGAGCTTCAGTCTTTCGCAAAAGCG----- 1951
 QY AlaGluMetTyraAsnGlnAsnLeuGluGluAspLeuGluThrLysThrLysLeuLys 797
 Db 1952 -----AACCTTAATCTTGAACCTTTTGGAGCA--ACAAAGCCTGCAAG 1996
 QY GlnGlnGluIleGlnLeuAlaGluLeuArgLys--ArgAlaAspAsnLeuGln----- 814
 Db 1997 CGGCAAGAAATT-----TCTCAGCTGAATTAATAATCATGCTGAACACTTAAGATTATA 2050
 QY Lys-----LysLysValArgAsnPhe-----AspLeuSerValSer 825
 Db 2051 ACTACACCAACCAAGCCTACCACTCATTCGCCAGCACGTAACAAATTAAGCCCTGAA 2110
 QY MetGlyAspSerGluLysLeuLysGluGluIlePheGlnLeuLysGlnSerLeuSerAsp 845
 Db 2111 ATGGGAACCTTGCTCTCTA-----TACACTCAGAAATTTAGCAATATTAGAT 2158
 QY AlaGluAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAsnLeu 865
 Db 2159 AATGATATATTAAAGACCACTTCCTCTGAG----- 2191
 QY GluLeuLysGluLysMetGluAspThrSerAsnTrpTyraGlnLysGluLysAlaAla 885
 Db 2192 -----ATGAATGAAACAACTTTT 2209
 QY SerLeuPheGlnLysGlnLeuGluThrGluLysSerAsnTrpLysLysMetCyluAlaAsp 905
 Db 2210 GAGGCCATTTCTGAAGACCTTAGAACAGTGAAGAAATGAGTCTTTTAAGCCAAA 2269
 QY LeuGlnLysGlu-----LeuGlnSerAlaPheAsnGluIleAsnTrp 919
 Db 2270 CTGATGTAAGAAAGACATTAATAAGCTTACAGCAGCATGTTGACAAATGGAACAT 2329
 QY LeuAsnGlyLeuLeuAlaGlyLysValProArgAspLeuLeuSerArgValGluLeuGlu 939
 Db 2330 CATCTACCCAAATG-----CAGGAGCTTTTCTCATCGAAAGAAATT--- 2371
 QY LysLysValSerGluPheSerLysGlnLeuGluLysAlaLeuGluGluLysAsnAlaLeu 959
 Db 2372 -----GATTGACCAAAACAGAGAGAGCTTCTCTCAAGTGAATGCTCTT 2419
 QY GluAsnGluVal---ThrCysLeuSerGluTrpLysPheLeuProAsnGluValGluCys 978
 Db 2420 GAAAGCAGCTTCAAGAGACTCAAACTTAATAAGCTTTTGAAGAAAGTGAATGATGAC 2479
 QY LeuLysAsnGlnIleSerLysAlaSerGluGluIleMetLeuLeuLysGlnGlu----- 996
 Db 2480 CTGCGAGTAGTCCCTCATTTGCTGCTGCAAGAGAGCTTCTTCAAGTGAATGATAGT 2539
 QY -----GlyGluHisSerAlaSerIleIleSerLysGlnGluIleIleMet 1011
 Db 2540 TCATTCAAAACGAATCAGAGAAAGAAATTCACAAACTTTTGAAGAACACATGATGTA 2599
 QY GlnGlnGlnSerGlnGluIleLeuGlnLeuThrAspGluValThrHisThrGlnSerLys 1031
 Db 2600 CAGCTTCAATTATGATATCTCAGGTTAAGAAACGAAAGCTCTTGAAGACCAAGCTCC 2659
 QY ValGlnGlnThrGlnGluGlnIleTrpLeuGluMetLysLysMetHisAspAspLeuPheGlu 1051
 Db 2660 CTACAGAGTATCTTATGACAACTTACAGAAATTAATGAATTTGAGATTGACCACTTCA 2719

982 nileserysAlaserGluGluIleMetLeuLeuysGInGluGluHisSerAlase 1002
 Db 1881 AGAAATCTTTGGCCCTTGAAGAGTTAGATTGCAGAAA----- 1917
 Qy 1002 rleleleserlysgIngluIleleMetGInglInserGInGluGluLeuLeuTh 1022
 Db 1918 -----AAGCAATCTCTCACAGAAAGTGAATAATTAATCTGGGACCTTCA 1961
 Qy 1022 rAepGluValThrHisThrGInserLyValGInGluGluGluGluGluLeu 1042
 Db 1962 GCAGAGACAGAGACTTACAGAACTGAATCTTGCAATGGAAGTTCT----- 2010
 Qy 1042 rlylyserMetHisAepAepLeuPheGluGluysrlyrlearg-----AsnLySerGluValaG 1061
 Db 2011 -----TTGAAAAAAGCTTACAGAAAACCAAAAATCAGTCAAA 2048
 Qy 1061 uAepLeuLeuAArgGluMetGluAenLeuLyserGlyThrMetGluSerValGluValysrI 1081
 Db 2049 AGATTG-----GCTGTTCACTCTGCAGAC 2072
 Qy 1081 eAlAepThrLySHisGluLeuGluGluThrIleArgAepLyGluGluLeuLeuHisG 1101
 Db 2073 TCAAAAAAATAAGCACAAATAAGAGATTACAGTC----- 2106
 Qy 1101 uLyserLyrrPhePheGlnAlaMetCInThrIlePheProIleThrProLeuSerAsp 1121
 Db 2106 ----- 2106
 Qy 1121 rleuProPserLyLeuValGluGlyAsnSerGlnAepProIleGluIleAsnApy 1141
 Db 2107 -----ATGCTTCAAAAAC----- 2121
 Qy 1141 rHisasnLeuIleAlaLeuAlaThrGluArgAsnAsnIleMetValCysLeuGluThrG 1161
 Db 2122 -----AAGACAGA 2129
 Qy 1161 uArgAsnSerLeuLyGluGluValIleAepLeuAsnThrGln-----LeuGInserLeu 1180
 Db 2130 ATTGAAAGCTTAAAGCATCACAGAGATCCCTTGAGCTGAAAACTCAAGTCTTAA 2189
 Qy 1180 nAlaGInserIleGluLySerAepLeuGlnLyserProlysGlnAepLeuGluGluG 1200
 Db 2190 GCAGACAA-----TATCAGACTGAATGGAATACTTAGGAAAGTGCAGACAGAAAA 2243
 Qy 1200 uValLySerLeuLeuGluMetGluLeuLeu-----LyGlyHisLeuThrAsp-----SerG 1218
 Db 2244 AGAAACATTTGTTGAAGACAGAAAGATATCTTCCAGGCCACATAGAAAGAAATGATGA 2303
 Qy 1218 nLeuSerIleGluLyLeuGluLeuGluAsnLeuGluValThrGluLyLeuGluThrle 1238
 Db 2304 AAAGCTTTAGAAAAGCTTGAATGTGAAGCAACAGAA-----CTGAAATCAATT 2351
 Qy 1238 uGInGluMetLyAsnIleThrIleGluArgAsnGluLeuGluThrAsnPheGluAs 1258
 Db 2352 ATCTTCTGAAGCTGTGAAGATATTAAGCCGCTCAAACTAGAAAGAGAACTTTCTGT 2411
 Qy 1258 pHeuLyAlaGluHisAepSerLeuLyGlnAepLeuSerGluAsnIleGluGInserI 1278
 Db 2412 TCTGAAGATCAAAACGATTAATAATGAAGCAGGATTAAGAGCCCAAGATGAT----- 2463
 Qy 1278 eGluThrGlnAepGluLeuArgAlaAlaGInGluLeuArgGluGluHisGInLeuVal 1298
 Db 2464 -----GAAACGAAAAAATCATCACAGACAGCAAGT 2492
 Qy 1298 lAepSerPheArgGInGluLeuLeuAspCysSerValGlyIleSerSerProAsnHisAs 1318
 Db 2493 TGACACT-----ATCATTAAGAAACACAGAGT 2519
 Qy 1318 pAlaValAlaAsnGInGluLyValSerLeuGluGluValAsnSerLeuGInserGluMe 1338
 Db 2520 ATCTATCCAGAGACTGAGAAAGGCATTAATAAGATCAAAATTAATCAACTT-----GAGCT 2573

Qy 1338 rLeuArgGluGluArgAepGluLeuGluGlnThrSerCysLyAlaLeuValSerGluLeuG 1358
 Db 2574 TCTCTTGAAGAAAGGAAACAGACATTTGAAAGAGATCAGGCTCATGTGAAATTTAA 2633
 Qy 1358 uLeuLeuArgAlaHisValLySerValGluGluGluAsnLeuGluIleThrLylylyle 1378
 Db 2634 G-----GCAGATATTAATAAGCTGAGAGGGAACCTCCAGCGGCACTCTGTAAGCT 2684
 Qy 1378 uAsnGluLeuGluLyGluIleLeuGluLySerSerGluGluSerGluValLeuLySerSe 1398
 Db 2685 GGACGCTTTTCACTCTTAC-----CAGAGTCCACACATGAGCAGACAAAGCAAA 2735
 Qy 1398 rLeuGluAsnLeuLyGluAepAsnAsnLySerLySerGluGluAlaGluGluTyrSerSe 1418
 Db 2736 TGAGAGAACAGTTGGCCCAATTCGACAGAGAGTTGTTGATTTGGAAACGAAAGAAATTC 2795
 Qy 1418 rLyGluAsnGlnPheSerSerLeuGluGluValPheSerGlySerGlnLyLeuValAepG 1438
 Db 2796 TCTTACCAAAACAG-----GTTGCTGAAAGTTGAGACACAAAGAAAGATGTTGTCTGA 2849
 Qy 1438 uIleGluValLeuLyAlaGlnLeuLyAlaAlaGluGluArgLeuGluIleLyAsnApy 1458
 Db 2850 GTTAGATGCTCACAAAATCCAGGTGCAGACTTAAATGCGCAACTTGAAAAACAAATATG 2909
 Qy 1458 GAepTyrrPheGluLeuValGlnThrAlaAsnThrAsnLeuValGluGluLyLeuGluTh 1478
 Db 2910 TGAATGAGCAAAAAGTAAATCTTTA---ACCCAAGCTATGACTCCAACTTGAAAG 2966
 Qy 1478 rProLeuGlnAlaAepHisGluGluAepSerIle----- 1489
 Db 2967 TGTGAACAAAGAAACAGAACAGACAAAGCAAAATCTTGCGTGAAGAAAGAAATATGATTT 3026
 Qy 1490 ---AspArgArgSerGluGluMetGluIleLyValLeuGluGluLyLeuGluArgAs 1508
 Db 3027 ACAAAATGAGAGAAAGACAGAAAGAAAGAAATAGATCTCACAGAAATTTGTCAGCCCA 3086
 Qy 1508 nGlnTyrrLeuLeuGluArgLeuGluGluGluLySerGluLeuSerAsnLyLeuGluI 1528
 Db 3087 GGAGACAGATATTCATATTTTGAATGAG-----GAATATGAACCAAAATTTAAAA 3137
 Qy 1528 eLeuGlnLySerGluMetGluThrSerValLeuLeuLyAepAepLeuGlnGluLeu-- 1547
 Db 3138 CCAAGAAAAAAGATGAGAAAAAGTTAAAGCAGAAAGCAAGATGCAGAAAGCGTTAA 3197
 Qy 1548 -GluSerLeuLeuSerGluAsnIleIleLeuLySerGluAsnIleAepThrThrLeuLySH 1567
 Db 3198 GAAAAAATTAAGTGCAGAGAGCCAAACTTAAAGAAAGAGCTTGAAATAACT----- 3249
 Qy 1567 SHIsSerAepThrGlnAlaGlnLeuGlnLyThrGlnGlnGluLeuGluLeu---AlaLy 1586
 Db 3250 -----GCTCTAGAGCTTGTGCAGAAAGAAAAACAGTTTAATGCCAA 3290
 Qy 1586 sAsnLeuAlaIleAlaAlaSerAspAsnCyAepProIleThrGlnGluLyGluThrSerAl 1606
 Db 3291 AATGCTGGAATAGGCACAGCTTAACCTCAGCTGGAATC-----AG 3329
 Qy 1606 AepCyValHisAepLeuGlu-----GluLyHisLeuLeuLeuThrGlu-- 1621
 Db 3330 TGATGACAGTGCAGAGCTTGAAACAAACCAAAAGAACAAAGAAAGCTTAACTGAGGT 3389
 Qy 1622 -----GluLeuHis-----GlnLyThrAsnGluGlnG 1631
 Db 3390 TCATGCAGACAGAACTCAATGATGTCAATCAATCTGGGAAAGAAAGAACTTAATCAGCAAG 3449
 Qy 1631 uLyLeuLeuHisGluLyAsnGluLeu-----GluGlnAlaGlnValG 1646
 Db 3450 TGAAGAACTTCAAGAAATATCATGAATCCAAATTACAGAAAGAAAGAGAGTACAGAGA 3509
 Qy 1646 uLeuLyS-----CysGluValGluHisLeuMetLySerMetI 1659
 Db 3510 ACTGAAACAAAGATCTCTTATTTGGGTGTGAAAAAGAAAGAGATGAACAGAAATAAG 3569
 Qy 1659 eGluSerLySerSerSerLeuGluSerLeuGlnHisGluLySHIsAepThrGluGlnGlnle 1679

Db 3570 ATGGCTGAAGAA-----GAGGCTGTTAAGCAGATACA-----ACATT 3608
 QY 1679 ULEUALALEUYSGLINMETGLNVALTHRGINGLYLSGLULEGNGLNTH 1699
 Db 3609 AAATGAATTACAGAAACAGTTAAAGCAAGAGTCTGCCATGTGAATCTCTTCCACAAAG 3668
 QY 1699 RHISGLNHSLEUTHALAGLVALASPHISLEUYSGLUASNILEGLULEGNYLEUAS 1719
 Db 3669 TGAACCTAACTGAAAGCT-----CATCTT---GAAAAGCTAGAGGTTACTTGAA 3716
 QY 1719 NPEHLYSASNGLVALAGLNGLNLYSTHRLYSGINGLYNYSLEUASNGLUASN- 1738
 Db 3717 T-----AAGTCTGGAAGGAAATACTTTCTTCAAGACAGCT 3755
 QY 1739 -LYSGIULEUGLNGLSERGNHISARGLEUINCYSGLNILEGLULEMETYSS 1758
 Db 3756 AGTTGAACCTGAAGATCTGCGACAGAAAGATTAAGCCGAGTTTCTGAGTTGACTAGCAA 3815
 QY 1758 RLEULYSAPPLYGLUSERALALEUGLUTHRLYSGIUSERSGLULEGNYVALILEAS 1778
 Db 3816 GTTGAATAACCAACGATGAAGAAATCCAGAGTTTGAATCTTCAATGAATAA----- 3867
 QY 1778 NLEUASNGINGLUMETGLUMETVALMETLEUGLUMETGLULEGNYLSHNSERGLNAR 1798
 Db 3868 -AGTAACAAGCCTAGAGACAAAGAGCTTGAAATTTAAAAAAGCTG----- 3912
 QY 1798 GTHRVALLIHALAGLARGHSPGLNLEGINASHPLEU--ARGLSERVALIGLUME 1817
 Db 3913 -----TCTGAGAACTAGCCGATTCAGCTAGATATTGCTGTAGAGAAACCAAGAC 3962
 QY 1817 TSERIEGLIUTHGLINASHPLEURGLYSALAGNGLUALALEUGLNGLNLYSAS 1837
 Db 3963 CTATTAGAAAGCT-----AAACAATGACCTATCAACTTAGTGTAG 4007
 QY 1837 PHYVALINGLULEUTHSERGNLESERVALLEUGLNGLYLSESERLEUGL 1857
 Db 4008 TAAACTAATGACATCTTTCTAGATCTCTCATTCACACCGACCACTAACTAATTTAA 4067
 QY 1857 UASNGINMETLEUTHYASNVALATHRYALLYSGLUTHRLUSERGLUARGHSPASPLE 1877
 Db 4068 GGAGGACCTGTTAATTAACCTTGACAGTTTCTGAA-----TT 4106
 QY 1877 UASNGINSERLYSGLNHSLEUPHESERGNILEGLUTHRLUSERLEUYSERGL 1897
 Db 4107 AGAAGCAAACTTAGACAGTTGACAGAGGCAAAATACATAATATTCTTTCAACA 4166
 QY 1897 ULYSGLUPHEALALEUGLNGLNALEGLUYASAP-----LYSNLASPVALA 1913
 Db 4167 GGCTACTCATGATTGAAGAAAGAAATCAATTAAGACATGACAGCTGATTTGA 4226
 QY 1913 AARGLYSTHRLIENPILETHRGILYSLSESERASNILEGLINGLNGLEUGLNG 1933
 Db 4227 AAGTCTT-----GTAACGAAAA-----GAAGCCTTACAGAAAGA 4262
 QY 1933 NALATHRASNLEUYSGLUTHRLYRGUARGUSERLEULE--GLCYSYSGI 1952
 Db 4263 AGGAGGCAATCAGCAAGGCTGCTTCTGAAAAGAGCTTGTATTAACACAGTTGAAGA 4322
 QY 1952 UGLINUALALEUASNTHGLNHSLEUARGIUTHRLUSERLYSASPVALALE 1972
 Db 4323 AAGATTATCTGAAAACATCAAT-----GCTGT 4349
 QY 1972 UGLYLSMETGLINGLNUARGHSPGLUALAASNLYSVALILEALALEUTHRGILY 1992
 Db 4350 CACATTGATGAAGAAGAGCTTAAAGAAAAAGTTAGATTAGACGCTTAGTAACA 4409
 QY 1992 SMETSERLEUGLNGLNGLNLEASNGLUASNVALTHRLYSGIUSGLYGLU 2012
 Db 4410 ACTTAACGATTGATGATCTTCAAAATAGCATC----- 4446
 QY 2012 YGLUYSGIUTHRLPHETYLEUGLNGLRPROSERLYSGINGLNSERSEERGLN 2032
 ||| ||| |||

Db 4447 -----AGCCTATCCGAAAAAGA 4463
 QY 2032 UGLIUEAURGUSERLEUTHRLYSHASPLEUGLNGLUALAGLULYSGIL 2052
 Db 4464 AGCAGCCATTTCATCATAGA-----AAGCATATGATGAAGAAAA 4505
 QY 2052 ESERGLUALATHRASNGLIILEYASNLEUTHRALYSLSESERLEUGLNGLU 2072
 Db 4506 ATGTGAATTGCGATCAGGTCCAGATTTATCTTTAAAGTTGACACTGAGTAAAGA 4565
 QY 2072 U-----ILEUGLNASNALASERILEUASNGLUALAVALSERGLUARG 2089
 Db 4566 GAAAATTTCTGCTCTTGAAGCAGATGACTGTGCAATAAATTTCTGAAATGGAAGA 4625
 QY 2089 NLEUARGHISERLYS-----GLNGLNUVALSERGLULEGNGLNUSE 2105
 Db 4626 GAAAGCACATGAAGATTTACACAGCATTAACACTGTAAAGAAATG--CAGATCCA 4682
 QY 2105 RLEUTHRLYLSERARGHSPHIALAPHEALAGNLSERLYSARGLULYSASPGLUAL 2125
 Db 4683 GCTTAGTTAAATCAAGAA-----GCTTATGAAGAAAGATGAGCA 4724
 QY 2125 AVALASNYSILIALASERLEUALIGLNUILYSLILEUTHRLYSGIUMETASP-- 2144
 Db 4725 GATTAAT-----TTATGAGAGAGCCTGATCAGCAAAATTAAGATTGATTG 4775
 QY 2145 -----GLUPHEARGHSPSERLYSGIUSERSLEUGLNGLNGLNSERSEHISLE 2161
 Db 4776 TTTAAAGGTGAATGAGAAAGACAGACAGCAAGATGAGAAAAGAGACTTAATTTAA 4835
 QY 2161 RGLUGLNU-----CYSTHTRYLY 2168
 Db 4836 AACAGAGTTAAAGTCTCAACAGCAAGAAATTAGATTAGAGCACTATTACCAGA 4895
 QY 2168 SFTH--GLUEUGLNETLEUYSGLN-----GLNLYSGIUSPIL 2181
 Db 4896 AACTATTGAATAGAGTCTTAAATGAAGTCTTAAATTAACAATCAACAAGAGATAT 4955
 QY 2181 EASNENLYS-----LEUALAGLU----- 2187
 Db 4956 TGAACACAAAGAAATGTTGTTACAGAACTTCAACATTTCAAGATTGAGAAAGAAAGA 5015
 QY 2188 -----LYSVALYSGIUALASPGLU-----LEULEGNHISLEUSERSE 2202
 Db 5016 CAACAGGTTAAAGAAAGCTGAAGAAATACTTAACACTTGAAANCCAAAGTTATTCAT 5075
 QY 2202 ULYSGLINGLNUASPGNILEGLMETGLUEN----- 2213
 Db 5076 GAAAGCTGAATGAAATTAAGAAAGAAATTAACATGTGAATTTAAGTGAAGAAG 5135
 QY 2214 -ARGASNGLUYSLUARGHSPHTRYGLU-----LE 2223
 Db 5136 CAAAGAGAGGAGTTAAAGGCAATTGGAAGATRGCTTGAGTCAGAAAGTGTCAAAAT 5195
 QY 2223 UCYSGLUYSMETASPILEMETGLULYSGLUILESERVALLEUARG-----LEUME 2240
 Db 5196 ACAGAGTTGAAGAAAAAGCTGAACAAATAATTCGTGCATTAAGACAGCTGTATTC 5255
 QY 2240 TGLNASNGIUPROGINGLNU-----GLUASHPVALALEGLUAR 2254
 Db 5256 TCAATGGAAGAGAAAGAAACAGTATTAATAAAGTACAGAAACCAATTTAGTGAGCT 5315
 QY 2254 GMETASPILEUGLUSERARGHSPHISGLNUILEGLNGLNUSEMETGLULYSLI 2274
 Db 5316 AAATCAAAATTTGCGAAGAAAGAAAGGAAAGTTCATCTTGGAAGAAAACTTAAGTC 5375
 QY 2274 AVALYRSEERGLINGL--HISHTHLEUEN-----SERSELEUSERSE 2288
 Db 5376 AGTGAAAGCTTACAGCTAGAAACATTAATTTATCCACAGATAGCAAAAAAGTGGCAC 5435
 QY 2288 RGLUENGLNYSGLUTHRLUALHISLYSHISCYSMETLEUASNILEYSGIUSER 2308
 Db 5436 ATATAGTGAACAAGAAAGAGATTTCCCAAGGCTGTGTGCGAAGACATATGAAGAAAA 5495
 ||| ||| |||

QY 2308 userSerThrLeuSerArgSerPheGlySerLeuGln----- 2320
 Db 5496 AATCAGTGTGTTTACAAAGAACTTAAGTCAAAAAGAAAGCTTTGACAGGGGTAGGCA 5555
 QY 2321 -----ThrglnHisValIySleuAenThrGlnLeuGlnThrLeu 2334
 Db 5556 CGAAAAAGAGAGACAGTTCTTCTCTCTGAAATGCGATGCGCAATACAGAGCGGCTT 5615
 QY 2334 uAenIySleuValIyValIyArgThrAlaIaValIySleuAenHisSerLeuIleIy 2354
 Db 5616 A-----ATAAAGCTGAGACATGCTGAGCAAGCAACATGAAATGATGATAG 5669
 QY 2354 sAerIyGlnIySleuAenIaIaGlnIySleuAenHisAerGlnLeuAenIySleu 2374
 Db 5670 TCATCTTCAAGAGAGCTTGAAGAAAAACAAAGAAATATTC-----TTGATAGTAC 5723
 QY 2374 uGlnCySleuGlnGlnHisGlyArgIySleuAerAserGlnIySleuIySleu 2393
 Db 5724 CCAAGCTGTGAGAAAAAGAGAGTAAATTAATACATACAGCAAGCAAAAGCTTGAAGAA 5783
 QY 2394 ---PheCySleuIleGlnPheLeuAenGlnLeuPheIySleuAlaIaIleIleG 2412
 Db 5784 TGTGTTTGAAGAGTCCAG-----AAACCTTCAGAGAGAGAGAACTTAAGCTGCTCA 5834
 QY 2412 nSerValGlnAerAerPheSerGlnIyValGlnValPheIy-----AsnGlnValG 2429
 Db 5835 GATTTTGAGCAAAAGATAAAGAGCTGATCTCTGTTAGTAAAGACAGAAAGAGTACA 5894
 QY 2429 ySerThrLeuGlnGlnIySleuGlnIySleuValIyPheMetGlnIyPheGlnIyP 2449
 Db 5895 TAGAGTTGAAATGAGAAAGAGTGAACCTCAAAATGAAATAATTCACAGCTTTACACAGAT 5954
 QY 2449 eGlyAerLeuHisValAerAlaIySleuSerGlnIyMetGlnGlnIySleuAer 2469
 Db 5955 GGATGAGAAATTAACCCACAGACATTTGGAAGAAAAACATGAGAAAGAAAGTCCAAA 6012
 QY 2469 gIleAerSerThrIleGlnLeuThrIySleuValIySleuValIyGlnIySleuIy 2489
 Db 6013 -----TCACATTTGGTCCAAACCAATTT 6035
 QY 2489 eGlnArgIleIleThrValIyLeuAenGlnPheGlnIySleu-----G 2505
 Db 6036 GCTTAATACATGAGAAAGCCAGCAATATCTGAGCTTAAATTTAGCCGGGAGAGAG 6095
 QY 2505 nGlnIySleuGlnIySleuAenIySleuMetArgAerMetGlnIySleuIyPheSer 2525
 Db 6096 GAGGAAACAGAACTGGGAGAGATTTGATTCAGAGAA-----GACCT 6143
 QY 2525 aSerValMetGlnIySleuAenIaIaArgLeuLeuGlnIyLeuIySleuThrValGlnAer 2545
 Db 6144 TCGAATTTGAGAAAGAGAGATCAGCAAGAAATGGAATTAATAAGAAAGAAATATGATCA 6203
 QY 2545 uSerIySleuGlnIySleuArgIleIySleuMetLeuGlnIySleuAenIySleuValIySleu 2565
 Db 6204 AGAAAG-----GAAGAGAAATCAACAGAGAGAGAAAGATCTTGAACCTGAAGCA 6257
 QY 2565 pAerAlaMetHisIySleuGlnIySleuValIaIaIleGlnAerIySleuLeuSerArg 2585
 Db 6258 TTCACATTA-----AAACAGCTGATGAGG-- 6282
 QY 2585 nAlaGlnIaIaGlnLeuAenAlaMetGlnValIySleuThrIySleuGlnAerAenIySleu 2605
 Db 6283 -----GACTTTAAT-----ACACAGCTGGGCAAAAGAGAAACAGAGCTGGA 6323
 QY 2605 nAlaIaIaMetIySleu-----IleGlnAenIySleuMetValIaIySleuValIaIyP 2624
 Db 6324 AATGACCATTAAGAAAGAACTATCAATAAGCCAGAGAGTGAAGCTTGAAGAG 6383
 QY 2624 oTyIySleuGlnIySleuAerAenIySleuThrIySleuValIySleuIleGlnIySleuIy 2644
 Db 6384 CCATCAAGAAAGACAAATCAGTTACTTAAAAAAATTCGAGAGAAAGAT---GATGATCT 6440

QY 2644 eIySleuIySleuAlaIleThrAerGlnIyIleAlaTyIyLeuIySleuCySleuGlnAer 2664
 Db 6441 AAAAGCAACAGCCAAAGAAAGATATGAGAAATC-----CTTATGCTCG 6482
 QY 2664 sGlnIySleu-----ArgArgLeuIySleuGlnIySleuAerArgAlaGlnAl 2680
 Db 6483 TGAAGAAAGAAATGACTGCAAAAGTAAGGACCTGACAGACTCAACCTGAGAGCTGAG 6540
 QY 2680 aAerAenAerThrThrValIySleuValIySleuAerIySleuAenIySleuThrPhePro 2700
 Db 6541 -----AAGAAATCCAGCAAAACCTAGACAGAGAGCA 6572
 QY 2700 IThrGlyGlnIySleuIySleuValIySleuThrAlaMetLeuValIySleuIySleu 2720
 Db 6573 GAACCTGGCAAT-----GATATGTAACATTAATGAGCTTACAGACACA 6617
 QY 2720 uIySleuAlaIySleuGlnAerGlnIySleuSerHisTyIySleuIySleuThrHis 2740
 Db 6618 GTAGCAGACAGAAAGACAGCTTAATCAGTGAATGAAAGACCAAGAGTTCAGAGA 6677
 QY 2740 gThrMetSerSerSerGlnAerArgIySleuThrIySleuValIySleu----- 2755
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 QY 2756 -----AerAlaHisSerSerHisThrGlnIySleuSerHisArgIySleu 2769
 Db 6738 TGTGGGACACCTTAACAAAGGTGGCAATTTGTACATACGATGCTCTACTCTTGGAGA 6797
 QY 2769 rProHisIySleuThrGln-----ThrTyArgHisGlyProValIh 2782
 Db 6798 ACCTACCGAATTTGAGTATTTGCAAAAGCTTTTGAATATATAGTGGTGTGAGAG 6857
 QY 2782 rProGlnAerSerGlnMetProSerLeuHisIySleuGlnIySleuProIySleuSer 2802
 Db 6858 TAAGACCATGCGCAAAAGTTATACACCGTACTGAAAGTCCCT-----GATATCA 6908
 QY 2802 rThrIySleuValIySleuProAerAerSerGlnIySleuSerGlnIySleuValIySleu 2822
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 QY 2822 oGlyIySleuThrGlnMet-----HisIySleuHisIleLeuSerProSerIySleuVal 2838
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 QY 2838 yLeuHisIySleuValIySleuAerProAerAerSerGlnMetProThrGlnHisValI 2858
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 QY 2858 eSerProGlnIySleuThrGlnIySleuHisIySleuAenIySleuThrIySleuPheAer 2877
 Db 7044 GACATTTGGGTGACTGCTGCTG--GAAGAGCTGCCACACTTGTCTCTTGAAGATGA 7100
 QY 2878 -----LeuSerSerProCySleuGlnIySleuValIySleuAenIySleu 2891
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 RESULT 15
 ; US-09-814-353-21776
 ; Sequence 21776, Application US/09814353
 ; Publication No. US20030165831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, John
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
 ; FILE REFERENCE: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: US 60/211,940
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: US 60/216,820
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: US 60/220,661
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: US 60/257,672
 PRIOR FILING DATE: 2000-12-21
 NUMBER OF SEQ ID NOS: 22037
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 21776
 LENGTH: 8063
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1, 7841, 7842, 7843, 7844, 7845, 7846, 7847, 7848, 7849,
 LOCATION: 7850, 7851, 7852, 7853, 7902, 7903, 7904, 7905, 7906, 7907,
 LOCATION: 7908, 7909, 7910, 7911, 7912, 7913, 7914, 7915, 7916, 7917,
 LOCATION: 7918, 7919, 7920, 7921, 7922, 7923, 7924, 7925, 7926
 OTHER INFORMATION: n = A,T,C or G
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 7927, 8036, 8037, 8038, 8039, 8040, 8041, 8042, 8043, 8044,
 LOCATION: 8045, 8046, 8047, 8048, 8049, 8050, 8051, 8052, 8053, 8054,
 LOCATION: 8055, 8056, 8057, 8058, 8059, 8060, 8061, 8062, 8063
 OTHER INFORMATION: n = A,T,C or G
 US-09-814-353-21776

Alignment Scores:
 Score: 5.51e-56 Length: 8063
 Percent Similarity: 1032.50 Matches: 618
 Best Local Similarity: 40.62% Conservative: 510
 Query Match: 22.25% Mismatches: 933
 DB: 6.99% Gaps: 717
 Indels: 129

US-09-724-584-1 (1-2954) x US-09-814-353-21776 (1-8063)

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 Db 331 GCCATGTTCAAGAAACGAAAGCAATACAGCAGAGACAGCAGCGCTCCAGCGCG 390
 QY 363 -----LeuGluSerSerSerGluThrLyAsnAlaGlnAlaMetAlaYsGlnGlu-HI 379
 Db 391 CTGGCTCTCTCTAGCGGCTCTCCCAATCTTCAACACCAACAGAAATAGAGACAGACA 450
 QY 379 sThrGlnLeuLeuAlaGluIleYsGlnLeuHISlySGluArGluAspArgIleTrpHI 399
 Db 451 TCTTCATTACAGAGCAACTTGATGAAGGTACAC---CCAAATGAGAGTCAGGTGACACA 507
 QY 399 sLeuThrAsnIleValAlaIaSerSerGlnGlnAspGlnArgValYsAr 419
 Db 508 C----- 508
 QY 419 glysArGArGValThrTrpAlaProGlyLysIleGlnAsnSerLeuHISAlaSerGlyVa 439
 Db 509 -----AGTCTTTTGCAAGAACTCCAG 531
 QY 439 lSerAsp-----PheAspMetLeuSerArg-----LeuProGI 450
 Db 532 CTCGGGGTCCCTCCGTGAGAGTCTTTGTTTCCAGAGTCGATTAAGAAATCTTATTCGG 591
 QY 450 yAsnPheSerLySlySAlaLysPheSerAspMetProSerPheProGluIleAspAspSe 470
 Db 592 TCTTCTTCAAGAGTCTTTGGTACGACATCTTCCAGAGAAATCCCTGATGACTT-GA 650
 QY 470 rValCysThrGluPheSerAspPheAspAlaLeuSerMetCysSerAsnGlyrI 490
 Db 651 CCTGACACTTCTACTGCGCAGTTTGATCCACCC---TCTGATATGATAGTACGAGGTGTA 707
 QY 490 eAspAlaGluTrpAsnLeuAlaSerLySValThrHisArgGluYs----- 505

Db 708 AGACTGTGAGCGAAT-----TCAGCACTCTCCAAAGAAACAGTTGATTCAGCGGTT 761
 QY 506 -ThrSerLeuHISGlnSerMetIleAspPhe---GlyGlnIleSerAspSerValGlnPh 524
 Db 762 CGCAAGATGAAAGCAAGCTTAAGTACTACAGGGGAAAAATATTCGACTTCTTACACG 821
 QY 524 eHisAsp-----SerSerLySLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 542
 Db 822 TTATCAGATCTCTCAGAGAGAGAAAGAAAGTACAAAGTATTTAAGTCAGAGTCAGGA 881
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 QY 582 uLeuGlnGlnGlnLeuSerValLySAlaYsAsnLeuGlnMetValThrAsnSer---Ar 601
 Db 981 GAAAGATCAGTATATCAGTGTCTCCAAACTCAGGTTTCTACTGAAACACGATTACG 1040
 QY 601 gGlnHISerIleAsnAlaGluVal-----GlnThrAspValGluYsG 616
 Db 1041 AAATGGCCCGATGAATGTTGATGATGTAACCACTTCTCAGCTGCAACACAGCTGTA 1100
 QY 616 uValAlaArgLySLeuMetSerValLeuGlyAspSerGlyTrpAsnAlaSerAsnSerAs 636
 Db 1101 AGCTTCTCACTAAGAAAGCAAT-----CCAGAAAGTGA 1133
 QY 636 pLeuGlnAspSerSerValAspGlyLySArgLeuSerSerSerHisAspGlyCysIleGI 656
 Db 1134 TCGAAGCCAGATGATGGAAGATGCA-----ACTTCGTGAA 1169
 QY 656 uHisArgLySMetLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 676
 Db 1170 AACACTGAAACACTCCACGAAAGAGTG-----AAGGCTCAAGGAACTTACT 1217
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 Db 1218 TAAAGCTTGAAGAAACAAATTCAGTCACATTAAGAAACAA----- 1257
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 Db 1297 -----CAACT 1301
 QY 736 uGluArSerLeuLySLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 756
 Db 1302 GGATGAAAGACTTCACAAACCTAGAAAGATAAGAGCACTTATATGCGCGAGAAAG----- 1356
 QY 756 rGlnLySLeuHISGlnAlaGlnLeuIleHISGlnIleGlySerLeuLySLeuValGI 776
 Db 1357 -----ACTAACTTATCACTAGTTCGCTGATGCAAGAAACTTAATTGA 1400
 QY 776 uAsnAlaGluMetLySAsnGlnAsnLeuGlnGlnAsp-----LeuGlnTh 791
 Db 1401 A-----CAGCTTGAAAGATTAAGGGAATGTATTCGACAGAGAC 1439
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1548 AGAAAGTCCGAAGAGCTGCTTTGAG-----GAACCTGAAAAAGCTTGAAGTACAGC 1601
QY
846 AGUAlaValThrArgAspAlaGlnLysGluCysSerPheLeuArgSerGluAenLeuG1 866
DB
1602 CCAAAA-----ACAGAGAGAGCAGAGAGAAA-----CTGAAGCAGAAATGATGATGA 1649
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DB
1650 ACAAAATAAAACCTTCGAAAAACAAGT-----GAGAGAGAACCATCACTAGT-- 1695
QY
886 rLeuPheGluLysGlnLeuGlnThrGluLysSerAsnTyLysLysMetGluAlaAspLe 906
DB
1696 -----CTTCAACAGAGATTAGTCGGGTGAACAGAGGTTGTTGATGT 1739
QY
906 uGlnLysGluLeuGlnSerAlaPheAsnGluLLeAsnTyLysAsnGlnLysLeuAlaG1 926
DB
1740 AATGAAA-----AAATCCTCAGAAAGAACAAATGTCTAGCTACAGAACTCATGAAA 1793
QY
926 yLysValProArgAspLeuLeuSerArgValGluLeuGluLysValSer----- 943
DB
1794 GGAAGCTGGCCAGA-----AAAGACAGAACTACCAAGAAAGCTTCAGACCCAGA 1844
QY
944 ----GluPheSerLysGlnLeuGlnLysAlaLeuGluGluLysAsnAlaLeuGluAenG1 962
DB
1845 AAGGAATTCACAGAACAAATGAAGTACCTTGAAGAAAGTCAA----- 1890
QY
962 uValThrCysLeuSerGlnTyLysPheLeuProAsnGluValGluCysLeuLysAsnG1 982
DB
1891 -----TCAGAAATATTGAAATCAGCCAGCAAAAGAAA-----CAGCA 1928
QY
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DB
1929 AGAATCTTGGCCCTTGAAGAGTTAGTTCGAGAAA----- 1965
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1966 -----AAAGCAATCCTCAGAGAAAGGAAATGAATTAACCTTGGGACCTTCA 2009
QY
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DB
2010 GCAAGAAAGCAGAGACTTACAGAACTAGAAATCTTGAATGAAAGTTCT----- 2058
QY
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DB
2059 -----TTGGAATAAAAGCTTACAGAAACCAAAATACAGTCAAA 2096
QY
1061 uAspLeuLeuArgGluMetGluAenLysGlnTyLysMetGlnSerValGluValLysI1 1081
DB
2097 AGATTGG-----GCTGTTCACTGGGAAGC 2120
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DB
2121 TGAATAAAATACACAAATGAAGAGATTACAGTC----- 2154
QY
1101 uLysLysTyLysPhePheGlnAlaMetGlnThrLLePheProLLeThrProLeuSerAspSe 1121
DB
2154 ----- 2154
QY
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DB
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QY
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DB
2170 -----AAGACAGA 2177
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QY
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DB
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QY
1200 uValLysLeuLeuLeuGlnMetGlnLeuLeu-----LysGlnHisLeuThrAsp-----SerG1 1218
DB
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DB
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DB
2512 -----GAAACAGAAATATCATCAGACAGCAAGT 2540
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DB
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DB
2733 GGAAGTTTTCAGCTTAC-----CAGAGTGCACACATGACGACCAAAAGCAT 2783
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DB
2784 TGAGGAACAGTTGGCCCAATTCAGCAGAGATGTTGGATTGGAAAACAGAAACATTC 2843
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DB
3075 ACAAAATGAGAGAGACAGAAAGAAAGAAATTTGAGATCTACACAGAAATTTGCAGCCAA 3134
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QY 1567 sHisSerAspThrGlnAlaGlnLeuGlnIlySerThrGlnGlnIleu- -AlaIly 1586
Db 3298 - - - - -GCTCTAGAGCTTAGTCAGAAAGAAAGAAACAGCTTAAAGCCAA 3338
QY 1586 sAsnLeuAlaIleAlaIleSerAspAsnCyProIleThrGlnIlySerGlnThrSer 1606
Db 3339 AATGCTGGAAATGCGACAGCTTACCTACCTGCAATC 3377
QY 1606 aAspCysValIHisProLeuGlu- - - - -GluysIleLeuLeuLeuThrGlu- 1621
Db 3378 TCATGCAGTGTCAAGCTCGAAACCAACCAAAAGAACAAATAGAAAGCTTACTAGAGCT 3437
QY 1622 - - - - -GluLeuHis- - - - -GlnIyStrAsnGlnGlnI 1631
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QY 1631 uLysLeuLeuHisgluLysAsnGluLeu- - - - -GluGlnAlaGlnValG 1646
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QY 1646 uLeuLys- - - - -CysGluValGlnHisLeuMetLysSerMetI 1659
Db 3558 ACTGAAACAAAGATCCTCTATTTGGGTGTGAAAGAAAGAGATGAAACAAAGAAATAC 3617
QY 1659 eGluSerLysSerSerLeuGluSerLeuGlnHisgluLysHisAspThrGlnGlnIle 1679
Db 3618 ATGCGTAGAGGA- - - - -GAAAGTGTTCAGACAGATACA- - - - -ACATT 3656
QY 1679 uLeuAlaLeuLysGlnMetGlnValIValThrGlnIlyLysgluLeuGlnGlnI 1699
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QY 1719 nPheLysAsnGlnIleGlnIlyStrThrThrLysGluGlnCysLeuLeuAsnGln 1738
Db 3765 T- - - - -AAGTCTCTGAGAGAAATACTTTCTTCAAGAGCAGCT 3803
QY 1739 -LysGluLeuGlnIlySerGlnHisArgLeuGlnCysGluIleGluIleuMetLys 1758
Db 3804 AGTTGAACCTGAAGATGCTGCGCAAGAAAGATTAACGGAAGTTTCTGAGTTGACTGACA 3863
QY 1758 rLeuLysAspLysSerLeuSerAlaLeuGlnIlyThrLeuLysGluSerGluGlnLysValIleas 1778
Db 3864 GTTGAAACCAACACAGATGAAGATTCACAGCTTGAAATCTTCACATGAAAAA- - - - - 3915
QY 1778 nLeuAsnGlnIlyMetGluMetValMetLeuGlnGluGlnIlyLysAsnSerGlnAr 1798
Db 3916 -AGTAACAAAAGCCTTAGAGACAAAGACTTGAATTTAAAAAACTG- - - - - 3960
QY 1798 gThrValIleAlaGlnArgAspGlnLeuGlnAspAspLeu- - - - -ArgGluSerValGluMet 1817
Db 3961 - - - - -TCGAGGAACTAGCAGATTGAGATATTGCTGTGAAGAAACCGAAGC 4010
QY 1817 tSerIleGluThrGlnAspAspLeuArgLysAlaGlnIlyAlaLeuGlnIlyLysAs 1837
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QY 1837 pLysValGlnIlyLeuThrSerGlnIlySerValLeuGlnIlyLysIleSerLeuGln 1857
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QY 1857 uAsnGlnMetLeuThrAsnValAlaThrValLysGluThrLeuSerGluArgAspAsp 1877
Db 4116 GAGGAGCACTGTTAATTAATTAATTCGACAGTTTCTGAA- - - - -TT 4154
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Db 4215 GCGTACTCATCAGTTAAGAGAAAAAATCAATTAAGACATGAAAGCTGATATTGGA 4274
QY 1913 aArgLysThrIleAspIleThrGlnLysIleSerAsnIleGluGlnIlyLeuGlnI 1933
Db 4275 AAGCTT- - - - -CTAACAGAAAAA- - - - -GAACCTTACAGAAAGCA 4310
QY 1933 nAlaThrAsnLeuLysGluThrLeuThrLysGluValGluSerLeuIle- - - - -GlnCysLysGln 1952
Db 4311 AGAGGCAATCAGCAAGAGCTCTCTGTAAGAAAGAGCTTTGTATTAACAGATTTGAAGAA 4370
QY 1952 uGlnLeuAlaLeuAsnThrGlnHisLeuArgGluThrLeuLysSerLysAspLeuAla 1972
Db 4371 AGACTTATCTGAAAACATCAAT- - - - -CCTGT 4397
QY 1972 uGluLysMetGluGlnGlnIlyArgAspGlnAlaAlaAsnLysValIleAlaLeuThrGln 1992
Db 4398 CACATTGATGAAGAAAGAGCTTAAGAAAAAAGTTGAGATTAGCAGCTTATGTAACA 4457
QY 1992 sMetSerSerLeuGluGlnIlyLeuGlnLysAsnValIThrThrLeuLysGluGln 2012
Db 4458 ACTAAGCTGATTGAATGTTGAGCTTCAAAATAGCATC- - - - - 4494
QY 2012 yGluLysGluThrPheThrLeuGlnArgProSerLysGlnGlnIlySerSerGlnMetGln 2032
Db 4495 - - - - -AGCCTTATCCGAAAAAGAA 4511
QY 2032 uGluLeuArgGluSerLeuLysThrLysAspLeuGlnIlyGlnAlaGluLysGln 2052
Db 4512 AGCAGCAATTCATCATCACTAAGA- - - - -AAGCAGTATGATGAAGAAAA 4553
QY 2052 eSerGluAlaThrAsnGlnIleLysAsnLeuThrAlaLysIleSerSerLeuGlnGln 2072
Db 4554 ATGTGAATGCTGCGATCAGAGCTCAAGATTTATCTTTAAAGTTGACACTGATGAAGA 4613
QY 2072 u- - - - -IleLeuGlnAsnAlaSerIleLeuAsnGlnAlaValAspGluArgGluAs 2089
Db 4614 GAAATATTCGCTGTTGAGCAGTAGATGACTGTCGCAATAATTCAGAAATGAGAA 4673
QY 2089 nLeuArgHisSerLys- - - - -GlnGlnLeuValSerGluLeuGlnLeu 2105
Db 4674 GAAAGCACAGTGAAGTTTACACACATCAAAAACCTGTTAAAGATTG- - - - -CAATCA 4730
QY 2105 rLeuThrLeuLysSerArgAspHisAlaPheAlaGlnSerLysArgGluLysAspGluAl 2125
Db 4731 GCTGAGTTAAATCAAGGAA- - - - -GCTTATGAAAAGATGAGCA 4772
QY 2125 aValAsnLysIleAlaSerLeuAlaGlnGluIleLysIleLeuThrLysGluMetAsp- 2144
Db 4773 GATTAAT- - - - -TTATTGAAGCAAGAGCTTCATCAGCAAAATAAATTTGATTG 4823
QY 2145 - - - - -GluPheArgAspSerLysGluSerLeuGlnIlyGlnIlySerHisLeu 2161
Db 4824 TTTAAAGGTGAATAGAAAGACGACACAGCAAGATGAGAAAAAGAGCTTAATTGACA 4883
QY 2161 rGlnGluLeu- - - - -CysThrTrpLys 2168
Db 4884 AACAGAGTTAAAGTCTCAACACAGCAAGAAATTATGGAATTAGAGCAATATTACCGCAA 4943
QY 2168 sThr- - - - -GluLeuGlnMetLeuLysGln- - - - -GlnLysGluAspI 2181
Db 4944 AACTTATTAAATAGAGTCTTAATTAAGAGTTCTTAAAAATTACAATCAACAAAAAGATAT 5003
QY 2181 eAsnAsnLys- - - - -LeuAlaGlu- - - - - 2187
Db 5004 TGAACACAAAGAAATTTGTTCAAGAACTTCAACATTTCAAGAGTTAGAGAAAGAAAAAGCA 5063
QY 2188 - - - - -LysValLysGluValAspGlu- - - - -LeuLeuGlnHisLeuSerSerLe 2202

```

Db	5064	CAACAGCGGTTAAAGAAAGCTGAAGAAATAATCTTAACTGTAAAAACAAGTTTATTCAT	5123
Oy	2202	uLysgluGluLeuAspGlnIleGlnMetGluLeu-----	2213
Db	5124	GAAGAGCTGAATCTGAATTAAGAAAGAAAGAAATTGAAACATGTGAATTTAAGTGTGAAGA	5183
Oy	2214	-ArgAsnGluLysLeuArgAsnTyrGlu-----	2223
Db	5184	CAAGAGAGAGAGATTAAAGGCAATTGGAAGATAGCGTTGAGTCAGAAAGTGTGCAGAAATT	5243
Oy	2223	uCyGluLysMetAspIleMetGlyLysGluIleSerValLeuArg-----	2240
Db	5244	AGCAGAGCTTGAAGAGAAAAAGCTGAACAAATAATTCCTCCATTGAAGAGCACTGTTATTC	5303
Oy	2240	tGlnAsnGluProGlnGlnGlu-----	2254
Db	5304	TCAATATGGAAGAGAAAGAAAGAAACAGTATTAATAAAAGGTACAGAAAGCCATTGTGAGAGCT	5363
Oy	2254	GMetAspIleLeuGlnuSerArgAsnGlnGlnIleGlnLeuMetGlyLysIleSerI	2274
Db	5364	AAATACAAATTTGACAGGAAGAAAGAAAGGAAGTTCCATCTTGGAAGAAAACTTAATGTC	5423
Oy	2274	avalTyrSerGluGln---HisThrLeuLeu-----	2288
Db	5424	AGTGGAAAGTTCAACAGTCAGAAACCTTATATGTATCCACAGATCAGCAAAAAATGTGGCAGC	5483
Oy	2288	tGluLeuGlnLysgluThrGlnuAlaHisLysHisCysMetLeuAsnIleLysgluSerI	2308
Db	5484	ATATATACGAACAAGAAAGAAAGCAATTCACAAAGCGTGTGTGCAGAAAGACATGTGAAGAAA	5543
Oy	2308	uSerSerThrLeuSerArgSerPheGlySerLeuGln-----	2320
Db	5544	AATCAGTGTTTTACAAAGAAACCTTAACGTAAAAAGAAAGCTATTGCAGAGGTAGAGCA	5603
Oy	2321	-----ThrGlnHisValLysLeuAsnThrGlnLeuGlnIleThrLeuI	2334
Db	5604	GGAAAAAGAGAGACAGACTTCTTCTCATTTTGAATGTGATGCCAATATCCAGAGAGCGTT	5663
Oy	2334	uAsnLysPheLysValValTyrArgThrAlaAlaValLysgluAspHisSerLeuIleLys	2354
Db	5664	A-----ATAAAGCTAAGAACATGCGAGCAAGAAAGCAATGAACTGAAATATGATGAC	5717
Oy	2354	sAspTyrGluLysAspLeuAlaAlaGluGlnLysArgHisAspGluLeuArgLeuGlnLe	2374
Db	5718	TCATCTTCAAGAGAGCTTGAAGAAAAACAAAGAAATATTC-----TTGATAGTAGAC	5771
Oy	2374	uGlnCysLeuGlnGlnHisGlyLysTyrSerAspSerLysAspGluLeuLys--	2393
Db	5772	CCACACATGTGGAAAAAGAAAGAGGTAAATAATACATACAGGCAAGCAAACTTGAGAAA	5831
Oy	2394	----PheCysgluIleGluPheLeuAsnGluLeuPheLysLysAlaAsnIleIleG	2412
Db	5832	TGTGTTTGACACAGCTCCAG-----AAAACCTCCAGAGAAAGAACTTAACCTGTCA	5882
Oy	2412	nSerValGlnAspAspPheSerGluValGlnValPheLeu-----	2429
Db	5883	GATTTTGAGACAAAGATTAAGAGAGCTGATCTCTGCTTAGTAAGACAGAAAGAAATACA	5942
Oy	2429	ySerThrLeuGlnGlnGluLeuGlnHisLysLysgluPheMetGlnTrpLeuGlnGluPh	2449
Db	5943	TAGAGCTTGAATGGAAGAGTTGACCTCAAAATATGAAAAATTTTACAGGCTTTTACAAACAGAT	6002
Oy	2449	egLysPheLysIleValAspAlaLysLysLeuSerGluLysMetGlnGlnIleAsnArg	2469
Db	6003	GGATGGAAAGAAATTAACCCACAGAACTTTTGAGAGAAACAACGTGAAGAAAGTCCAAA--	6060
Oy	2469	gLeuLysSerThrIleGlnLeuLeuThrLysArgLeuLysAlaValGlnSerLysI	2489
Db	6061	-----TCACATTTGGTCCAAACCAAAATT	6083
Oy	2489	egLysArgGluLeuLeuThrValTyrLeuAsnGlnPheGluAlaLysLeu-----	2505
Db	6084	GCTTAGTACATGGAAGCCAGCAACAATGATCTGAGATTTTAATTTAGCCGGGGCAGAAAGC	6143

QY	2505	ngllylylsygluclnlnshlysglyulemeArgrgmeGlnlnshlselgProseral	2505
Db	6144	GGAAAAACAGAAATCTGGGCAAGGAGATGTGATTCAGAAA-----GACCT	6191
QY	2505	aseValmeclnclnclnlnshlnalArgrLeuGlylIeclnlythrValGlnaPrG1	2545
Db	6192	TCGAATGTTGAAAGAGGACATCGACAGAAATTTGAAATCTTAAGAAAGAAATATGTATCA	6251
QY	2545	userlylylsygluclnserArgrlyIeIysmeLeuGlnaPrGlyleuashnleuashnVallybae	2565
Db	6252	AGAAAG-----CAAGAGAAATATCAAAACAGAGACGAAGATCTTGAACGAAACACAA	6305
QY	2565	paPrAlamechlslysglyclnlysvaIaIleleuGlnaPrlyleuashnleuashnVallybae	2585
Db	6306	TTCCACATTTA-----AAACAGCTGATAGAG--	6330
QY	2585	nalGlnAlAGluLeuashnAlameclnVallyleuThrlylysglnshnashnleuG1	2605
Db	6331	-----GAGTTTAT-----ACACAGCTGGCAAAAGAACAGAGCTGGA	6371
QY	2605	nalAlameclnysGlu--IleGlnaLeuGlnlysmetValAlalyeGlyAlaValPr	2624
Db	6372	AATACCATTAAGAAACATTCATATAGGCCCCAGAGCTGAGAGCTTATAGAAAG	6431
QY	2624	oTyLyrsGlnGlnllleashnleuLystrlylysvaIvallyslleGlnmetGlnlysl	2644
Db	6432	CCATCAAGAGAGACAAATCATGTTCTTAATAAAATTCGTGAGAAAGAT--GATGATCT	6488
QY	2644	elyTySerlyshAlaThrashnGlnllleAlaTyLeuLysserGlyshnleuashnlybae	2664
Db	6489	AAAACGAACGCCAAAGATATGAAAGAAATC-----CTTATGCTCG	6530
QY	2664	sgLlnGlylyleu-----ArgArGlylyleuGlnleuashnArgrAlaGlnl	2680
Db	6531	TGAAGAAAGAAATGACTCGCAAAAGTAAAGGACCTCGACACTCACTTACGAGAGCTCGAG--	6588
QY	2680	aasPrashnashrThrValCysvalProlysaPrTyGlnlyshAlaSerThrPheProva	2700
Db	6589	-----AAGAAATACCAACAAAGCTAGACGAGAGA	6620
QY	2700	lThrcysGlyclnlyserGlylevalGlnserThrAlameclnValleuGlnserG1	2720
Db	6621	GAACCTCGGCAT-----GATATGTAAACATTTATGAGCACTTACGACGACACA	6665
QY	2720	ulysAlAlaleuclnArgrGlnleuSerthIstrlylylylylytyxthlnshleuserAr	2740
Db	6666	GCTAGCAACAGAACGACTTAAATCATGACTGATTTGAAATTTAAGACGAAGAGTTTCAGAGA	6725
QY	2740	gThmetSerSerSerGlnaPrArgrlylylystrlylysvaIlyseSer-----	2755
Db	6726	ACAAATTCACATTTAAGACCGTTTGAAGAAATAGAAAGAAATGATATATGCAACAAC	6785
QY	2756	-----AapAlahlsSerSerthIstrGlySerSerthlsArgrlyse	2769
Db	6786	TGTGGGACACCTTACAAAGTGCAATTTGTACATACGAGATGCTCATCTTTGGAGA	6845
QY	2769	rPrshlnlylythrGlu-----ThrTyArghlslelyProvalTh	2782
Db	6846	ACCTACCGAAATTTGAGATTTCGGAAAAAGCTTTTGAAGTATATGATGGCTGTGAC	6905
QY	2782	rPrGlnArgrSerGlnmetProSerleuThlsleuGlySerProlylyshSerGlnserse	2802
Db	6906	TAAACACATGCGAAAAATTTAACCACCCGATCGAAGTTCCCT-----CATGATCA	6956
QY	2802	rThlylysvaIvalSerProashnArgrGlnllleTySerGlnleuValmetSerPr	2822
Db	6957	GACTCAAAAAATTTTG-----GAAAGAGAAAGAT-----GCTCGGCTGATGTTTACTTC	7004
QY	2822	oGlylylyThrGlymet-----HlylyshlsleleuSerProserlylysvaIgl	2838
Db	7005	ACCTCGAGAGTGAATCTTCTAGTAAACCAACAGTCTGGCTTATGATTAACATGTGTGATG	7064

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QY      2838 YLeuHISLeYsArgAlaLeuSerProAsnArgSerGluMetProThrGlnHisVal11 2858
Db      7065 GCTC-----CGATCTTCATCTTGAAGAAGA-----GT 7091
QY      2858 eSerProGlyLysThrGlyLeuHISLysAsnLeuThrGluSerThrLeuPheAspAsn-- 2877
Db      7092 GACATTGGGTGACTGCTGCTTG---GAAACTGTCCACACTGCTACTCTTTGGAATGA 7148
QY      2878 -----LeuSerSerProCysLysGlnGlnLysValGlnGluAsnLeu 2891
Db      7149 AGTTGCATTCAGGGCCCTCATGTAGCCAAAGACCAAGAAATACTG 7197

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Search completed: October 23, 2003, 03:02:08
 Job time : 2885 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 21:06:57 : Search time 33 Seconds
(without alignments)
3787.463 Million cell updates/sec

Title: US-09-724-584-1

Perfect score: 14769

Sequence: 1 MSEGDAVAVCVRRVRLIORE.....QAENWYBAKKEAECTS 2954

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3615	24.5	2662	4	US-09-595-684B-31
2	1148.5	7.8	3248	1	US-08-353-700-1
3	1148.5	7.8	3248	5	PCT-US95-16216-1
4	1055.5	7.1	2482	1	US-08-328-254-6
5	1051	7.1	1388	4	US-09-572-191-2
6	1051	7.1	1388	4	US-09-723-262-2
7	1051	7.1	1388	4	US-09-723-219-2
8	1020	6.9	3878	4	US-09-914-259-11
9	953	6.5	1234	4	US-09-592-054-8
10	945.5	6.4	1232	4	US-09-592-054-2
11	943	6.4	1231	4	US-09-595-684B-23
12	906	6.1	1375	4	US-09-722-139-2
13	906	6.1	1375	4	US-09-721-832-2
14	906	6.1	1375	4	US-09-721-689-2
15	890	6.0	963	4	US-09-914-259-20
16	887	6.0	963	4	US-09-914-259-22
17	877.5	5.9	1031	4	US-09-914-259-24
18	874	5.9	967	4	US-09-914-259-21
19	873.5	5.9	957	4	US-09-914-259-16
20	868.5	5.9	975	4	US-09-914-259-19
21	867	5.9	956	4	US-09-914-259-17
22	866	5.9	10182	4	US-09-134-001C-3159
23	856	5.8	1032	4	US-09-914-259-26
24	847	5.7	1027	4	US-09-914-259-27
25	841.5	5.7	1279	4	US-09-724-517-2
26	841.5	5.7	1279	4	US-09-641-807A-2
27	841.5	5.7	1279	4	US-09-723-096-2

28	812.5	5.5	935	4	US-09-914-259-25	Sequence 25, Appl
29	795.5	5.4	928	4	US-09-914-259-23	Sequence 23, Appl
30	770.5	5.2	815	4	US-09-914-259-18	Sequence 18, Appl
31	769	5.2	3696	4	US-09-134-001C-5080	Sequence 5080, Ap
32	763	5.2	955	2	US-08-428-414A-3	Sequence 3, Appl1
33	759	5.1	955	1	US-08-006-676B-1	Sequence 1, Appl1
34	759	5.1	955	1	US-08-282-845-2	Sequence 2, Appl1
35	759	5.1	955	5	PCT-US94-0034-1	Sequence 1, Appl1
36	758.5	5.1	1066	3	US-09-541-782-8	Sequence 8, Appl1
37	758.5	5.1	1066	4	US-09-723-820-8	Sequence 8, Appl1
38	756.5	5.1	1637	4	US-09-718-692-2	Sequence 2, Appl1
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45	744.5	5.0	2101	1	US-08-467-781-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1

US-09-595-684B-31

Sequence 31, Application US/09595684B

Patent No. 6544766

GENERAL INFORMATION:

APPLICANT: Berand, Christophe

APPLICANT: Ohashi, Cara

APPLICANT: Sakowicz, Roman

APPLICANT: Waisberg, Eugeni

APPLICANT: Wood, Kenneth

APPLICANT: Yu, Ming

TITLE OF INVENTION: Human kinesins and methods of producing

TITLE OF INVENTION: and purifying human kinesins

FILE REFERENCE: cytop036

CURRENT APPLICATION NUMBER: US/09/595,684B

CURRENT FILING DATE: 2002-06-24

PRIOR APPLICATION NUMBER: 09/295,612

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 31

LENGTH: 2662

TYPE: PRT

ORGANISM: Human

US-09-595-684B-31

Query Match 24.5%, Score 3615, DB 4, Length 2662;

Best Local Similarity 32.0%, Pred. No. 2,6e-169;

Matches 995; Conservative 570; Mismatches 935; Indels 614; Gaps 85;

QY	1	MSEGDAVAVCVRRVRLIORE--GQANLQWRAGNNTTSQVDGTSFNFDRVFNHSTG	58
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QY	59	QIYQEIAPVIRISALQVNGTIFAYGQTSSTGYTMMGTPLNSLGIIPOAIOEVPKIIQEI	118
DB	61	NYVEEIAPIIDISALQVNGTIFAYGQTSSTGYTMMGTPLNSLGIIPOAIOEVPKIIQEI	120
QY	119	PRREFLLRVSYMEINETYKDLLCDRKKPLEIEDFPKRVNVVADLTETELVMVPERHVG	178
DB	121	PRREFLLRVSYMEINETYKDLLCDRKKPLEIEDFPKRVNVVADLTETELVMVPERHVG	180
QY	179	WIKKGEKRNHYGETYKNDHSSRSHITFRMIVSRPNRDNPTNSGNDGAVMVSHLNLDVDA	238
DB	181	WIKKGEKRNHYGETYKNDHSSRSHITFRMIVSRPNRDNPTNSGNDGAVMVSHLNLDVDA	237
QY	239	GSERAAQTGAAGVRLKEGGINRSLFIIGQVIRKLSDGQAGFVINYRDSKLTIRIIONSG	298
DB	238	GSERAAQTGAAGVRLKEGGINRSLFIIGQVIRKLSDGQAGFVINYRDSKLTIRIIONSG	297

QY	299	GNAKIVIICTIPVPEFDELSTJQASPAKHYRNPVHNVYDDPALLKRRKELTJDK	358
Db	298	GNPKRIICTTIPVSEFDELTRJQASTAKTKNPNVYVSTDBALLKRRKELTJDK	357
QY	359	QLENSSSETKAQMAKEBHTQJLAELKQJHKEDEIRIMHJTNIVASQES--QODRV	417
Db	358	QLE--EVSLETRAQAMEKDOQLAELKEKDLQKQVNEKINENLTRLVYSSSLTJQELKA	415
QY	418	KRKRVTYVAPKQJNSLHSGVSDPDMJSLRPGNFSKAKFSQDMSFPEIDDSVCTEFS	477
Db	416	KRKRVTWJLQKJNKKNKSNYADQPN--IPTNITTYTHKLSIMJLREIDSVCSBESD	471
QY	478	FDDALSMDSNSGIDAEMLASQVTRHEKTSJLHQSINIDGQJSDSQVHDSKKNQJLYR	537
Db	472	FSNTJDTJS---ELEMPATKJLQOE-----	494
QY	538	KDSGDMACRKAQFPEKJITTSJQOQJQSKEEKEKJLQVSEFKJALBEQJLSVAKNLEMV	597
Db	495	-----NIESE	499
QY	598	TNSRPHSINAQVQIDVEKEVVRKENSJVLGDSGYNASNSDLQDSSVDGKRLSSHDECHE	657
Db	500	LNS-----	502
QY	658	RKMJEQKJVDLEEFJENLNKKSSENDQKSSBQDPHESJQLOEBAJMAKAMJLEJALMRD	717
Db	503	-----LRA	505
QY	718	NFDNIIENETJKEBIADJLERSJKEQNETPEJLEKETQHEHQELIHEJGSLKJLVEN	777
Db	506	DYDNLVDYQJRTKEMELKJRKNDLDEEALERTKQDQEMQJLHEJLSNJKLVKH	565
QY	778	AEVYNQJLEBDJETKJLKQEOJQJLAELRKRAQNLQKQVNFJLSVSMGQSEKJCEBIF	837
Db	566	REVVYQJLENEJLSKVEJLREKEDQIKKJQOYIDQKJENIKMDJSTL---ESIEDPK	621
QY	838	QJQJSLSAEAVTRQJQKQCSFTJSENEJLEKEMEDTJNMVYNQKEMKASJLEKQJLETFKS	897
Db	622	QKQJTLFPAETVALDAKQESAFJRESENEJLEKEMELATTKQJEMENDJQJQJQJLEA--	679
QY	898	NYKKMEADJQKQELQSAFNEJNYNLQJLQKVPJDLJSVEJLEKQVSEFSKQJLEKALEEKN	957
Db	660	--KQJQVJLEKQJSAFNEJITKJLSJLQKVPJDLJCLBEJGKJTDJQKJLNEVEBENE	737
QY	958	ALENEVJTLSEKJFLPNVEEKLQJQISKASEJIMJLQJGHSASJISKQJIIWQJQSEQ	1017
Db	738	ALREEVJLJLEKJLSPSEVERJLREJQJQKSEBHIITSEKQJFSEVYVHKSRAVQJLLE	797
QY	1018	JLQJLDEVTJHQSKQJQTEBOJQJLEKKNHNDJLFKY-----JRNKSEADJLREMENT	1070
Db	798	JGKTJDDJLATTQSNYKSTDOEFQNKJLAMPFOEQKYKVLNEENRMOJIVNLSKEAQKF	857
QY	1071	KJGMEVSEVKAJDTJGHEJLEETJJDKEQJLHEKQVFPQAMQJTIPTJPLSDJLPSKJLVG	1130
Db	858	DSJSLGKJTLBJSYKJQJQJLEKJREJQJLNEJQJLEKQJLEN--RDSJQJYEREXJLTITE	915
QY	1131	NSQJQJIEJNDYVHJLJALATERNNJWJLCTERNJSJKEQV-----JDLNTQJLSQJQAS	1183
Db	916	KJQJQJL--EJVKTJQJQKDJLQJQJQESQJERDQJKSDJHDJVMNNJIDQJQJLNAJESL	973
QY	1184	JEKSDJQKQJQDLEGEVJLJLMEJLKGJLTD---SQJLSJEKJQJLENJEVTEKJQJLQ	1239
Db	974	KJQJETJNLTKJQJISE--EVSJRNJLMEJNTGETJKEFQJQKQVQJIDKQ--DJL--AKNTQJTLT	1029
QY	1240	JEKKNJITJ-----ERNJQJTFEJDLKQJHSDJLQJLJSGNTEQJQJSETQJDEJLRAA	1287
Db	1030	ADVQKJNEJIEQJQKJFSLJQJKNELQJQJLSEVJAEKQJLKTJDLKENJEMTJENQJEBJRL	1089
QY	*1288	QJELREKQJLVDSFQJQJLQJDSQVJSGJSPNHDAVANAQJQVSYSGJEVNSJQJSEM---LRGE	1342
Db	1090	GJELKQJQJQJIVAEQJKNHAKJ--KEGJLSJSTQJRLAEVEKJLKEKQJQJQJQJQJLQJQJLE	1148
QY	1343	JQJDELQJTSKALVSEJLEJLRAVKS-----VEGENJETTKJLNGJLEKEJLJGKSEBSEVJ	1395

Db	1139	MSENQCK-----INLENKAKELKAKKELLLENHETBERLEAKKLLENBEVANSITKERVYL	1204
Qy	1396	KSMLENKEDNNKLEQAEYSSKENPDSLEEVFSQKLVDEIVLKAQKAAERLEI	1455
Db	1205	KELQSPETERDHLRGY-----IREIATGICHTKEELKIAHILKEHQETIDE	1252
Qy	1456	KDRDYFE-LVQPTANTNLVEGLTEPRLQD---HEED-----SIDRSEEM-EIKVLG	1502
Db	1253	LRRSVSEKTAQIINTQDLE-KSHTKLOEIPVLHNEEOELLBNVKKVSTQSTQNMNELLELT	1311
Qy	1503	EK-LEBNQYLLERLOEEXLESNKLEILOKEMETSVLLKDLOOLKEBLSYENITLKENI	1561
Db	1312	EOSTTKSDTTLARIEMERLYRNEKFOEBOEIKSLTERDYLKTIKELBYKHQOKENI	1371
Qy	1562	DTTLKHSDDTOAOKTOQOELQALAKNLAAASDNCPIITQEXE---TSADCVHPEEKILL	1618
Db	1372	RETL-----AKIQESQSQEOGSLNMKEKNETTKIIVSEMEQFKPKDALLRIEIMVLG	1424
Qy	1619	LTEELHQKTNOEQKILHNEKMLEBOAQVHLKEVEHLMKSMYESSLSLELOEHKNDTBOQ	1678
Db	1425	LSKRLQESHDMKSVAKKEDLOLQLOEVLQESQOL-----KENIKEIYAKHLEETEE	1477
Qy	1679	L-----LALQOQOVAVTOEKKELQOOTHENTHLYAEVHLKENIE-LGLENFNEAQOKTTQEOC	1733
Db	1478	LKVAHCCIKKEBEETINELRVNLSEKE---TEITIQOKALINDKQIANKIQLIYEKBEQ	1533
Qy	1734	LLENKELEBQSHRLQCEIEBELMKSJKDKESAEITLKESEQVNL-----NOQEMEV	1786
Db	1534	L-NIKQISEVQENVN-ELKQFKERAKQDASALQSI---ESKMLELTVRLQESQEBIQIM	1587
Qy	1787	MLEMBELKNSQRTIYAERDQLODDLRESVEMSIETODDLRAQALQOQKQVLELSQI	1846
Db	1588	IKKEBEMKRVQEAQIERDQLEKNTKEIVAKMKSQOE-KESQOLKQTVAVNETEKMCEI	1645
Qy	1847	SVLOEKJSL-----LEN-----OMLY-NVATVUKETLSERDDLNQSKOHLFSEIETLS	1892
Db	1646	EHLKEQETQKLANENIETENIRLTQIHLHNELEMRSVYTERDRLRSVEETLKXERDQK	1705
Qy	1893	LSLXER-EFALEQAEKDK-----ADAAKRTIDITEKISNIEBOLLQOATNIKETL-YERE	1945
Db	1706	ENLBEETIRPLEQEKBELKIYMHLMKEHQETID---KLRGIVSEKTNEISNMQKLEHSND	1762
Qy	1946	SL-----IOCKQALNTEHLEFETLSKQDLAGKQOEERDEAKNVATLTEMSSLEBGIN	2001
Db	1763	ALKAQDOKTIOBELIYAHNHLKEQOETIDKLRGIVSEKTTDKLSNMQKLENSNAKLOEITQ	1822
Qy	2002	ENVTTLKEGEBEKRTFYLORPSKOSSQOMELYESIKTQLOJQEBABKEISEATNETIKN	2061
Db	1823	E-----LRANEHQIITLKQDVNETQKYSSEHQKKQIKQOSLTLSKL-----ETEN	1869
Qy	2062	LTAKISSLEEBILONASILEAVERENLRHSHKOQVSELEQSLTL---KSRDHAPAQ	2117
Db	1870	L-----NLAQGLHNLEEMKSVMERONLNRVBEETIKLERQOLKESIQOETVARDLQOE	1924
Qy	2118	-----SKREK---DEAVNKIASLAEIKILYTEMDEFRDQSKSLQESQSHSEELCTY	2167
Db	1925	LKTARMLSKSEKETVQDKIREKISSEKTIQIADIQDLDK---SKDELQKQIOELO-----	1975
Qy	2168	KTELQMLKQOEEDINNNKLAEKVKEVDEL-----LOHLSLSKEQLODOIOM	2211
Db	1976	KKEIQOLLR-VQEDVNMGS-HKKINIMEQOLKQOFBNYIJSKEMDNFOLTKLHESLEEBTRI	2033
Qy	2212	ELR-NEKLRNVELECKMDIMEKIESVLRML-----QNEPQOE-EDDVAESMDILS	2260
Db	2034	VAKRDELRIRKESLQKYE-RDQFALATREMIARORONQVQKPERKLLSDGOQHIMESLRE	2092
Qy	2261	RNOEIOELMEKISAVYSEQHTLSSLSSELOKETEAKHQCMLNKESLSTLSRSFGSLQ	2320
Db	2093	KCSIRIKELLKRYSEM-VDHVECLNRLSLDLEKELEFHR-----	2129
Qy	2321	TEHKLMTQLOTLNKRKV--YTTAVKEDHSILKQYEKDLAAEQKHDELRLQLOCLE	2378

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Db 2130 -----IMKLTAVLSYVTKIKEOEHCINKFEMFIDEVEKOKELLIKIQHLQ 2177
Qy 2379 QHGRKMSDASBEIKCEIEFLNELLPKANIIOQVDDPSEVQVNLNGVSTLOEELH 2438
Db 2178 QD-----CDVPSRELRLKLNQNMWL-----HIEILKPFSEBE--FPSIKTEFOQVLN 2225
Qy 2439 KGFQWMLFEFDLHDVAKKLSGMOQENRIASTQLTLTKLKAJVSQSI---OREITV 2495
Db 2226 RKEMTQFLEWMLNTRFDIKLKNGIOKENDRICQVNNFPNNRIAIAMNSTEREEBSATI 2285
Qy 2486 YLNOFEAKLOEKKOEONKELMRMRHHGSPASVMEENBARLGLTKTVODE-----SKKL 2549
Db 2286 -SKWEQDLSLKEKNEKLEFKVYQTLTKLSAQVNL-----PTQONKMPHYVSRAT 2337
Qy 2550 Q---SRIMKLENLVKKDDAHKGEKVALLODKL--LSRNAEELNAMOYKLTCKODNIQ 2605
Db 2338 QUTTEKIRELENSLHAKESAMHESKIIKQKELEVTNDIIDLK---QAKVHESNKLE 2394
Qy 2606 AAMKEIENLOKAVKAVPYKEIDNLKTRVYKIEKIKYSKATDOEIAVLKSCLEDE 2665
Db 2395 KTKETIQLVLDKVALGAKPYKEIEDLKKLVKIDLEKNAKAEFEKEISATKATVEYOK 2454
Qy 2666 EGLRLKLELRBAQDNITTVCPKDYQKASTFPVTCGGSGIVOSTAMLVIOSEKALE 2725
Db 2455 EYIRLLREMLRKSQAQODTSVISEHTDPQPSNKPPLTCGGSGIVQNTKALLIKSEHIRLE 2514
Qy 2726 RELSHYKKKKYHHLSTRMSSEDEKKTAKASDAHSSTGSHRSGPKTITYR---HGPLYT 2782
Db 2515 KEISIKLKQONQOL-----IKQKNELLSNNQHLSNEVKTKEKERTLKEBAKQYT 2562
Qy 2783 PRSEMPSLHSGPKKSESSTKRVVSPNNSIYLSQVMSPKTCMHKHLISPSKVLGHLK 2842
Db 2563 CE-----NSPK-----SPKVTGT-----ASKK 2579
Qy 2843 RALSPNREMPTOHYVISPCKTGLHKVLTSTLFDNLSPCKQKVOENL--NSPKGLRD 2900
Db 2580 KQITP-----SOCKERNLDDPVPKSPKSCFPD 2607
Qy 2901 VAKSKMPY--CPSQFQDNKSLGDFSELTNTAESNDKSAENWYBAKETIPECKT 2953
Db 2608 SRSKSLPSHPVPRYPDNSSLGLCPVONAGAESVDSQPGPMHASSGKDVPECKT 2661

RESULT 2
US-08-353-700-1
; Sequence 1, Application US/08353700
; Patent No. 5599919
; GENERAL INFORMATION:
; APPLICANT: YEN, TIMOTHY J.
; APPLICANT: RATTNER, JEROME B.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A
; TITLE OF INVENTION: TRANSGENICALLY-EXPRESSED KINETOCHORE PROTEIN,
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DANN, DOREMAN, HERRELL AND SKILLMAN
; STREET: 1601 MARKET STREET, SUITE 720
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,700
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, JANET E.
; REGISTRATION NUMBER: 36,252

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; US-08-353-700-1

Query Match 7.8%; Score 1148.5; DB 1; Length 3248;
Best Local Similarity 20.5%; Pred. No. 3,3e-48;
Matches 716; Conservative 605; Mismatches 1159; Indels 1019; Gaps 139;

Qy 81 FAYGQTSSGKTYTMMGTSPSLGIIIPQALQEVKIIQEIPIRREFLRVSYMEIYNETYKDL 140
Db 99 FOEGQLNSGK-----KQIEKLDELRLCKSELEERSQAAQASADVSUN 140
Qy 141 LDDDRK--KPLEIREDFENRVVYADLTFEELVMVPEHYIQWIKKGEKURHYGETKMDH 197
Db 141 PCNTPOKFTTTLTTSQYISGSKY--EDLKEKYNKEVE-----ERKLEAVKALQA 190
Qy 198 SSRSHITFMIVIESRD--RNDPTNSE--NCDGAVWVSHNLVDLAGESRASQTAGEVRLK 254
Db 191 KKAQQLPQATNHHDDIANHQAASSVFSMQEKTSHLS-----SNSQRT----- 235
Qy 255 EGCNINRSLFLIGQYIKLSDQAGFIYRDSKLT-----RLNLSLGNAKTVICTI 309
Db 236 -----PIRDPFSASYFSGELEVTPTSRSTLQIGKDANSSFPGNSS----- 275
Qy 310 TPVSPFDELSTLOFPASTAKVANTPHVNEVLDDLEALKRYKREIDLLKQLENNLESSSET 369
Db 276 SPHLID-----QLKQNOELRN--KINEL--ELRLQHEHE--MKQVVKFQ----- 316
Qy 370 KAQAAKEBHQLAEIKQLHKEREDRIWHLTNIVASSQESQODQVRK-----KR 421
Db 317 ELQOLEKAKVELLIEKEKVLNKCDELVATTAQYQASATKYVALQKLLKLEDSQCRQ 376
Qy 422 RVTMAPGKIQNSLHASGVSDPMLSRLPGNF-----SKAKKS--DMPSPPEIDDSVC 472
Db 377 NAEARSCLSEQKIKEKEKEFOEELSRQGRSFQTLDOECIQMKARLTOELQCAKMMHNVILQ 436
Qy 473 TEFSDFDALSMWDNGIDAEWNL-----ASKVTHREKTSLSHOSMIDFQISDSVOFHS 527
Db 437 AELDKLTVKQOLENNLEFFKQKLCRAEOAFASQIKENELRSHBEMKKENNLKSHSE 496
Qy 528 SKENOLOYLPKDSGMAECRKASPEKEITSLQOOLQSKKEEKELVQSEFLKIALEBOL 587
Db 497 QKAREVCHLEALKNIKQCLNOS-----QNFALBKAKAKTSGETMLRDLQEKINQOENSL 551
Qy 588 SYKAKLEKVTNRSRHSINAEVQTVDEKEVVRKENSVLDSGYNANSNDLQSSVDGKRL 647
Db 552 TLEKLKLVAA-----DLEKQDSCDILLKRR-----EHHIEQLNDLSTKTERESKAL 598
Qy 648 SSHHOCIEHRCMLKOKIVDLEEFLENLNLK-----SENDK-----QKSSSEDDPMS-----IQ 696
Db 599 USA-----LELKKEVEYELKEEKLTFSCWSENEKLLTQMBSEKENLQSKINHLE 648
Qy 697 LC-----EAIMAKANALEBELALMBDNFNILLENETTLKREIADLERS-- 739
Db 649 TCLKTQOQIKSHENYRNVATLEMDRENLSVEIRNLNVDSDKSVEVETQKLAIMELOQKAE 708
Qy 740 -----LKENQETNEFEIILEKETQKHEADQIHEIGSLKKLVENAEYNOVL 785
Db 709 FSDQKHQKEIENMCLKTQLTQGVDDL-----EHKLQLLS-----NEIMDXDRCY--QDL 756
Qy 786 BEDLETTKRLKLEGEIQL-----AELRK 808

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Db 757 HAEYESLRDLKSDASLVTHNEHORSRLAFDOOPAMHSPANIGGSGMPSEBRSRCL 816
 QY 809 RADN-----LOKVENFDLSVM-----GDSEKLCFEEFOLKOSLDAEAVTRDQKE 856
 Db 817 EADQSPKNSALIONRVDLSLEFSLESOQMSDLQOKOEBELVOIKGELE--ENLMKAQOM 874
 QY 857 CSFLRSNLELKEKEMEDTSNWN-----OKERASLFEKQETESNKKME-- 903
 Db 875 QSFVAETSORISLQOEDTSAHONVAETLSALEKKEKELQDLNDKVTBQAEIOELKKS 934
 QY 904 ---ADLOKELO-----SAPFNINVLNGL-----AKVRPDL 933
 Db 935 HLEEDSLKEJOLSETLSLEKENSIIISLNKREIEBELTQENGTLAKINASINQOKXNLI 994
 QY 934 SRV-----ELEKKVSEFSKOLE-----KALEKNA-- 958
 Db 995 QKSESFANYIDEREKSISELSDQYKQKLLQRCBETGNAYEDLSQKYAAGEKKSLE 1054
 QY 959 -LENEVTCLSEYKFLPNEVECLKNQISKASEETML-LKQEGHSAIISKQEIIMO-- 1012
 Db 1055 CLINECTSLCENR--KNLELOQLKEAFKHEQEBFLTKLAFEEHNNQIMLELFTVOQALRS 1112
 QY 1013 -----BOSE-----OILQLTDEVTHOSKV-----QOTEOYLEMKKMH--DLFEK 1052
 Db 1113 EMTDNQNSKSEKAGLKOELMTLKEBONKQKEVNDLLOENBQIMKMKTKHQCUNLESE 1172
 QY 1053 YIRNKSEADLLREMENTLKQTM-----SVEVKIADTKHELEETTRDKE 1096
 Db 1173 PIRNSVAKERSEHNOQCFQMDLVEKISLDSYNAQVLQLEMLNKLKLOESKEKE 1232
 QY 1097 QLLHEKKYFFQAMOTIPITPLSDSLPPSKYLVGNSODPPEINDY-----HNU 1144
 Db 1233 CLQHE-----LOTI-----RGDLTSLNQMOSQOESISGLKDCIDEKYSISGPHLE 1279
 QY 1145 IALATERNNIMVCLETERNSLKEQVIDLNTQLOSLQASIE-----KSDQKQKODL 1196
 Db 1280 STSQONNAHOCSLQTTANKLNE--LEKICEILOHEKELVTELEBDSRSECTITATRK 1335
 QY 1197 EBEKVLLLEMLLKG-----HLLD 1216
 Db 1336 AEEVGLKLENEVKILNDSCGLHAGELVEDIPGEGFBGEPNQHVPVSLAPIDESNVEHL-- 1394
 QY 1217 SQSIEKLOENLEVEKQOTLOEBMKNTIENNELOTFEDLKAHDSLKODLSNINQ 1276
 Db 1395 --LSDREVQMFALQEKELSLQSEHKILHDOHQMSKMSKSELQTYVDSLK--ABNLVL 1449
 QY 1277 SIETODELRAAOBELREOKOLVDSFRQOOLDCSVGISPNHDAVANOQKVSLOEVNLSQS 1336
 Db 1450 S-----TNLNFQODLVKEMQL--GLEBGLVPSLSSCVDPSSLS--SLGD--SSFYR 1497
 QY 1337 EMLRGERDELQTSKALVSELE-----LIRAHVKSVEGENTETTRKNG 1380
 Db 1498 ALLE-----QTGDMMLSLNLBGAVGSANOCVDEVFCCSLQTYVDSLKAENLVLSTNLN 1551
 QY 1381 LEKEILKGE--ESFVLKSMLENLKEPDNNKLK-----FOAEYS-- 1417
 Db 1552 PGODLVKEMQLGIEBGLVPSLSSCVDPSSLSLSDSSFYRALLEQTGDMMLSLNLEGV 1611
 QY 1418 SKENOFSLSEEV-----SGSQKLVDEI--EYTKAQLKAAERLE-- 1454
 Db 1612 VSANQOSVDEVFCSLOEBENLTKETPRSPAKGVLEBESLCEVYRQSLKEBKESQOI 1671
 QY 1455 IKORDYFELVOTANTVLE--GKLETPLOQDHE--EDSIDRSEMEIKVGLKERNQYL 1511
 Db 1672 MNKKELOEBOLLSERROELDCIRKOYLSENEQOQKLSVTLMESEKLAQKQEQS 1731
 QY 1512 LE-----RLOEKLEISNKLLEIIOKEMETSVLLKXDLQOQLESLSNIIKKNIDITLKH 1567
 Db 1732 LELVAKLOLOGIDUSSR-----SLGIDIEDAIOG-----RNSCISKXH 1773
 QY 1568 HSDTOAOLQK-----TOOELOL-----AKNIIAASDNCPTQOKET----- 1604

Db 1774 TSETTERPKHDVHOICDHOAOQDLNLDIEKITTEGAVKPTGECGSGQSPDTNYPEPBGD 1833
 QY 1605 ----SADCVHPL-----EKKILLTEELHOKTNEOKELHKEKNELEQAO 1644
 Db 1834 KQOGSECSISELSPSPNALVMDPLGNQEDIHNLQKRVKETSNEMLRLHLYIEDRDR-- 1891
 QY 1645 VELKCEVHLMKSMIESKSLSLQHEKHDTEQOULA-----LKQOMVVOEKKELQ 1697
 Db 1892 ----KVESILNEMKEIDSKL-----HLOEQVQMTKIEACIELEKIVGELKENSJLS 1939
 QY 1698 QTHENHTAIVDHLKENIEL--GLNFKNEAO--QKTIKEQCLLNENK-----ELEOS 1744
 Db 1940 EKLEYFSCDHOELQVETSEGLNSDLEMHADKSSREDIGDVAVAKNSWKSRFLDVERE 1999
 QY 1745 OHLQCE-----LELMKSLDKESALETIKESPOKYI--NINQEMEMVLMEMEL 1793
 Db 2000 LBRINSEKASIHENHAYLEADLEVQVOTELCLCEKNENKQKIYVLEBELSVYTSERNOL 2059
 QY 1794 KNSQRTVIAER--DQLODDRESEVMSTET-----QDLRKAQOALQOQKDK 1838
 Db 2060 RGEIDTMSKKTALDQISEKMEKETO--ELESQSECLHCIOVAEAVEKETEELLOTLSSD 2118
 QY 1839 VOELTSQISVLOEKISLENQMLVNAVATYKETLSERDNLQSKOHLFSEITFLSLSEK 1898
 Db 2119 VSELKDKTHQEKQSLSEKOSQALSTKCELENGIOALNKEKELLVSESLQARLS 2178
 QY 1899 EF-----ALEQAEKDYADAARKTIDITEKISN-----EEOQLQOATVL 1937
 Db 2179 DYKELNVSALAEALVKEGFALRLSTQOEBVHOJRGIEKLRVNIADDEKQOHLAETL 2238
 QY 1938 KETLYRESLQOCKQOLANTHEBELTKSDQALAGNKEOERDEANRYALITKMSLSLE 1997
 Db 2239 KERERENDSL--KQVLENLELOMSSENEBELVI--LDAENSKA-----EVELTK 2284
 QY 1998 EOINENVTTLKEGE-----GEKETFYLOPPSKQOSSOWEELSESUKTQOLOJEPEK 2050
 Db 2285 TOIEEMASLKFELDVLTTLSSEKNLTQIOEKGQSLSELDKLSSTRKSLLEEKQOAI 2344
 QY 2051 EISEAT-----NEIKNLTAKISL--EEBEILQ--NASLINEAVSERENLRHSKOQV 2099
 Db 2345 QIKESKTAVENTLOQLKEINBAVALGQDEIMKATQSDLPRIEHHQJRNSTEKIRA 2404
 QY 2100 ELE-----QSLTSLSRDHAFAQSKREKQDVAUNKIASLAEIKILTMD--EFRSK 2150
 Db 2405 RLEADEKKOCLVLOOLK-----ESEHNDLKGREVENLEBELIARTQOENALAEANSK 2459
 QY 2151 ---ESLOQSSHLSBELCTYKTELQMLKQOKEDINNKLAEKVKEVDELLOHLSLKEQD 2207
 Db 2460 GEVETLYAKIGMTQSLGELBDVYTTISEKENLTNLELOKQOERSEL----- 2507
 QY 2208 QIOMELRNEKLRNVELCEKMDIMEKELSVLRMONEPQOEDDVAERNDILESNOEIOE 2267
 Db 2508 ----EINSSPEN-----ILOKEQEKVQMEKKSSTAMEMLOT--QJKE 2545
 QY 2268 LMEKISAYVSFOHTLS--SLSSLOKETBAHGHCMANTESLSTISRSFGSLQTHV 2324
 Db 2546 LNERVAAAHNOEACRAKQONLSQVE-----CL-----ELEKAOQLQGLDEAKNYYI 2593
 QY 2325 KLNTQLOTLNKKFKVYRYTAVKEHDSLIKDYEKDILAEOGRHDELRLQCLCEOHGRKW 2384
 Db 2594 VLOQSVKVLQIE-----VEGOKKLEKKEDEIRIKKNQIDQOQOLVSKL 2637
 QY 2385 SDSASEELKF--CEIEFLNELLFKKANIITQSVQDDSEVOVFLNOVQSTLOELE--HK 2439
 Db 2638 SQVBEHOLMKEONLDELNLTLVELEOKIQOVQSKNASTLODTLEVLOQSSYKNLENELETLK 2697
 QY 2440 KGFQOMLEEFQ-----DLHVDACK--LSEGOQOENRRIASITQILTRKRAV 2485
 Db 2698 MDKQSFVKKVNMKTAKETELQERHWEHMAQKAELOEBLSGKNRLAGLOLLEBETIS-- 2755
 QY 2446 QSKLOREITVVLNOFEALQEKKEQONKELMRMEHGHGSPASVMEENARLLGLITKTVODE 2545
 Db 2756 -SKDQ-----LKELTLENSBELK--SLDCMKKQDYKEKG--KYREE 2791

QY 857 CSEFLRENIEMKEMDTSNWN-----QKKAFLFEKOLETEKSNYKME----- 903
 DB 875 QSFVAETSORISKLOEDTSAHQNVAVETLVALENKEKEJQLLNDKVEETOAELOELKKN 934
 QY 904 ---ADLOKLO-----SAPNEINYLGL-----AGVRPDL 933
 DB 935 HLEBLSKLOLSETLSLEKEMSSISLANKREIELQENOTLKEINASLNQEKNNLI 994
 QY 934 SRV-----ELEKVSEFSKOLE-----KALEKKA--- 958
 DB 995 QKSEFANYIDEREKISELSDQYKOEKLIILQRCETGNAVEDLSQKYAAQEKNSKLE 1054
 QY 959 -LENFTCSEYKFLNEVECLKNQKSKASEIML-LKQEGHSAISIKQELIMQ----- 1012
 DB 1055 CLNBECTSLCENK--KNELBOLKEAPAKEHOFETYLAFAERNQNLMELETVOQALRS 1112
 QY 1013 -----EOSE-----OILLOTDEVTHTOSKV-----OOTEBOYLEMKMHMD--DLFEK 1052
 DB 1113 EMTDNQNNKSEAGGLKOEIMTLKEBQNKQKEVNDLQENBOLMKVMKTKHECQULESE 1172
 QY 1053 YLRNKSADBLREMEMLKGTME-----SVEVKIADTYHELEETTRDXE 1096
 DB 1173 PIRNSYKERESERNQCNFKPQMDLEYKEISLDSYNQOLVOLBAMLNKEKLOQESKEKE 1232
 QY 1097 QLLHEKVFQAMQTFPITPLSDSLPRKLVGNSQDPLEINDY-----HNL 1144
 DB 1233 CLQHE-----LOTI-----RGDLTSLNLOMOQOEISGLKCEIDAEKXISGPHLE 1279
 QY 1145 IALATERNNIMVCLTERNSLKEQVIDLNTQLOSLQASIE-----KSDLQKRPDL 1196
 DB 1280 STSQNDNALQCSLOTTMKNKNE-----LEKICEILOAEKVELTELNDRSRSECTITRCK 1335
 QY 1197 EEGEVLLLEMLLKG-----HLLD 1216
 DB 1336 ABEVGLKLNBEVKILINDSGLLHGLVEDIPGGEFGQPNQHPVSLAPLDESNSYEHLLT- 1394
 QY 1217 SOLSTEKLOENLEVEKLOTOLOEMKNITIERNELOTNPEDIKAHDSIKOLSNINQ 1276
 DB 1395 --LSDDEVQMHFAELOEKFLSTLOSEHKILHDQHCQSSKXSELQTYVDSLK--AENLV 1449
 QY 1277 SIETODELRAAOELREKQKQVDSFRQOLDCSVGSSPNHDAVANQEKVSLGEVNSLOS 1336
 DB 1450 S-----TNLKNFGQDLYKEMQL--GLEBGLVPSLSSSCVDPDSSLS-----SLGD--SIFR 1497
 QY 1337 EMIRGERDELQTSKALVSELE-----LIRAHVKSVEGENEITTKLNG 1380
 DB 1498 ALLE-----QTDGMSLLSLNBGAVSANGQSVDEFCSLQTYVDSLKAENLVSLTNLAN 1551
 QY 1381 LEKEILIGSE---ESEVLKSMLENLAKEDNNKL-----FOABEYS----- 1417
 DB 1552 FGQDLYKEMQLGLEBGLVPSLSSSCVDPDSSLSLGDSSFYRALLQOTGMSLLSLNEGV 1611
 QY 1418 SKENQPSLEBEV-----SGSQKLVDEI---EVLKQOLKAAEBRL----- 1454
 DB 1612 VANQCSVUBVFPSSLOEBNLTTRKETPSAPAKVEBELESCEVYRPSLEKLEKMSQGI 1671
 QY 1455 IKRDYFELVOTANTNLVE--GKLETPLOADHE--EDSIDRSEMEITKVLGEKLEBNQYL 1511
 DB 1672 MKNKEIOTLEQLLSSRQELDLCKQYLSENEQMOQKLTSTVLEMESKLAEEKQTEQLS 1731
 QY 1512 LE---RLQBEKLELSNKLEILOKEMETSVLKDLOOLKESLSLENNILIKENIDITTLGH 1567
 DB 1732 LLEVARLOLOGLDLSR-----SLLGIDITDEALQO-----RNESCDSIKSH 1773
 QY 1568 HSDTOQLOK-----TOEOLO-----AKNATAIASDNCPTIOKET----- 1604
 DB 1774 TSETTRTRTKRHYHOICDKDAQODLNDLEKITEGTAVKPTGCSQESQSDTYPERGED 1833
 QY 1605 ---SADCVNPL-----BEKILLTEELHQKTNOBKLIHEKNELEQAO 1644
 DB 1834 KTOGSSECTISELFSGPNALVPMDFLQNGQEDHNLOLRVAKETSNENMLRLHVIEDRDR-- 1891

QY 1645 VELKCEVEHLMKSMIESKSLSELOHEKHDTEQOLLA-----LKQOMQVTOEKELO 1697
 DB 1892 ---KVESLNLMBELDSKL-----HLOEVOLMTKIEACIELEKIVGELKKNSDS 1939
 QY 1698 QTHEHLTAEVDDLKENIEL--GLNFRNEAO--OKTTKEOCLLENK-----ELEOS 1744
 DB 1940 EKLEYFSCDHQLOLRVETSEGLNSDLEMHAKSSREDIGDVAKVNDSMKERFLDVENE 1999
 QY 1745 QHRLOCE-----IEELMSKLDKSALETLEKESOKYI--NLNOMEMVMLEMBL 1793
 DB 2000 LSRIRSEKASIEHEALYLEADLEVVOOTEKLCLEKONENQKVIICLEBELSVATSERNOL 2059
 QY 1794 KNSORTVIAER---DOLODDLRESEVMSIET-----ODDIRAKOABALQOQKDR 1838
 DB 2060 RQELDTMSKKTALLOLSKMEKQO--ELESFQSECLHIOYVAEAEVKTELLQTLSSD 2118
 QY 1839 VOELTQSISVLQEKISLEENOMLYNVAIVKETLSRBDLNSQKHLFSEITFLSLKEX 1898
 DB 2119 VESLLKDKTHLOEKLOSLQESLEKQALSTFKCELENOIQALNKEKEILLVKESESLQARLSHS 2178
 QY 1899 EF-----ALQAEKRDADARKTIIDITEKISNI-----EEOLOQOATNL 1937
 DB 2179 DYKLVNSKALBAALVEKEFEALRLSSTQEBVHQLRGIEKLRVRIEADKQOLHIAEKL 2238
 QY 1938 KETLYERESLQCKEOLALNTEHLRETLKSKDLALGKMEQERDEAANKVIALTEKMSLE 1997
 DB 2233 KERERENDSL--KQKVNLRELOMSENOGLVI--LDAENSKA-----EVETLK 2284
 QY 1998 EQINENVTTLKEGE-----GEKETFYLRPSQOSSQSSQMELEBSLTKDLOLEBAK 2050
 DB 2285 TQIEEMARSLKIFELDLVTLREKENLTKQIOEKQOQSELKLLSPKSLLEKQOAEI 2344
 QY 2051 EISEAT-----NEIKULTAKISL--EELILO--NASILNEAVSERNLHNSQOLVS 2099
 DB 2345 QIKESKTAVENTLOQLEKLNBAVALGQDOIMATEQSLDPLPIEEHQLNKSLIEKLA 2404
 QY 2100 ELE-----QSLTLKSRDHPAQSKREKDEAVNKIASLAEIKILTKEMD-----EFRRDK 2150
 DB 2405 RLEADEKQOLCVLOQK-----ESEHHDLLKGRVENLERELIARTNOEHAALEENSK 2459
 QY 2151 ---ESLOEQSHLSEELCTYKTELQLOKQEKEDINNKLAEKVYEDELLQHLSSLKEQLD 2207
 DB 2460 GEVETIKAKIEGWTQSLRGLIEDVVTIRSEKENLNLNELOKEORISEL----- 2507
 QY 2208 QIQMBLREKLANVELCEMDIMEKEISVLRQMBQPOEEDVARMIDLESRQEOIE 2267
 DB 2508 ---EINSSPEN-----ILOKEQEKVQMKKSSVTAMMLQO---OLKE 2545
 QY 2268 LMEKISAVYSPQHTLLS---SLSELOKETEAMKHCMLNIKESLSTLSRSFGSLQTEHV 2324
 DB 2546 LNERVAALHNDQBACKAKQONLSQVE-----CL-----ELEKQOLQIDEAKNNVI 2593
 QY 2325 KLNTOLOTLINKFKVYVTAAYKEDHSLIKDYEKDLAABQKXHDRLQLOCLCEQGRM 2384
 DB 2594 VLQSSVKGLOE-----VEDQKQLEKDEEISRLKNGIQOQEOQLVSKL 2637
 QY 2385 SPSASBELKF---CEIFLNLFRKANNIISQVODDFEVQVFLNQVSTIOEEL--HK 2439
 DB 2638 SQVEGHQOMKEONDELRLNLVLELOKIQVOLSKNASLODTLEVLOQSSYKNLENEBELTK 2697
 QY 2440 KGFQWOLEBEFG-----DLHVDARK---LSEGMQOENRRIASTQLTLTKRLKAVV 2485
 DB 2698 MDMKSFVEKVNMTAKETLEQEMEMQKTALELOELSSEGNRLLAGELQLLBEIKS-- 2755
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 DB 2756 -SKDQ-----LKEILTLENSLKK-----SLDCMHKQOVEKEG--KVRE 2791
 QY 2546 SKKLOSRITMLENELNLVDDAMHNGEK--VALLODKLLSRABAEALNMQVLTQKQON 2603
 DB 2792 IAEYOLR-----LHEAEKQOALLD--TNKOYEVEIQTAREKLTISKEC 2834
 QY 2604 LOAAKKEIENLOKVAKAVPYKEEIDN-----LKTQVVIKLEMEKIKY-----SK 2648

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      2835 LSSQKLEIDLLKSS-----KEELNNSLKATTOGLEELKKTQMDNLKYVNOQLKKENER 2886
Qy 2649 ATDQETAYKSC--LEDKEEGLRLKEELRRADNDTVVCYPKDYOKASTPVTGCGGS 2706
Db 2887 AOGKKKLLIKSCOKLEEKEKIILOKELSQLQAQOEKOKT----- 2924
Qy 2707 GIVOSTAMLVLOSE-----KALE---RELSHYKKKYVHLSRTMSSSEDRKKTAKSDAHS 2759
Db 2923 GTVMOTKDELITTEIKELKELEKTEDEYLDKICSL--LISHEKLEKAKEMLETVOY 2981
Qy 2760 SHTGSSH-----RGSPHKTEYRHGVPVTERSEMPSL-----HLGSPKSSSS--- 2802
Db 2992 AHLGQSQSKQSDRGSP-----LLGVPVHGSPPIPSVTEKRLSSQGNKASGKRGQSSGIM 3035
Qy 2803 -TKRVSPNRSRITYS---QLVMS-----PEKTM 2827
Db 3036 ENGSGPTPATPEFSFKSKKAVMSGIHPAEDTEGTEFEPEGLPEVYKKGFIADIPGKXISP 3095
Qy 2828 H-----KHILSPKVGILH-----KKRALSPNSEMPQHVISPCKTG 2864
Db 3096 YILRRTTARTSPRLAAQKLLALSPUSLGKENLAESSKPTAGGSRQKVKVAQRSPVDSG 3155
Qy 2865 --LHKNTLSTLFDNLSPCKQKQVQENLNSPKGLF-----DYKSK----- 2904
Db 3156 TILREPTTKSVPNVNLPEPSPTDSREGLRVKGRLVPAPKLDMSQLAVRTVRSSEALCV 3215
Qy 2905 SMPYCPSQFPDPSKLGDFS 2923
Db 3216 SDPMEVQSLIDRLCLQDFG 3234

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RESULT 4

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US-08-328-254-6
; Sequence 6, Application US/08328254
; Patent No. 5710022
; GENERAL INFORMATION:
; APPLICANT: Zhu, Xueliang
; APPLICANT: Lee, Wen-Hwa
; TITLE OF INVENTION: A No. 5710022e1 Nuclear Mitotic Phosphoprotein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,254
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,239
; FILING DATE: 22-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CJ 1191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8849
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2482 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-08-328-254-6

Query Match 7.1%; Score 1055.5; DB 1; Length 2482;
 Best Local Similarity 21.8%; Pred. No. 8.7e-44;
 Matches 615; Conservative 482; Mismatches 937; Indels 781; Gaps 115;

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Qy 545 ECRKASFEKETSLOOOL---QSKEEKEKELQSPFELIABEEOLOSVAKNLEWNTSR 601
Db 2 ESEKENLOSKINHLETCLEKTOQIKSHFYNERRRTLEMD---REMLSVIEIRLHVLDISK 57
Qy 602 EHSINAEVQDVEKEVREKMSVLDSGY--NASNSDIQDSSVDGKRSSSHDECIHR- 658
Db 58 --SVAVETQKLAWELOOK--AEFSDOKHOKIEEMCKLTSQLTQO-----VEDLEHKL 107
Qy 659 KMLEQKIYDLEEFINLKKSEN--DKQSSQDPMESIQLCEALMAEKYALAEALMR 716
Db 108 QLSNEMDKOCYODLAHAEYSLDLKSKASLVTEHDQRSLL---AFDQAPAH 162
Qy 717 DNFNIIIE-----NETLKREIADLERSLKENQETPEILEKE 755
Db 163 HSFANIIIGQSGMPSEBSECRLEADQSPKNSAILQNRVDSLEFSLQKQNM-----SD 216
Qy 756 TQKEHEAQLIHEIGSLKLVENAEMYNQNLBEDELTCTKLKEQEIQLAEIKRADN--- 812
Db 217 LQKOCE-ELVQIKGEIIEENLMAEQMHQSPV--AETSQRISKLQEDTSAHQVVAETLSA 273
Qy 813 LQKVRNFDLSVMSQDSEKLEIFOLQKSLSDAVALTRDAQKESFLSENLEKEKME 872
Db 274 LENKEKELOLNDKQETEO--AEIQELKRS---NHLLSDSLKELQL--SEFLSLEKEM 326
Qy 873 DTSNMYNOKERKASLFEKQLETESKNYKMEADLOKE---LOSAFNEINYNGLLAGV 928
Db 327 SSTISLNKRE-----IEELQENGTLKEINASLQECMNLQKESFANYID----- 373
Qy 929 PDDLRSVLEKXVSFSKOLE-----KALEKXNA---LE 960
Db 374 -----EREKISISLSDYQKQEKILLORCETGNAYEDLSQYKAAQENSKLECLL 425
Qy 961 NEVTLSEYKFLPNVECLKNOISKASEIML-LKQEGHSASISKQEIIMQ----- 1012
Db 426 NECTSLCENR--KQELQOLKEAFKQHEFLTKLAFAERNQNLMLLEETVQOALRSEMT 483
Qy 1013 -----EOSE-----QIQLTDEVTHTOSKV---QOTEEOYLEMKKMD--DLFEKYIR 1055
Db 484 DNQNNKSSBAGGLKQELMTLKEQNKQKQEVNVDLQENBOLMKVKKTKHQCQNLSESPR 543
Qy 1056 NKSEAEDDLREMEMNLKQME-----SVEVKIADTKHELEETIRDKQQL 1099
Db 544 NSVKERESEBRNQCNFKPQMDLEVKETSLDSYNAQLVQLEAMLRNKLKLOQSEKKECQL 603
Qy 1100 HEKKYFFQAMQTIPIPTPLSDSLPPSKLVEGNSQDPIEINDY-----HNLIATL 1147
Db 604 HE-----LOTI-----RGDLSTSNQDMQSOISGKQCEIDAEKXYISGPHLETS 650
Qy 1148 ATERNNINWCLETERNSLKEQVYIDNTQLOSLQAOSIE-----KSDLOKPKDLEEG 1199
Db 651 QNDNAHLQCSLOTTMKNLNE---LEKICEILOAKYELVTELANDSRSECTITATRKMAEE 706
Qy 1200 EVKLLEEMELKLG-----HLTDSQL 1219
Db 707 VGLKLINEVKIINDSGLHGLHGLVEDIPGEGFGEQNEQHPVSLAPLDSNSYEHILT--L 763
Qy 1220 STEKLOLENLEYTEKLOTLQOEBMKNITERNELQTNFEDLKAENDSLKODJSENIEOSTE 1279
Db 764 SDKEVQMHFAELQEFSLQSEHKILHQHCQMSKMSKSELQTVYVDSLK---AENLVLS-- 818
Qy 1280 TQDELRANQEBLREQKQVDSFRQQLDQSVGISPNHDAVANQKSVSLGEVNSLOSEML 1339
Db 819 --TNLRNFQGDVAKMOL--GLIEGLVPSLSSSCVPDSSSLG---SLGD--SFPYRALH 868
Qy 1340 RGERDELQTSKALVSELE-LLRHVKSVEGENLEITTKLNGLEKELIGKSEES----- 1392
Db 869 E-----QTGDMSSLISNNEGAVSANQCSVD---EVF--CSLQGENITLRETPEAPAKG 916

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QY 1393 -EVLSMLENLEKEDNNKLEKQAEVYSKKNQSPLEEFSGQKLVDEIYVLKAQKAAEE 1451
DB 917 VEELSELCVYRQSIJEKLEEKMEQSGIMNK-----EIOELFOLSSERQ 961
QY 1452 RLEIENDROVFLVQANNTLVGKLETPLOADHEEDSIDRSEEMEIKVLEKTERNOYL 1511
DB 962 ELDICRKOYLS-----ENEMOQOKLTSVTLVEMESKLAEEKQTEQLS 1003
QY 1512 LE-----RLOEKELELNKLEILOKEMETSVLLKDLQOKLESLSLENIILKENIDTTLKH 1567
DB 1004 LELEVARLOLOGLDLSR-----SLIGITDEAIOG-----RNESCDISKEH 1045
QY 1568 HSDTQAOLOK-----TOEIOLO-----AKNLAIAASDNCPIPTOKET----- 1604
DB 1046 TSETTERTPKIDVHOICDKDAQODLINDIEKITERGALKPTGEGSGEQSPDTNVEPPGED 1105
QY 1605 ----SADCVHPL-----EEKILLTTELHOKTVEQEKLEHKKNELOAO 1644
DB 1106 KTOGSSSECISELSPSGNALVPMDFLGNQEDIHNLQIRVKETSNENIRLHTVEDRDR-- 1163
QY 1645 VELKEVEHLMKSMIESKSSLESLOHEKHDTQOOLLA-----LKOOMQVVTQEKKELO 1697
DB 1164 ----KVESILNEMKEIDSKL-----HIOEVQDMTKIACICILEKIVGELKKENDLS 1211
QY 1698 QTHEHLVAEVDHLEKNIEL--GLNFKVBAQ--OKTTKEQCLINENK-----ELEQS 1744
DB 1212 EKLEYPSCDHOELLQORVETSEGLNSDLEMHADKSSREDIGDNVAKVNDSWKERFLDVENE 1271
QY 1745 QHRLOCE-----IEELMKSLDKRESALETETKESQKVI--NINOEWEMVLMEL 1793
DB 1272 LSRIRSEKASIEHEBALYLEADLEVVOETKECLEMDNENKOKIVCYCLEELSVTSENOJ 1331
QY 1794 KNSGRVIAER--DOLODDLRESVENSIF-----QDDLKRAQOALQOQKDX 1838
DB 1332 RGEIDTMSKKTALDOLSEKMEKETO--ELSHOSECLHCIOVAEAEVKEKTELOTLSSD 1390
QY 1839 VOELTSGIVLOEKISLLENQMLYNVATVETISEBDNOSQHLFSELETLSLKLK 1898
DB 1391 VSELLKXKTHLOKLOSLKEDSOALSTKCELENQIAOLNKEKELLVKESSELOARLSHS 1450
QY 1899 EF-----ALBOEKDKADARKTIDITEKISNI-----EEOULLQOATUL 1937
DB 1451 DYKLTNVSKALEALVEKGFALRLSSTOEYHQLRGIEKLRVIREADEKKQHLHAETL 1510
QY 1938 KETLYERESLIOCKEOLANTEHLRETLKSKDALGKMEORDEANAKVIALTEKMSISLE 1997
DB 1511 KEBERENDSL--KDVENLIERELQWSEENQELVTL--LDAENSKA-----EVEETIK 1556
QY 1998 EOJINENVTLKEGE-----GEKETFYLORPSPKQOSSQOMELERESLTKDLOLEBAEK 2050
DB 1557 TOIEEMARSLKVFLDLVTLRSEKENLTKQIOEKQOSLELDKLSSPFLSLEBKEQABI 1616
QY 2051 EISEBAT-----NEIKULAKISL--EELILO--NASLINEAVSERENLRHQOVLVS 2099
DB 1617 QIKESKTAVEMLOQOLKEINBAVALCGDOEIMKATEOSLPPIEBEHOJLNSIEKTRA 1676
QY 2100 ELE-----OLSTLKSBDHAFASCKREKDEAVNKIASLAEEIKILTKEMD-----EPRSK 2150
DB 1677 RLEADEKKQOLCVLOOLK-----ESEHHDLLKGRVENERLELEIKARTOEHAALEAENSK 1731
QY 2151 ----ESLOBOSSHLSSEELCTYKTELOMLKQOKEDINNKLAEKVXEDVLLLOHLSLKEOLD 2207
DB 1732 GEVETLKAKIEGMTQSLRGLIEDVVTIRSEKENLTNELQKEGERISEL----- 1779
QY 2208 QIOMELRNEKLYNELCEKMDIMEKEISVLRIMQNEPOEEDVAAERNDIIESRNOEIOE 2267
DB 1780 ----EINSSPEN-----ILOKEQEKVOMEKESSTAMEMQOT--OLKE 1817
QY 2268 LMEKISAVYSEQHTLLSSLESELQETEAHKCMINIKESISTLSRSFGSLQTEHVKN 2327
DB 1818 LNERVALAHNDQ-----BACK-----AEQUNLSQVECLEHEKXQOL 1854

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QY 2328 TOLOTLINKKVVYRTPAAVEDHSLIKDYEKDLAAQKHDE---LRLQLOCLIEQHRKM 2384
DB 1855 QGLDEAKNNYIVLOSSV-----NGLIOVEDGKOKLEKDEISRLKNGIDQOGLVSLTL 1909
QY 2385 SDASSELKEF-----CIEFLENLEPKKANILIOVODDFSEVOVFLNOSTLOEILE-HK 2439
DB 1910 SOVEGEHQMLKEONLEIRNLVYELBEKQIOVLQKNASLODTELEVLOSSYKNIENLELT 1969
QY 2440 KCFMOWLEERG-----DLHVDACK--LSEGMQOENRRIASTIQLTKRLKAV 2485
DB 1970 MDKMSFEVKYNNKTAKETELQREHMHMAQTALEQELISEGKRLLAGELQILLEIKS-- 2027
QY 2486 OSKIOREIVYINQPEAKIOEKKQONKELMRMHHGSGASVMEENARLLGILKTVODE 2545
DB 2028 -SKDO-----LKELTLENSELK-----SLDCMHNDQVEKEG--KVARE 2063
QY 2546 SKRLQSRIMLENEINLVKDDAMHGEK--VALIODKLLSRNAEALNAMOVLTKRKDN 2603
DB 2064 IAEYOLR-----LHEAEKKHQALLD--TNQOYEVEIOTYREKLSKEC 2106
QY 2604 LOAMKEIENLOKMAKGAVPYKEIDN-----LKTQVVKIEMEKIKY-----SK 2648
DB 2107 LSSOKLEIDLLKS-----KEELNNSLKTATQIILELKKTKMDNLKYVNLKENER 2158
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QY 2707 GIVOSTAMLVLOSE--KAALF--RELSHYKKKYHNLSTWSSSEDRKKTAKSDAHS 2759
DB 2197 GTVMDTKVDELTELTELKELEKTEKREADEYLDKYGSL--LSHEKLEAKKMLTQV 2253
QY 2760 SHTGSSH-----RQSPHKTETRYRHGPTPESSEPSL--HLGSPKSESSTKRVG-- 2808
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QY 2809 -----PNRSEIYS--OLWS-----PGKTGM 2827
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QY 2828 H-----KHILSPKVGILH-----KKRALSPRSEMPTOHVISPEKGTG 2864
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DB 2428 TIREPTTKGVPVNNLPERSPDPSPRGLAVKGRVLVPSKAGLESKGSNCKVQ 2482

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RESULT 5
 US-09-572-191-2
 ; Sequence 2, Application US/09572191
 ; Patent No. 6355466
 ; GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Wood, Kenneth
 ; TITLE OF INVENTION: No. 6355466e1 motor proteins and methods for
 ; FILE REFERENCE: 1017
 ; CURRENT APPLICATION NUMBER: US/09/572,191
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1388
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-572-191-2

Query Match 7.1%; Score 1051; DB 4; Length 1388;
 Best Local Similarity 24.5%; Pred. No. 7.4e-44;
 Matches 417; Conservative 304; Mismatches 548; Indels 434; Gaps 60;

2 SEGDAVVCVVRPPIORE---QGOANLQWAGNNTTISOVDGT---KSFNDRVFNSSHE 55
 22 NEGDAIKVFRIRPAERSGSADGEO-NCLSLVSTSLRLSHNBPBKFTTDDHADVDT 80
 56 STSQIYOEIAPDIISALOGYNGTIFPANGOTSSGKTYTMMG-----TPNSLGITPOAI 108
 81 TQESVATVAKSIVESCMGNYGTIFAYGOTSGKFTTMMGPESDNFSHNLRGVYPRSF 140
 109 QVEFKIQEI-----PNEPILRVSMETVNTVDLLCDPRKPKPLEIREPNNVYA 163
 141 EYLFELIRREKEKAGAGKSFLOKCSFIEIYNEQIYDVL--DSASGLYIRHRIKGVFPV 198
 164 DLTEELVWPEHVIOWIKKGEKNRHYGETKXNDHSSRSHITPRMAYESRDR-NDPTNSN 222
 199 GAVEOVVTSAAEAYOVLSGGMNRKRYASTSMNRSSRSRAVFTTIESKEKNEIYN--- 255
 223 CDGAVWVSHNLVLDLAGSERASOTGAGVRLKEGKNINSFLPGVILKLSGQAG-G 280
 256 ---IRTSILNVLVLASERQKDTAEGWRLKEAGNINSLSCLQVITALVDVGKQOR 311
 261 FINVDSKULTRILQNSLGNNAKTIVITCTTPVS--PDELSTLQRPASTAKHVRNTPHNE 338
 312 HVCYSDSKLTPFLRDSLGNNAKTIIANYHPSRCFGETLSTLNFAPORAKLTKNAYVNE 371
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 372 --DTQGNVSQDAEYKRLKEQLAELASGOTPPESFTRDKKKTNYWEIYQ----EAMLF 424
 399 HLTNIVASQORSQODORVYKRRRYTWAPGKIONSLHAGSVDFMLSLRPNFSKAKAF 458
 425 F-----KKSBEQEK-----SLIEKVQLEJDLTKKEKF 452
 459 SDMPSPFPEIDSVCTEFSDFDALSMDNSNGIDAEMNLASKYVTHREKTSLSHOSMIDFGOI 518
 475 ---KESRGGFLPEEODRL---SELRNBIQTLRQIEIHHHPVAYKAMENSHL 520
 579 KIAELEQDLSYAKKYLEWYTNRSRHSINAEVQDVEKEVVRKEMSVLGDGYNASNDLQ 638
 521 R---EENRRRL--LEPVKRAOE----- 538
 639 DSSVDGKRLLSSHDECIHRKMLEQKIVDLEEFENLNKSSENDQKXSEQDPMESIQC 698
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 575 PCLFA-----NTEKLAQOLQIOTELNNSQOEIEF---KEIT 609
 758 KEHEQOLHEIGSLKULVENAMENYONLEBEDETKTLKEOEIOIAELRK-RADNLO-- 814
 610 RKRQLELSELOSLOKA-----NUNLENLEA-TKACKROEV--SOLNKHAEETLKTI 659
 815 ---KVRNF--DLSVSMGDSERKCEBIFOLKQSLSDAEAVTRDAQKESFLRSEN 865
 660 TTPTAAYOLHSRPVKLSPMGSPGSL--YTQNSSIINDIILNEPVPE----- 706
 866 ELKEKMEQTSNMYNOKEKAAASLFEKOLETEKSNYKMEADLOKE-----LOSAREIN 919
 707 ---MNEQAFEAISELRLTVQDEOMGALQKDEEHRKMLKLOOHVDCLEH 752
 920 INGLLAKVPRDLRVELLEKKEVSEFSKOLEKALEKXALENEV--TCLSEYKFLPNEVEEC 978
 753 HSTOM-----QELFESSERI---DWTQOEELISQANVLEKQLOETQTKANDFLKSEVND 802
 979 LKNQISKASEEITMLLKQJ-----GEHSASIIISKQEIIMQOSQOILQIDEVHTHOSK 1031
 803 LRVLHSHADKELSLSVKLEYSFKNQOEKFPNLSERHHMVHQQLDNLRLLENKLLLESKAC 862

1032 VQOTEEOYLEMKNKMHDDLFEXYIRN-KSEABDLREMENTLKGTMESVEVK-----IA 1082
 863 LQDSVDNLQETWKFEIDQSRNLQNFKKENETLKSDLNMLLELBAEKERRNNKLSLOFEE 922
 1063 DTKHELEETIRPKEDOLHEK-KYFQAMQITFPITPPLSDSLPRLKVEGNSODPIEINDY 1141
 923 DKENSKEILKYLEAVROEKQETAKCEQAKAVKOLEEST----- 963
 1142 HNLILATERNNIIMQLETERNSLYKEQYIDNTLOLSQAOAGIEKSD-LQKPKOLEE 1200
 964 ---LATEK--VISLEKSRDSKVVADLMNOLOELRSSVCETETITDILKQELKDN 1016
 1201 VK---LLEMEBLYKHLTDSQSLSEIKOLENLEVEKLTQLOEEMKNITIERNELOTFE 1257
 1017 CKYNSALVDR-----ESRVLKQGVLDLDEKTLR-----LRILSE 1054
 1258 DIKAEDSLKODLSNIEQ-----SIETODELRAOEELREKQOLVDSFROQLDCSV 1310
 1055 DI--ERDMICEDLAHATEQLNMLTBAASKHSGLSQAOBELTKKALLOELOHKL----- 1107
 1311 GISSPNHNAVANOEVKSLGEVNSLOSEMRLRGRDELQTSKALVSELELRAHVKSVEGE 1370
 1108 ---NOKK-----EVEQKKNYFNFRQOL-----EHVDSAAE 1137
 1371 N-----LEITKKLNGLEKEILGKSESEVYLSKMLENLEKEDNNKLKE--QAEYS 1417
 1138 DQOSKTPRPHQTHLAKLLETOEGBI---EDGRASKTSLEBLVTKLMBDRVKNAEILR 1193
 1418 SKENQSLSEVPSSQKLVDEIVLKAOLKAAEFLKIDRDYFELVOTAN----- 1468
 1194 MKEQREMENLRLESQOLIEKMWLLQGOLODDIKROKENSQDQHPNOQLKNEQESIRER 1253
 1469 ---TNLVGKLETPQADHEEDSIDRSEMEIKVLGSEKLEBNQVLLRLOEKELNSK 1525
 1254 LAKSKIVEMBK--KRADEVOGALYNKMECRLMTBEVERTOTLESKAFQEKQOLNSK 1311
 1526 LEILOKEMETSVILKDDLOQKLESLSSEN--IILKENIDTTLKHSSTOALOQTOQELQ 1583
 1312 LEEMEYERBERSQEMEMLRKQVECLAENGKLVGHQNL-----HOKIYVVRLLKENVR 1365
 1584 LAKNLAIASDNCPTIOKETSTA 1606
 1366 LAEETEKLEAENVFLPEKERSBS 1388

RESULT 6
 US-09-723-262-2
 ; Sequence 2, Application US/09723262
 ; Patent No. 6379912
 ; GENERAL INFORMATION:
 ; APPLICANT: Beraud, Christophe
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Wood, Kenneth
 ; TITLE OF INVENTION: No. 6379912el motor proteins and methods for
 ; FILE REFERENCE: 1017
 ; CURRENT APPLICATION NUMBER: US/09/723,262
 ; CURRENT FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: US 09/572,191
 ; PRIOR FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1388
 ; TYPE: prt
 ; ORGANISM: Human
 US-09-723-262-2

Query Match 7.1%; Score 1051; DB 4; Length 1388;
 Best Local Similarity 24.5%; Pred. No. 7.4e-44;
 Matches 417; Conservative 304; Mismatches 548; Indels 434; Gaps 60;

2 SEGDAVVCVVRPPIORE---QGOANLQWAGNNTTISOVDGT---KSFNDRVFNSSHE 55

QY	56	STSQIYQEIAPVPIHNSALOGYNGTIFAYGQTSSTGKTYTMMG-----TPNSLGIIPQAI	108
Db	81	TOESVFATVAKSIVSCMSGVNGTIFAYGQTSSTGKFTMMGSESDNFSHNRGVIPRF	140
QY	109	QEVFPIIOEI-----PNREFLRVMEYNETVVDLDCDDPRKKPLREDFPNRRVYA	163
Db	141	EYLSLIREKEKAKAGKSFLLCKGCFEILYNEQIYDL--DBASAGLYIREHIKKGVPV	198
QY	164	DLTEELVWVPEHVIOWIKKGEKNRHYGETKANDHSRSHTTIPRMIVESHDR--NDEPTNSEN	222
Db	199	GAVEQVTVSAEAYQVLSGGMWRNRVASTSMRRESSRSHAVPTITLESMEKEINYN---	255
QY	223	CDGAVMNSHLNVLDAJGSEPRASQTAGEVRLKEGCNINRSLFICQVYKLSDGQAG--G	280
Db	256	---IRTLNLDVLDJAGSEROKDTAEAGMRLEKADNINRSLSCICQVITALVDVANGKOR	311
QY	281	FINYRDSKLTNLIOWSLGNKTVIICITTPS--FDELSTLQPASTAKYHRNPHNE	338
Db	312	HVYCRDSKLTFLRLSLGNAKTAIIANVHPESRCFGETSLTNPAQRKLKNRAVNE	371
QY	339	VLDDEALIKRYAKIELDKOLENLESSSETQAQMAQEAHEHTQLAEIKOLHKEEDRIW	398
Db	372	--DQGNVSQIQAQAEVYKRLKEQJAEIASQOTPEPESLTJTDKKTNYMEYFQ-----EAMLF	424
QY	399	HLTNIVASSQESQODQVRKKRRVTWAPGKIQNSLHASGVSDFMLSLRPNFSKAKAF	458
Db	425	F-----KXSEQEKK-----SLIKVQTLJEDTLTKKEKF	452
QY	459	SDMSPFPIIDSVCTEFPDFDALMSMONGDAEMNLASKYTHREKTSLHOSMIDFQI	518
Db	453	-----IQSNKVIYFR--EDQIIRLEK--LH-----	474
QY	519	SDSVQFHDSSKENOLOYLPKDGDMAEGRKASFKEITSLSQOOLSKKEEKELOVSEFL	578
Db	475	-----KESRGFLPEEDRLL---SLRNEIQTLRQIEHHRPVAKYAMENHSL	520
QY	579	KIABEQLSVYAKNLEWNTSRHSINAEVOTDVEKVERKEMSVLGDGYNASNDLQ	638
Db	521	R-----EENRRRLR--LEPVKRAQE-----	538
QY	639	DSSVDGKRLSSHDECIEHRKMLEQKIYDLFEFLENLANKSSNDYOKSSQDFMISIQLC	698
Db	539	-----MDAOTIKLEKAFSEISGMEKSDK--NQOQFSPKAOKE	574
QY	699	EAIMAEKANALBELALMRDNFINILLENETLKREIADLERSUKEN--QENNEEILEKERO	757
Db	575	PCLFR-----NTEKLAQIQLQIOTELNNSKQEEEF---KELT	609
QY	758	KEHEQOLIHEIGSLKLTVENAEWYNQNLNEEDLETYKLLKEQOEIOLAEYLRK--RADNLQ--	814
Db	610	RKROLELESELOSLQK-----NLNLENLLEA--TKACKREBV--SOQNKIHAETIKI	659
QY	815	--KKVRNF-----DLSVSGMDSKLCCEEIFOLKOSISDAEAVTRDAQECSFLRENL	865
Db	660	TTPTKAYQJLHSRPVPLKSLPEMGSFGLS---YTQNSSIJDNDILNEPVPE-----	706
QY	866	ELKEMEBTSNMVYNQKEKASLFEKQOLETEKSNYKXKMEADLOKE-----LOSANEINYN	919
Db	707	-----MNEQAFEAISELRTVQDQMSALQKIDEBEHKIKLIKLOOHVDKLEH	752
QY	920	LNGLLAGVPRDILSRVLELEKKVSEFSQLEKALEEKKALENEV--TCLSEYKFLPNEVAC	978
Db	753	HSTQM-----OELPSSERI-----DWTQOEBELSLQNLVLEKQLEBOTQKNDPLSEVND	802
QY	979	LKNOISKASEEIMLLKQF-----GEHSASIIISKOEIIMQOSQOILQLTDEVTHTOSK	1031
Db	803	LRVLVSHADKELSVKLEYSSFKTQOEKFNKLSERHHNHVQOQLDNLRLNENKLESKAC	862
QY	1032	VQOTEQOYLEMKKMHDDLFEKTIYR--KSAEADLLAMEKYLKQTMSSVEYK-----IA	108
Db	863	LQDSYDNIQOEIMKFEIDQLSRNLQNFKEKETLTKJDLNNIMLELAEKERNKNSLSIQEBE	922

QY	1083	DTKHELEETIDDKQOLJHEK-KYFQAOAGTIFPTPLYSDDSPRSLKVGNSQDDPIEINDY	1144
Db	923	DKENSSKTLVLEAVROEKOKEFKAACEQNAKXOKLEESL-----	963
QY	1142	HNLLALATERNNINWCTETERNLSLKEQYDIDNTLOSLOAOSIEKSD-LQKRODLERGE	1200
Db	964	-----LATEK--VYSIEKSRSDSDKKVAVADLMNOQOELRSSVCEKTEHTIDTLQKGLKOIN	1016
QY	1201	VK--LLLEMLKLGHLTDSQSLSTFKLOLEMLVTEKQTLQOEEMKMITTERNELQTNFE	125
Db	1017	CKYNSALVDRE-----ESRVLJKQOVDILDKEETLR-----LRILSE	1054
QY	1258	DLKAEHSDLKODLSENINQO-----SIETODELRAAOEELREOKOLVDSFPROOLDSCV	1311
Db	1055	DI--ERDWLCEDLHATBQMLMTBASKKSHGLIOSAOBELTKKALLQOELQKL-----	1107
QY	1311	GISSPNHDVANOEVKSLSGEVNSLOSSEMLRGERDELQTSKALVSELELRAHVKSVEGE	1370
Db	1108	-----NQKK-----EEVEQKKEUYNFKMQOL-----EHVMSAAE	1133
QY	1371	N-----LETTKTLNGLEKEIILKSESEVLSKMLLENKEDNNKKE--QAEYS	1411
Db	1138	DPOSKPTPPHFOTHLAKLELTOEOEI-----BDGRASKTSLSHLVTKLNEDERVKNAEILR	1193
QY	1418	SKENQFSLEEVFGSGOKLVDEIEVLVKAQOLKAAEERLEIKDRDYELVOTAN-----	1466
Db	1194	MKEQURENENLRLESQOLIEKMWLLQSDDDIKKQKENSDDNHPNOQLKIQEESIKER	1255
QY	1469	--TNLVGKLETPLOADHEEDSIDRSESEMEIKVLGKEERNOYLLERLOEKEKLETSNK	1522
Db	1254	LAKSIVBEMLK--MKADLEEVQSALVYKMECCLMTDEVERTQTLSEKAFQEKQLRSK	1311
QY	1526	LEILOKEMETSVLKDDLOQKLESLSBN--IILKENIDTLIKHSDPQAOLOKTOQOELQ	1588
Db	1312	LEEMVEERERTSQEWMEMRKQVECLAEENGKLVGHQNL-----HQKIQYVRLKKEVNR	1365
QY	1584	LAKNLAIASDNCPTQKETSQA	1606
Db	1366	LAETEKRAENVFLPEKKRSES	1388
RESULT 8			
US-09-914-259-11			
; Sequence 11, Application US/09914259			
; Patent No. 6495336			
; GENERAL INFORMATION:			
; APPLICANT: Makowski, Lee			
; APPLICANT: Hyman, Paul			
; APPLICANT: Williams, Mark			
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES			
; FILE REFERENCE: 8471-010-999			
; CURRENT APPLICATION NUMBER: US/09/914,259			
; CURRENT FILING DATE: 2000-11-21			
; NUMBER OF SEQ ID NOS: 180			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 11			
; LENGTH: 3878			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-914-259-11			
Query Match			
Best Local Similarity 19.0%; Score 1020; DB 4; Length 3878;			
Matches 691; Conservative 639; Mismatches 1146; Indels 1152; Gaps 143;			
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Db	3	DEEROKLEAGKAKIEELSLAFVLVROLQAFORAKQASDGSGPSKKOKKR--KTSSSKH	59
QY	198	SSRSHTTFRMVVEGRDRNDPINSENCQCAVWVSHNLVLDLAGSEFASQTAEGCVLK---	254
Db	60	DVSAHHDINDINQOCNENMYINNSORVESTVLPSTIMKTLHSGELTSHGQFSVLESEI	119

QY 255 ---- EGCN--INRSLEIIOQVIAKKUSDGAGGFINYRDSKLTIRILONSJGNAKTVIICT 308
 Db 120 STTADDCSEVNGCSFVM----- RTGKPTNLLREEBFG----- 152
 QY 309 ITPVSDLELSTLQFPASTAKVHANTPHVNEVLDDEALLKRYKEILLDKOLENLESSE 368
 Db 153 ---- VDDSYS----- EOGADSPHLEMMESSELGAKOH--ELIELRELEEMKVTYG 198
 QY 369 TKA-----QAMAKEH---TOLLAEIKOLHAKEREDRIWHLNTIYVWASSQESQODQRYK 418
 Db 199 TEGLOOLQOFPAIKORDGITTOULTANLOQAREKETWREFEL-----TEGQOKIO 251
 QY 419 RRRRYTAPGKIONSILHAGVSD-----FMLSRLPGNFESK----- 454
 Db 252 IQFOOLQOASETLRNSTHSTADLLQAKOQIILTHQOQLEODHLEIDYOKKKEDFTMQJS 311
 QY 455 ---- KAKSDMPSFPEIDSVCTERSDFPDALSMNSNGIDAE--WNILASKVTHREKT- 506
 Db 312 FLQEKIKVYEMODKKVENSKEEIOEKETIIEELVTKIIIEBKTLLEKDKLTADKLL 371
 QY 507 -SLHOSMIDFGO-----ISDSVOFHDSKKNOLQVLPKDSGDMAEGRK-----ASPE 552
 Db 372 GELQEOIVOKNOEIKMKLELTNSKOKEROSSEITQLM---GTYBELQKRNHKSQPE 427
 QY 553 KEITS-LOOQLOSK--BEKKELVQSPFKIAELBEOL--SVAKULEWVTNSR--EHSI 605
 Db 428 TIVQMEQETQKLEQLAELEDMYGGQIVQWKQELIRQHMAGMEKTRHKGEMENAL 487
 QY 606 NAEVQTDVKEVYVRKMSVUGDSGYAHSNDLQDSSVDGKRILSSHDECIEHRKMLEQKI 665
 Db 488 RSYSNITTVEDQIK--LMNVAINELNIKLODTNSOKEKLELGLILLEKCALQROL 542
 QY 666 VLEEFIEHLNKSEMDKSSRODFM-----ESIQCEAIMAKANALE--ELAL-- 714
 Db 543 EBLVEILSRQEOIQAROTIABQESKLANBAKXSITVEDIKAEIYASASEKKELELKE 602
 QY 715 ----MRDNFIILENETLREIADLER-----SLKE----- 742
 Db 603 AEVTNYKIKLEMLEKKNALVDPMASQOE-ABELERLTQOLFSHEBELSKLEDELEIHR 661
 QY 743 ----NQTNEFEIL--EKETOKEHQAOLIHETGISAKKULEVNA 778
 Db 662 INIEKLDNIGIHYKQOIDLQONEMSQKIETMQPEKDNLITKONQILIEISKDKLOQS- 720
 QY 779 EWMYONULEE--DLETRTKULIKE-----OEIOL-----AELRKRADNQ 814
 Db 721 -LVNSSEEMTLOINLOKEIILRQEBEKEKTLBEVQELQKTLLEKQKMEKENDIQ 779
 QY 815 KVRNFDLSVS-MGDESKLCEEIIFOLQSLSDAEAV-----TRDA--OKESGFLRS 862
 Db 780 EKFAQLEANSITLKDEKTLDEMLKIHTPVQSEERLIFLDSIKSKSDSWEXEIEILIE 839
 QY 863 EN-----LELKEKNEEDTSNMNYQEKAKASLPEKOLETEKSYKKNEMDLO--KEL 910
 Db 840 ENEDKQOOCIOINLEIEKORNTFSFAKNEVANYQELQEBYACLLVYKDLBESKXKQEL 899
 QY 911 Q-----SAFNEINYLN-----GLAGKVPRLD-- 933
 Db 900 EYKSKIKALNEBELHORINPTTYKMSVSPDEDKTVAETLEMGAVEVEKDTTELMKLEV 959
 QY 934 ---SRVELEKVSEFSKOLEKALEKNALENEVTCLSEYK---FLPNEVECHKN----- 981
 Db 966 TKREKLELSQRLSDSEQLKQKHGEISPLNEBEVKSJKQEKQVSLACRELEIILINNRAE 1019
 QY 982 ----QISKASEEIMLKQBS-EKSASTISK-----QEIIMQOSQO 1017
 Db 1020 NVQSCDPTQVSLIDGVVITVTSRGABGSVSKVNSFPEESKIVEDXVSENNMVTGEBESQO 1079
 QY 1018 ----ILOLTQEBVHTOS--KVQOTEEOYLE-----MKKMDLPEKVIARKSEAE----- 1061
 Db 1080 EQLILDLHLSVTKESSLRATQSENDKLOKELNVLSBQNDL-----RLQMEKQRICTSL 1134
 QY 1062 ----DLIRE-MENLKGT-----MESVEVKIADTKHELE-ETIR-----DKEO 1097
 Db 1135 VYSTHVDQVREYMEKAKALCSLKEELIFQAEKIKELQKIHOLELOTMKTOETGDEGK 1194
 QY 1098 ILH-----EKKYFQAMOTIFPIPLPSLSPSKLVESNODPIEINDY----- 1141
 Db 1195 PHLHLIGLQKRAVSECSYFLOTLCV-----LGEYTPALKCEYNAEDKENSQYISEN 1249
 QY 1142 ----HNILATERNNIMVCLTERNSLKEQVIDLNTQLOLQAO 1182
 Db 1250 EDPQLQDYREYQDFQENMHTLANKVTEENYKLVLOLRLSKIMQOCTD-----GM 1300
 QY 1183 STEKSDLOKPKQDLEBGEVKKLLEMLLKGHLTDSQLSIEKQLENLEVT--EKQTLQOE 1240
 Db 1301 KLEFGEENLPKE-----ETEFLSIH--SQMT--NLEDIDVNHKSKLSSLOD 1342
 QY 1241 EKMNTIRBRELQTNFEDLKAHSDLSKODLS----- 1272
 Db 1343 ----LEKTLQEBQVQELBSLSSLOQKQETEQNYAEIHCLOKRIQAVSESTVPSL 1396
 QY 1273 ----NIEQSIETQDELRQAQE-----ELREQKQLVDSF 1301
 Db 1397 PVDVAVITESDAQRTMYPGSCVYKKNIDGTIERSGEFGVKEETNIYKLEKQYOQOLEBEV 1456
 QY 1302 ROQLLDCSVGI-----SSPHNDVANOQEKVSLGEVANSLOSEMRLGERD 1344
 Db 1457 AKVIVMSIAFAQOTELSRISGKENTASSKQAHAVCOQEOHYFNMKLSODQIGFOTPE 1516
 QY 1345 ELQTSCKALVSEL--ELRAHVYKVEGEN-----LEITKULNGLEKE--ILGKS 1389
 Db 1517 TVDVKFKKEFKPLSKELBHGKEIILNSDHPDIDESKDCVULTIEEMFSKKTIVQOS 1576
 QY 1390 ESEVILKSMI-----ENLKEDNNKLEQAEVYSSKENQFSLAE--VFSQSOKLV 1436
 Db 1577 IHDEISVSMASRQMLNEBQLEDMDQOELVQYQEHQOATQSSIDNENILVSEBRVLL 1636
 QY 1437 DEIEVLKQOLQAABERL--ETQDRDYFELVQNTANVLYEGKLETLQADHEDSDIDRSE 1494
 Db 1637 BELLEALKQULSAGREKTLCCCEJENSS--TOTONENQOGEVE--EOTFKERKIDRKE 1689
 QY 1495 EMEIKVLQEKLERNOYLLERLOEKEKLELNKLEIIOKEMETSVLLKDD-----LOOK 1546
 Db 1690 DVPPEILSNE--RYALQOKAN-----NRLKILLEVYKTTAAVEITIGRHVGLDRS 1739
 QY 1547 LESLSENIILKENIDTTLK--HNSDTQAOLOK-----TOQELQ 1583
 Db 1740 SKSQGSASILWRSBAEASVKS CVHEHTRVTDESIPSYSGDMPRNDINMMSKVTBEGTE 1799
 QY 1584 IAKNL--ALASDNCPIITQOE-----KETADCVHPLBEKILLT 1620
 Db 1800 ISQRLVRSFGAGTEIDPENEBELMNISSRLQAAVEKLELALISSETSSQLEHAKVTQTELMR 1859
 QY 1621 BELHQKTNEOEKL-----LHEKNEL--EOAQVELCEVENHLKMSMIESKSSLESIOH 1670
 Db 1860 ESFROKQOATEBSLKQOEBELREHLHESARABQAVELS--KAGGVADYADEKTLTEROQ 1918
 QY 1671 EKHND--TEQQLLAKQOQVYVTOEKKELQOETHELHTAEVDHLKENIELGINTFNEAQO 1726
 Db 1919 EKTDIIDRLQOELLQANSRLQELBAEQOIOERELLRSQKAMK--ABAG----- 1967
 QY 1727 KTTKQOCLINENKELQOSQHRLOCEIEBELMSLKIKESNLETUKSEQOVNULNDEMENV 1786
 Db 1968 --PVEQOULOETEKMLKRELEVOCAQKVRDLOQOVALE-----IDIVEQVSR- 2015
 QY 1787 MLEMEELNNSQRTVAERDQLODDRESVEMSIETQDDLRKAQFALOQOKDQVOELTQOI 1846
 Db 2016 FIELEOEKNTIEM-----DLRQONQALEKOLEMKRFLDQO 2051
 QY 1847 S-----VLOEKISLENOMLYNVAVYKETLSERDDLQNSKQHLFSEITFLSLSLEK 1898
 Db 2055 AIDREHERVDFQOEIOKLEQOQ--KVVPFQCISE-----HOTREVEQLAHLKEX 2100
 QY 1899 E-----FALQAEKQADARKTIIDITEKISNIEBOLQOATNLKETLYRRE--SLQOC 1950

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Db      2101 TDKCSLLSKSQQLOQDIOERNEIEKLEFRVVELEQALLVSADTFQKVEDRKHFGVAE 2160
Qy      1951 KQOLAMNT--EHRLETKSKDIALGKMEQ-----RDEANKVIALTEKMSLSLEQINENV 2004
Db      2161 KPELSLEVOLQMERDAIDRKEKEITNLEBQLOFRELLENKNEEVOQLHMOLEIQKEST 2220
Qy      2005 TTLKEGEKKEFTFYLQRPKQOQSSQMEELRESLTKDLOLEBAE-----KEISEAT 2056
Db      2221 TRLQELQENKLF-----KDMETGLAIKESDAMSTQDQVNLFGKFAQIQOE 2270
Qy      2057 NEIKULTAKISLEEEIIONASILNBAVERENLRHSKOOLVSEBQSLTKSRDHARA 2116
Db      2271 VEIDQNEQVTKLOOL--KITDNKVIE-----KNELIRDETQTECLMSDQECVK 2321
Qy      2117 QSKREDEAVNKIA-----SLAEELKILTKENDERDSKESIQEOS 2157
Db      2322 NRREBEIEQNLNVEIKLQLOELANIGQKTSMAHSLSEADSLKHQDVLVIAEKLALEQOV 2381
Qy      2158 SHLSEELCTYKT-----ELQMLKQOKEIDNNKLAEKVDE-----LLOH 2198
Db      2382 ETANEMTMRKVNLKETNFKMNOLOELFSLKRESV-----EKIQSIPENSVAVAIH 2436
Qy      2199 LSLKQLODOIOME-----LRNEK--LRNYLCEKMDIMEKISVLR 2239
Db      2437 LSKDPELEVLITEDALKSLENOQYKSPENGKSIINLETRILLOLESTVSAKDLELQ 2496
Qy      2240 -----NONEQOEBDVAERMILIESKNOEIQELM--EKISAVSEQHTLSSLSSEQ 2291
Db      2497 CKQIKDMOQOQFE-----TEMLQKIVMLQKIVEKVA-----ALVSOIQ 2539
Qy      2232 KET--EAHNGMLN-----IKEL--SLSTLSRFSGLTEHVKANT 2328
Db      2540 LEAVEBVAFCODNOTISEPERTNIQNLQREBELSGDIALTRISLESOVEEMT 2599
Qy      2329 QLOTLNFKKVVYRTPAVKEHSLIKDYEKDLAEGRHDELRLQLOCEHGRKWSDA 2388
Db      2600 SL--ILEKQVEIAEKNVLEKEKLELOKLEBNEKKQRE-----KKRSPD 2647
Qy      2389 SEELK-----FCIEPL-----NELLFKANTIQ 2412
Db      2648 VEVLKTTTELFHNSNESGFFNELALRAESVATKELASKEKAEKLOELLVKETN--MT 2706
Qy      2413 SVQDDFSEQVFLNGVSTLQ-----ELEHKKG----- 2441
Db      2707 SLQKQLOVHRDLAEKKEKSLIEKEDETEVOESKACNFBPLPIKLSIASQDTGTLK 2766
Qy      2442 -----FMQLEBFGDLHYDAKKLESGMQO 2465
Db      2767 ISSNOTQILVKNAGIOINLOSECSSEVTEIISQFTKIEKMOELH-----AEILDM 2821
Qy      2466 ENRRIAST-----IQLTKR--LKAVVOSKIQREITVYLNQ----- 2499
Db      2822 ESRHISETETLKREHYAVQOLKEBGTAKAVIQCLRSKEVGFYMMCFTSLCDGSDWG 2881
Qy      2500 -----FAKQOKEKQON-----KELMRMHHGSA----- 2525
Db      2882 QGITVTHSGFPIASBEGSESESATDSFPKKIKGLLRVHNHGQVSLTESPYSDGD 2941
Qy      2526 -SVME-----EENARLLGILKTVODESCKLQSRIMLEENLNVYDDMH-----KGE 2572
Db      2942 HSIQOVSEPMLEERKAVINTISSLKDILTKM-----LOREAVYDSSGSHSFSFDMKE 2996
Qy      2573 KVALIQDKLL-----SRNAEALINAVQVLTQKQDNLQAMK----- 2609
Db      2997 LLLALQOVFLERSVILAAFRTELTALETDAVGLNLCLEORIIOEGVAYQAMCLOKA 3056
Qy      2610 -----EVENQKRVAKAVPYKEID-----NLTKE-----VVAIEBKIKY 2646
Db      3057 DRRSLISETQALHAQNGRKITLKREQSEKPSQELLENIQOKOSQMLEMVELSSMK- 3115
Qy      2647 SKATQOEIAYLKSCELEDEKGBRLKEELRRAQADNDTVCVPKYOXKASTFPVTCGGS 2706
Db      3116 DRATE-----LOEQLSSEKVVVAELKSELAQTKLELLETTLLKQOHGHLK----- 3158

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Qy      2707 GIVQSTAMLVLOSEKAAERELSHYKKKYVHLHLSRTMSSEDR-----KKTAKSDAH 2758
Db      3159 -----ELBAFRLVKDKTDEYHLNDLNTLASQOKKSRELQMALEKAK----- 3201
Qy      2759 SSGTSSHRGSPAKTETYRNG--PVTPERSEMPSLHGSFKSSESTKRVVSPNRSEIYSQ 2817
Db      3202 ---LGRSEERDKEELEDLKFSLSESQKQNLQNLLEBQKOLNNSQOKIESQRMLYDQ 3258
Qy      2818 LVMSPGKTGMKHIIISPSKVGLHKRRAISPNRSEMPQHVISPGKTGLHKULTSTLPDN 2877
Db      3259 LSEEGRMLEOVLLSESEKVRIREMSSTLDRERELHAQLQSSDGTGOSRPLPSEDLKE 3318
Qy      2878 USSPC--KOQKVQENTL--SPKGLFDVKSX 2904
Db      3319 LQKQLEBKHSRIVELNTEKYLQSLQTR 3348

RESULT 9
US-09-592-054-8
; Sequence 8, Application US/09592054
; Patent No. 6440684
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Finet, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; TITLE OF INVENTION: their use
; CURRENT APPLICATION NUMBER: US/09/592,054
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: Human
; US-09-592-054-8

Query Match      6.5%; Score 953; DB 4; Length 1234;
Best Local Similarity 25.3%; Pred. NO. 4,1e-39;
Matches 358; Conservative 245; Mismatches 444; Indels 370; Gaps 55;

Qy      3 BGDVAVCVVRPLIORE--QGDQANLQWKAGNNTISOVDGT--KSFNDFRVFNSHESTSQ 59
Db      6 KQIPVRVALRCRQPLPKPKEISEGQWCLSFVPGETGV--VVGTDKSFYDFVDPCTEOBE 63
Qy      60 IYQELAVPIISALQGVNGTIFAYGQTSKGTYTMG-----TPNSLGIIPQAIQBFV 112
Db      64 VNKAVAPLIGIFFGYNAVTLAVGQTSKGTYSGAVYTAQENEPVGIIPVYQLLF 123
Qy      113 KIIQEIIPREFLLRYSVEIYNETVQDILLCDRRKPKLEIREDFNRVNVVADLTIELVMV 172
Db      124 KEIDQKSPFETLKYSYIEINBELDLLCSREKAQININEDPREGKIYGLTEKTVLV 183
Qy      173 PEHVLIQIKKGEKNRHYGETKXNDHSSSHITFRNIVESRDRNDPTNSENCDAVMVSHL 232
Db      184 ALDVTSCLEQGNNSRTVASTMNSQSSRSHAIFTLSLEQKKSDKNS-----FRSKL 236
Qy      223 NLVYDAGEBPASQTAEGVRRLKEGNTNRSLEFILGOVYKKLSDGAGGFVNRDSEKTRI 292
Db      237 HLVDLAGEBRKKTAEGBDRLEGINIRGLLCLGNVTSALGDDKGSFVPRDSEKTRL 296
Qy      293 LQNSLGNAGTIVICTIPV--SPDETSLTQFASSTAKGVNTPHVNVDLDEALLKRYR 350
Db      297 LQDSLGNSHLTMACVBPADSNLEETISTLRVADRAKIKNKPVYV-----IDPHT 348
Qy      351 KEIIDLKQLENLESSSETKAQAMAKEEHTLLAEIKQLHKEREDRIWHLNIVVASSQE 410
Db      349 AELNHLKQOVQOL-----QVLL----- 365
Qy      411 SQQDQVRVKKRRVYMAPKIQNSLHASGVSPFDMLSRLPGNFKKAKFSDMSPFEIDS 470

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Db      366  -----LQAHG-----GTLPSISIAE-----PS-----382
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Db      383  -----ENLQSLMEKN-----OSLVE-----ENE 400
QY      531  NOLQYLPRKSGDMAEGRKASFEKEITSLQOOLSKKEEKE-----LVQSFELKI 580
Db      401  KLSRCLSKAAGQAFQMLERILITE--QVNEKLNALKEILGHAKCLDLOKLVETLEDQ- 457
QY      581  AELEEQSLVAKNLEWNTNSREHSI--NAEVQDVEKVEYVRKEMSVLGDSCGNASNDL 637
Db      458  -ELKEVEVEIICNLQOILITQSLDDETVACTAAIDTAVEEE-----AQVETS 501
QY      638  ODSSVQGRKLSHDECEIHRKMLQOKIVDLPEFI-----ENLKSSENDKQKSEDDPME 693
Db      502  PETSRSDDAFTTQH--ALHQAOQSKVEVELNNAALKEALVRKMTQNDQ-----IQ 551
QY      694  SIQCEALMAEKANALEELAMRDNFDNIILENETLKREIADLERSL--KENQETNEPE 750
Db      552  PIQF-----QYQDNIKNLELEVINLQKEKEELVRELOQAKKANQAKLS 595
QY      751  ILEKETQKEHEAOL-----IHEIGSLKLVENAEWNTNLEEDLETKTKLKEQETQLA 804
Db      596  EHRKRLLOLEGOIADLKKKLNQOSKLLKLESTERVSKLNOEI--RMKNQGRVOL- 650
QY      805  ELKRAKDNLQKVRNFDLSVSGDSEKLECEIFOLKQSLSDAEAVRDAQKESFPRSEN 864
Db      651  -WRQMEDAE-KRQW-----KQKRDKEVLOKE-----RDRKQO-----YEL 686
QY      865  LELEKEMEDTSNNYNQKEKASLFEKOLETEKSNYKMEADLOKELQSAFNEINYNGI- 923
Db      687  LKLERFQOSQNVLRKTEBAANAKRLKDALQKQEV-ADKRKETQS-----RQME 737
QY      924  -LAGKPRDLISVELEKVKSEFSKOLEKALEKNALENEVTLSSEKFLPNEVECLKQO 982
Db      738  GTAARVRNMLGMEIEVWVSTEEKRHLNDLEDRKLIADVOVLOKE-----783
QY      983  ISKASEIMLKEQEGSHASIIISKEIIMQOSEQIOLDEVTHTQSKVQOQTEQYGLM 1042
Db      784  -----KKSRENPPPKLAKCTFSISEYNGQVLESDCIT--KOIESLETMEEL 829
QY      1043  KQMH-DLPEKYIRNKSSEADLRE-MENLKGTMESEVEVXKADTKHELEBITRDEQLH 1100
Db      830  RSAQIADLOQKLL--DAESBDRKQCMENIATILEA--KCA-LXVLIGELVSSK--IH 880
QY      1101  EKKYFQAMQTIPTIPPLSDSLPSPKLVESGNSQDPIENDYANLILATERNNINVCLET 1160
Db      881  -----VTKLENSLRQSKASCADMQKML-FEBOHFSEIETELQAEIVRMOQ 925
QY      1161  ERNSLKEQYIDLNTQOSLO--AQSIKES-----DLQPKQODEEGEV 1201
Db      926  QH--QEKVLYLVQLOESQMAEKOLEKASKEPEQVSTLQOCQDELEKMEVECEQNO- 981
QY      1202  KULLEWELLKGHLTQSLSEKLOLEN--LEVTETKLOTLQOEBMKIITERN--ELQOTPF 1256
Db      982  QLLQEBEITIKOKLILQVASRQKHLPNNDTLSPDSSEFYIIPRKRKSRYKKEKLEBSMDI 1041
QY      1257  EDLK--AEHDSLKQDISENIEQSIETODE-----LRPAQEBELR-----EQQOLVD 1299
Db      1042  EDLKCTSEHSVNEHEGDDGDSDEADDEWKPTKLVKVSARKNIQCSCKMGKNQOC-- 1099
QY      1300  SFRQOOLDCSVGIS--SPNHDVAVNOEKVSLGEVNSLO 1335
Db      1100  GCRKQKSDCGVDCSCDPTKCRNRQQSKDSLGTVEQTO 1136

```

RESULT 10
 US-09-592-054-2
 ; Sequence 2, Application US/09592054
 ; Patent No. 6440684
 ; GENERAL INFORMATION:

```

; APPLICANT: Beraud, Christophe
; APPLICANT: Finer, Jeffrey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Wood, Kenneth
; TITLE OF INVENTION: No. 6440684e1 motor proteins and methods for
; FILE REFERENCE: 1016
; CURRENT APPLICATION NUMBER: US/09/592,054
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1232
; TYPE: PRF
; ORGANISM: Human
US-09-592-054-2

Query Match      6.4%; Score 945.5; DB 4; Length 1232;
Best Local Similarity 24.6%; Pred. No. 9,6e-39;
Matches 372; Conservative 275; Mismatches 499; Indels 369; Gaps 61;

QY      3  EGDVAVKVCVRPLIORE--QGDQANLQWKAGNNTISQVDT-KSFNPDVFNHSHSTQ 59
Db      6  KQIPVRVALRCKPLVPKEISEGQCLSFVCEPQV--VGTDKSFTYDFVDPSTBOBE 63
QY      60  IYOEIAVPLIRSALOGNGTIFAYQOTSSGKTYTMMG-----TPNSIGIIPQAOEYF 112
Db      64  VENTAVAPLIKQVFPVGNATVLAQOTQSGKTYSGAVTAQOEHEPTVGVIVITQLLF 123
QY      113  KIIQELPNREPLLRVSYMEIYETVKDILCDRRKKPLEIRDPENRNVYVADLTIELVY 172
Db      124  KEIDKSPFEFLKYSYLEIYNEIILDLCPREAOQINIRDPREGIKIVLTKETVLY 183
QY      173  PEHVQWIKKQKGNHYGETKNDHSRSHTFRMIVSRDNDNTSENCGAAVWSHL 232
Db      184  ALDVTSCIEQGNNSVTVASTANSSQSRSHALITTSLOGKSKDNSS-----FRSKL 236
QY      233  NLVDLAGSERASQTAGEGVRLKEGGINRSJLILQOVIKLSDQAGGFINYRDSKLTRI 292
Db      237  HLVDLAGSERQKTAEGGRLEKGINIRGLICGNVISALGDDKKGFPAPYRDSKLTRL 296
QY      293  LQNSIGNAKVIYICTTPV--SPDETSLTQFASHTAKVNTPHVNEVLDEALLKRYR 350
Db      297  LQDSLGGNSHTLMICVSPADSNLEETINTLRVADARKIKKPTVN--IDPQT----- 348
QY      351  KEIILKKOLELJESSSEFTKQAMAKEHTOLLAETKQLHKEREDRIWHLTNIIVASSQE 410
Db      349  AELNHLKQOVOL-----QVLL-----365
QY      411  SQODQVRKRRKRVTPAPKIQNSLHAGSVSDPDMLSRLPGNFSKAKFSDMPSPFIDDS 470
Db      366  -----LQAHG-----GTLPGSIYVE-----PS-----382
QY      471  VCTEFSDDALSMDSNGIDAEWNLASKVTHREKTS--LHOSMIDFQGISDVSQFHDS 528
Db      383  -----ENLQSLMEKN-----OSLVE-----ENE 400
QY      529  KENQOYLPRKSGDMAEGRK-ASFEKEITSLQOOLSKS-SEKKELVOSFELKIALEBO 586
Db      427  NE-----KQNAKIEELRQHAACKLQKLVETLEDELEKNEVEITCNLQOLITQSLDE 479
QY      581  ISVKANLEWNTNSREHSINAEVQDVEKVEYVRKEMSVLGDSCGNASNDLQDSSVDGR 646
Db      480  -----TVACMAAALDTAVEQEAQVETSP-----TSRSSAPFTQHALR 518
QY      647  LSSSHDECEIHRKMLEQKIVDLPEFIENLKNK--SENDQ--KSSBDDPMEISQOLCEATIAE 704
Db      519  QAOQSKLELVELNKALAK-----EALARKMTQNDQLOPIQYOYQDNI-----561
QY      705  KANALEELAMRDNFDNIILENETLKREIADLERSKENOETNEPELEKETQKEHEAOL 764
Db      562  KEPELEVINLOKEK-EELVLELOQAKKANQAKLSERRRKLQLEGOIADLKK-----615

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0Y      765SHEIGSLKVLVNAWMAWNONLEEDLETPTKLKEGEIOELABRKXADNLQKKVRNFDLSV 821
0Y      616LNEOSKLLKKESTERTYSKLNQET-----RNMKNORVOL--WRQKCEAB-KFROW---- 664
Db      825SMGDSEKLCCEEFLQKOSTSDAEATRAPOACEPSLRASENTELKEMEDTSNMYOKEKA 884
Db      665---KQRKDKEYIQKE-----RRKRQ-----VELLKLENPFQKSNVLRKTEE 706
0Y      885ASLFEPKOLETESNYKKMEADIQEKLOSAFNEINYNGU--LAGKVPRDLLSRVELEKV 942
Db      707AAANAKRLKDALQKOREV-ADRKETQS-----RCMEGTAAWVKWLINIEIWMYST 757
0Y      943SEFSQJLEKALEBKALENEVTCSEFYKFLPNEVBCLKNQJSKASEEIMLKQGBEHAS 1002
Db      758BEAKHLDLLEDKRIILQAODVAQLKE-----KKEGENDPP 793
0Y      1003IISKOIIMOQOSEQILOLDTDEVTHQTSGVOOTEBOYLEMKMHNDLPFKYTRNKSEAD 1062
Db      794KLRRRTESLTREVRGVSESEDSIT-KQLESLETEHFESAQIA-DLOQKLL--DAEBD 848
0Y      1063LLRE-----MENIKGTMESVEVKIADTKHELEB--TIADKQULHEKKYF 1105
Db      849RPKQWENIATILEAKALKTYLIGELVASKIQVSLESSLQKTSKSCADMQKMLFEERNH 908
0Y      1106FOAMOTIPITPLSPSLPEPSKYLBEGNSODPIEINDYNHLALATERNNIMVCTLETNRSL 1165
Db      909FAEIETEL-----QAEIVRMEOQHPEKV---LYLLSQLOOSQWA----EKOL 948
0Y      1166KEOVIDANTOLOS-LQAOSIEKSDOKPKODLEBGEVULLMEMLEKGLTIDSOULEKL 1224
Db      949EESVSEKQOQLOSTLKCD--BELKKREVCEBNQ-OLLENEIIKOKTLTLOVASRQK 1004
0Y      1225QLEN---LEVTEKLOTLOEMKNKITERN--ELQTFEDLK-----AEDHSUKODLSE 1272
Db      1005HLPRDTLSPDSFSFEYVPQPKPRSVKEXKFLQGSMDIEDLKYCSHNVNHEDDGDGDE 1064
0Y      1273NIEOSIELQDELRAAOEELR-----EQXQVDSFFQQLDCSYG-ISSPNHDVAVANQ 1323
Db      1065GDDEWKPFTKLWNVSRRKNIQGCSCCKMGCNKQC-GCRKQKSDCGVDCCDPTRCNRNQ 1122
0Y      1324EKVSLGFVNLSQSENLRERBELQTSKCALVSELRLAHVKSVEGENLETTKLNGLRK 1383
Db      1123GKDSLGYTERQ-----DSESSFK-----LE-----DETETPGLSFPNP 1157
0Y      1384EILKSESEVYLKSM--LENLKE-----DNKLEQEAEEY-----SSKENOFSL 1425
Db      1158--VCATPRSKILKMCVDVEQVLSKTPAPBPFLDLPELKHATVTEQENKSGKKKKRALA 1215
0Y      1426--EEVFSGSQKLVD 1438
Db      1216SNTSFSGSCPREE 1230

RESULT 11
US-09-595-684B-23
; Sequence 23, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Onashtl, Cara
; APPLICANT: Roman
; APPLICANT: Sakowicz, Eugenii
; APPLICANT: Valsberg, Eugenei
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; TITLE OF INVENTION: and purifying human kinesins
; FILE REFERENCE: cytopo36
; CURRENT APPLICATION NUMBER: US/09/595, 684B
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295, 612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ IDS: 105
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ. ID NO 23
; LENGTH: 1231
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-23

Query Match      6.4%; Score 943; DB 4; Length 1231;
Best Local Similarity 24.5%; Pred. No. 1,3e-38;
Matches 376; Conservative 258; Mismatches 491; Indels 410; Gaps 608

OY 3 EGDVAVCVVRVPLLORE--OGDQANLQMKAGNNITISQV DGT-KSFNFDKRVFNSHSTSQ 59
Db 6 KQIPRVAVLRCPRLVPKKEISEGCMQMLSVPRPQV--VGTDKSTTYDVFPRPSTQEE 63
OY 60 IYQEIAPVPIRSALQOYNGTIFAYGQTSGGKTYMWG-----TNSLGIIPQAIQEVF 112
Db 64 VENTAVAPLIKGVFKGVGNATVLA YGGTSGKTYSMGCAVTAEGENEPVGVIPRVIQLLF 123
OY 113 KIQEIAPNREFLLRVS YMEIYVETVKDLLCDDBRKRLPIREPFNNVYADLTIELMYV 172
Db 124 KEIDKSDPFEFLKVSYLEIYNEEILDLCPSEKQKQIIRBEPKEGIKVGLTETKVLV 183
OY 173 PEHVQWIKKGEKNHYGETKKNDDSSRSRHTI FRMIVESRDNRDPNSENCDGAVWVSHL 222
Db 184 ALDTVYSCIEQGNNSKTVASTAMNSOSSRSHALFTISEQKSKSDKNS-----FRSKL 226
OY 223 NLVDLAGSERASQTGAEGVRLKEGCNINSLF ILGVIKKLSDQAGGFINYRDSKLTRI 232
Db 227 HLVDLAGSEROKTVAEGDRLKEGININNGLLCIGNVISALGDQKKGAFAPYRDSKLTRL 236
OY 233 LQNSLGSNAKYIITCTTV--SFDETSLTQPASTAKVVRNTPHYNEVLDEALLKRYR 350
Db 237 LQDSLGSNSHTIMICVSPADSNLEETLNTLRYADAPARKIKKPIYV--IDPQT----- 348
OY 351 KEILDKQLEMLESSSETKQAMAKKEHTTOLLAELIKQHKREBRIWHLTNIVVASSQE 410
Db 349 AELNHLKQOQVQL-----QVLL----- 355
OY 411 SQQDQRYVKRRVTPWAPGKIQNSLHSA GSVDFCDMLSRLPNGFSKAKFSPMPSPETIDS 470
Db 366 -----LQAHG-----CTLPGSITVE-----PS----- 382
OY 471 VCTEFSDDDALSMDSNGIDAEMNLASKVTHREKTS--LHOSMIDFGQISDSVQPHDSS 528
Db 383 -----ENLQSLMEKN-----QSLVENEKLSRGLSAAQGTQAOILERRIIWTEQA 426
OY 529 KENCQIYLPKSGDMAECR-----VASPEKETSLLQOQOSKEEKEKELVQSELMIAEL 583
Db 427 NE-----KNNAKLEELRQHAACKLIDQKLETVLIDQEL-----KEVAEIIICNLQOILITOL 475
OY 584 EEOLSVAKNLEMYNVSREHSINAEVQTPVEKEVVRKEMSVLGDSCYNASNSDLODSSVD 643
Db 476 SDE-----TYACMAAIDTVAEQNAQVETSE-----TSRSSDAFTQH 514
OY 644 GKRLSSSHDECIEHRKMLQOKIVLDEEPIENLKK--SENDKO--KSESDQFMESIQCEAI 701
Db 515 ALRQWQSKELVELKALKALK-----EALARKWTQWDSQLOPQIQYQYQDNI----- 560
OY 702 MAEKANALBELALMNDNFNIILENETLKREIADLERLSKENQETNEFEILEKETQKEHE 761
Db 561 ---KEPELEVINLOREK--EEVLVEIQTKKDNQOKLSRRRRKRLQOELGQIADLKK-- 614
OY 762 AOLHIEISLKLVLNAEMYNQNLBEODETKTTLKKEQEIQALAEKLRADNLOKKRVNFD 821
Db 615 ---LNEQSKLLKLKSTERTYSKLQEI---RMKNQVRQL--MRQMEDAE-KRQW-- 663
OY 822 LSVMSGDEKLCCEIFQOLQOSISDAEAVTRDAQEKCSFLRSENLEIKEMKEDTSMVYNOK 881
Db 664 ---KQKDKVEIQLKE-----RDRKQKQ-----YELKLERNFQKQSNVLRK 702
OY 882 EKASLFLPKQLETSKNYKKMEADLOKELQSAFNEIYINGL--LAGKVPDRLSLVELE 939
Db 703 TEEAANAANKRLDALQKQREV-ADRRKETQS-----RQMEGTAAARYVMYMGNEIYV 753

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QY 940 KVVSEFSKQLEKALEKNALENEVITCLSEYKFLPNEVECLAKNQISKASEIMTLKQEGH 999
DB 754 VSTEAKRHLNDLLEDRKILAQDVAQLKE-----KKESEGEN 789
QY 1000 SASIISKOEIIMQOSEQIOLQTLDEVHTQSKVQOOTEBOYLKMKHMDLFEKYIRNKE 1059
DB 790 PPPKLRRTFFSLTEVRGOV-----SE 810
QY 1060 AED-LIREMENIKGTMESVEVAKIADTKHEL---EETIRDKEO-----LLEHEK---KYFF 1106
DB 811 SEDSITKQIESLEFETMEFRSAQIADLOQKLDABEDBEPKORWENIATILEAKCALXYLI 870
QY 1107 -QAMQITPITPLSLSPKSLVEGNSQDPIEINDYHNLALATERNNIWCLETERTNSL 1165
DB 871 GELVSSKIQSVKSLTESLSKQSTSCADMQKML-FEERNHFAIETELQAEIVRMEOQH--- 926
QY 1166 KEQVINDLNTLOSLQAOQSIK-----SLOKPKODLEGEVYKL 1204
DB 927 QEKVYVLSQOQ--QSQMAEKQLEBSVSEKQOQLSTLKCQDELEKREVECEQNO-QLL 983
QY 1205 LEMELKGLTDSQSLSEKQLEN---LEVTEKLQTLQEMKNITTIERN--ELQTNFEDL 1259
DB 984 RENELIKQKLTILQVASHQKHLPKDTLLSPDSFEVYQPKRPSRVAKEXLEQSMQIEDL 1043
QY 1260 K-----AEHDSLKQDLESENI EOSIETQDELRQAQELR-----EOKQVDSFRQO 1304
DB 1044 KYCESHSVNHEHEDGDDDEGDEEMKPTKLVNVRKNIOGSCGKMGCKQC--GCRKQ 1101
QY 1305 LLDSCVSG-ISSPNHDAVANOEKVSLGEVNSILOSEMELGERDELQTSKALVSELELRAH 1363
DB 1102 KSDGVGDCDPTKCRNRQOGKDSLGTVERTQ-----DBESSFK-----LE--- 1142
QY 1364 VKSEGENLEITTKLNGLEKEIIGKSESEVYLSKM--LENLKE-----DNKLKE 1411
DB 1143 -----DPTVTPQLSPFNRP--VCATPNSKILKEMCVBEQVLSKTPPAPSPDLPELWH 1194
QY 1412 QAEY-----SSKENQFSLEVPFSGQKLVD 1438
DB 1195 VATEYOENKAPGKKKKRALKALASNTSFRSGCSPISEE 1229

RESULT 12
US-09-722-139-2
; Sequence 2, Application US/09722139
; Patent No. 6355471
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6355471el motor proteins and methods for
; FILE REFERENCE: 1055
; CURRENT APPLICATION NUMBER: US/09/722,139
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1375
; TYPE: PRF
; ORGANISM: Human
US-09-722-139-2

Query Match 6.1%; Score 906; DB 4; Length 1375;
Best Local Similarity 25.5%; Pred. No. 9, 5e-37;
Matches 413; Conservative 247; Mismatches 531; Indels 430; Gaps 71;

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QY 105 PQAIOEVFKIIOEI---PNEEFLLRVSWEIYNETVKKLDCDRRKP-----LEIREDEN 157
DB 123 PRICEGLFSRINETTRWDBASFTEVSYLEIYNERVRLD---RRKSXTFLRVREHFX 179
QY 158 RNVYVADLFEELVMVEBEHVIOMIKKEGKRNHGETMTDNHRSRSTIF--RMIVSRDRN 215
DB 180 EGPYVEDLSKHLVONGVBEELMDKGINIRTTAAQGMVDSRSSHAIFITKFTQAKPFSE 239
QY 216 DPTNSNCDGAVVSHNLVLDAGERASQTAGEVRLKEGCNINRSILFILOVYKIKLSD 275
DB 240 MP-----CE---TVSKIHVLVDLAGSEBADATGATVRLKEGGINIKSLVTLGAKKQV-- 289
QY 276 GQAGFIRYRDSKLRILQNSIGNAKYIITCTIP--VSPDETLSTLQFASSTAGHVNT 333
DB 290 -----FVPRDSVLTWLMDSLGNSKTIMATISPAOVNGETLSTLRVYRANRINIK 344
QY 334 PHNVEVLDDEALLKRYKEIIDLK-----KQLENTLESSSETKAQMAKKEHTOL-LAEI 386
DB 345 PTINEDANVK-LIRELRABEIALKTLNLAQNGQIALDSEP-----ALSMEEKLOQNEARV 398
QY 387 KQHLKEREDRIWHLNIVVASSQESQDQRYKRRRTWABGKIQNSIHASGVSDPMLS 446
DB 399 QELTKEWTKN-WNET-----QNLKEQTL-----ALRKEGIG----- 429
QY 447 RLPGNFSKKAKRSPDPSPEIDDSVCT-----ERSDPDALSMD--SNGIDA 492
DB 430 -----VLDSELPHLIGIDDLSTIGIILYHLKEGQTYVGRDASTEDQIVLHGIDL 481
QY 493 E-----WNLASKYTHREKTSLHQSMIDFQGISDVQFHDSS-----KENOLOY-LPRKS 540
DB 482 ESEHCIFENIGIYAT-LIPLSGSQSVNGVQIVAEATHLNGQAVILLRTNMFRRNHKEA 540
QY 541 GMAECRK-----ASFPEKITSLQOOLSKSEKKEVLQ-----SEFLKALELEQULSVK 590
DB 541 AKLREKRSGLSSFSYSMTDL-----SKRENLSAVALNYPGLEFRQOREELEKLESK 595
QY 591 AKNLEMYTNSREHSHINAEOQ--TDVEKEVVRKENSVLGDSGNASNSDLODSSVDGRKLSS 649
DB 596 RKLIEEM-EBKQSDKALEMROEQEVETQKKEIIV-----QLO-----IR 635
QY 650 SHDECIEHRKM-LEQKIVDLBEFTENLNKKSSENDQKSSQODFMESIQLCEAIAEKANA 708
DB 636 KOESLSLRSPFHINKKDL-----LAEKEKEEBERLRQ----- 670
QY 709 LEEALMRDNFNDIILENETIKREIADLER--SIKENQETNEFEILEK--ETQKEHEAOL 764
DB 671 -QEIELOKRR-----QEEFTFLAVQEBLQRLKELNNKAEKQIFQEBDLOKEXBOY 724
QY 765 IHEIGSLKULVENAE---MYONLEEDLETK--TKLKEOEIQLAEIRKADNLQKV 817
DB 725 A-KLEIEKKRLEBOEKEQVWLVAHLEQULREKQEMIQLLRGEVQWVEEKR----- 775
QY 818 RNFPLSVMSDSEKLCBEIFQLOKOSLS---DAEATRDQKCSGLRSENELEKEMED 873
DB 776 -----DLGIRBSLRLVAKARAGDEDEELEKQLRFEFRKQVLVNLKEXD 825
QY 874 TSNWYNQEKRAASLFEKQLETERKSNYKWEADLOKELQSAFNEINYLNLGKAGVRDL 933
DB 826 LVOQKILKKEVQEOEILECLCKEHDKESRLLEKXIDESVTD-----VTEVPQDDE 876
QY 934 SRVELEKXSEFSKQLEKALEKNALENEVITCLSE-----YFPLPNEVECLKN--QISK 985
DB 877 KIRPVEYRLQYKERQIQ-----YLLQNLPTLLEKORAFILDRGPLSLNNTLYOYVK 930
QY 986 ASEEMILLKQEGHSASISKOEIIMQOSE-----QILOLTQEVN---HTOSKYQOQREE 1037
DB 931 EMBE-----KEBOLAQYQANANOQKQLOATEFTFANLARQEKYRKKEK 974
QY 1038 QYIEMKAMMDLFEKYIRNKSADLILREMNULKGTMSVEVAKIADTKHE--LEETIRKE 1096
DB 975 EILS-----REKQOREALERLALRLERRHSLQ-----RHSTIGTEIBOR 1016

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Db 1095 PLMDARINAYIE-----EVQRRLQDHRVISSECGSTADTMKDNKEXLHNGTIOBKLY 1148
Qy 1254 TNFEDLK-----AEHDSLKODLSENI EOSIETODEL-----RAOEELREBK 1295
Db 1149 ELCRDLCLVLMPEPDAAACANHPILQODL---VQSLDMKTEIPDLVLPNGVQVSSKQOT 1205
Qy 1296 QLVDSFRQOOLDGCSGISPNHDAVANOBYSLGEVNSLOSEMLRGERDELQTSCKALVS 1355
Db 1206 TLVDNI--YFLHGNMEVNP-----SLAEVQULLTYTKVMGDSGHDQCSQILV- 1251
Qy 1356 ELELIRAHVKSVE-----GENLEITKKNLGLK-----ELIGSESESV 1394
Db 1252 ---LNTHTALVKECCVFPRIIRSNIPRPAQDPVL-KCHALSEPRCVVPEKKNVSTV 1307
Qy 1395 LKSMLENKEDNNKKEQAEEYSKEN--QPSLEEVSGSQKLVDEIEVLKAOLKAABER 1452
Db 1308 ELVFLQKLKPSVSGSRNSPPEHLOEAPNVQLFTTPLYLQSGQNVAP--EVMKLTJNSQDEA 1365
Qy 1453 L 1453
Db 1366 L 1366

RESULT 14
US-09-721-689-2
Sequence 2, Application US/09721689
Patent No. 6440685
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6440685el motor proteins and methods for
FILE REFERENCE: 1055
CURRENT APPLICATION NUMBER: US/09/721,689
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1375
TYPE: PR1
ORGANISM: Human
US-09-721-689-2

Query Match 6.1%; Score 906; DB 4; Length 1375;
Best Local Similarity 25.5%; Pred. No. 9.5e-37;
Matches 413; Conservative 247; Mismatches 531; Indels 430; Gaps 71;

Qy 6 AVKVCVRVPLIQRGGDQAN--LQWKAGNNTISQV-----DGRKSFNFDVYF 51
Db 3 SVKVAVRVRPMNRREKDLKAKFLIOMEKSTITITNLIKIEGGTGDSGRERTKTYTYPDSF 62
Qy 52 NSHSTST-----QIYQELAVPIIRSALOGYNGTIFAYGOTSSGGTYTMMGTSPNSLGI 104
Db 63 YSADTSPRYVQEMFKTLGTDVVSAAFEYNACVFAYGQSGSGSYTMGNSGDSGLI 122
Qy 105 PQAIGEVFKIOET---PNREFLRLVSYMEIYNETVKDLCDRKKRP---LEIRDEPN 157
Db 123 PRICEGLFSRINETRWDBASFRTEVSYLEIYNERDRL---RKSSKTFPLRKREHPK 179
Qy 158 RNVYVADLLEELVMPENHYIOWIKKGEKRAHGETRKMDHSRSHITF--RMIVESDRN 215
Db 180 EEPYVEDLSKHLVQNGVDVEELMDAGNIRRTAATGMNDVSSRSHAFITIKFTQAKPDS 239
Qy 216 DPTNSCNGAVMVSHLNLVDLAGSEPRASOTGAEGRVLEKGCNINRSIFLIGOVYIKKSD 275
Db 240 MP-----CE---TVGKIHVLDLAGSEPRADATGATGRVLEKGNINXSLVTLGAKKQV-- 289
Qy 276 GGAGGFIVRDSKLRILIONSLGNAKTVITITRP--VSPDETSLTIOFASSTAKHYANT 333
Db 290 ---FVPRDSVLTMWLKDSLGNSKTIMIATISPADVNYGETLSTLRVYANRAKNIINK 344
Qy 344 PHNVEVLDEALLLKRYREIIDLK-----KQLENLBSSETKQAOMAKEHTOL-LAEI 386

Db 345 PTINEDANVK-LIRELRABIAKTLAAGNOIALIDSTP-----ALSMEEKLOONEAV 398
Qy 387 KQHKREDRIRIHLINIVVASSOESOODRVKRRRTVAPKGIIONSLHAGSVSPDMLS 446
Db 399 QELTKEMTNK-WNET-----ONILKEQTL-----ALRKEGIG----- 429
Qy 447 RLPGNSSKAKFSDMSPFEDDSVCT-----EFSDFDALSMDP--SNGIDA 492
Db 430 ---VVDSELPHLGIDDDLTSTIGIILYHLKEGOTVYGRDASTODIYVHGLD 481
Qy 493 E-----WNLASKVTHREKTSLHOSMIDFGQISDSVOFHDSS-----XENOLQY-LPKDS 540
Db 482 ESEHCIFENIGTIV-LIPLSGSQSVNGVQIVKATHLNGQAVILLGTTNMRFPNHPREA 540
Qy 541 GMAEGRK---ASFKEKTSIQOOLQSKKEEKELVQ-----SFEKIALFELQSLSVK 590
Db 541 AKIREKRSGLSSFSLSWTDL-----SKSRNLSAVMLYNPGLFEPERQOREELEKLEBSK 595
Qy 591 ANNLEWNTSRSHSINAEOV-TDVEKEVVRKEMSVLGDGYNASNDLQDSSVQGRKSS 649
Db 596 RKLIEEM-BEKQSKDALELRMQQEVETQKETEIV-----OLQ-----IR 635
Qy 650 SHDECIEHRKM-LEOKIVDLEEFLENLKKSSENDKQSSQEDFMESIQLCBAINAERANA 708
Db 636 KOEBSLKRSFPIENKLDL-----LAEKEFEERLRQ----- 670
Qy 709 LELALMRDNFQNIILENETLKREIADLER--SLKENQENTFEILEK--ETQKENEQOL 764
Db 671 -QEILQOKR-----QEBETFLRVOEELQRLKEILNNEKAKRFQIFQELDLOQKEKEQY 724
Qy 765 IHEIGSLKLVENAE---MYNONLEBDLETK---TKLKEQETQLAEIRKADNLQKV 817
Db 725 A-KLELEKRLBEQKEQVMLVAHLEBQLRKQWIMQILRRGEVQWMEBER----- 775
Qy 818 RNFDSVMSGSEKLCBEIFQLOKSL---DAVAVTRDAQKESFTLRSENLEIKERMED 873
Db 776 ---DLEIGRESLRLVKERAGGDEGELEKAOQRFEPFRQQLVTKLVNLEKD 825
Qy 874 TSNWYNOKERKAASLFEKQLETEKSNYKMEADLOKEQASAFNEINYLNGLAGVPRDL 933
Db 826 LVQOKDLIKKEVQGEQELBECLKCEHDKESRLKHEBSYTD-----VTEVPDPE 876
Qy 934 SRVLEKKVSEFSQLEKALEBKALBNVTCISE---YKLPNEVECLKN---QISK 985
Db 877 KIKPEVRYLQYKERQLO---YLQNHLPITLLEKQRAFEILDRPLSLDNTLVQVEK 930
Qy 986 ASEEMIMLKQGEHSASIIKQELIMQOSE---QILOLTDVY---HTQSKVOQTEE 1037
Db 931 EMEB-----KEBOLAQYQANANOLQLOQTFEFTANIAEQEERKKEK 974
Qy 1038 QYLEMKRMHDLFEKYIRNKSSEADLLREMENTKGTMSVEYKIADTKHE-LBEITRDKE 1096
Db 975 EILLES-----REKQREALERALARLERRHSAQO-----RHSITGTELEBOR 1016
Qy 1097 QULHEKKYFFQANGTIFPIPLPDSLPSPKLVAGNSQDPEIENDYANLIALATERNNIV 1156
Db 1017 Q-----KLASLNGS-----SREDSGLQA 1034
Qy 1157 CLETERNSLKEQYIDINTQLOSLQASIEKSDLOKRODLEBEV-KLLLEMLLGHGLT 1215
Db 1035 STEBQERALEKQDERLEVEIQOLKOKIYVDVQKHGHGLBEKVASSSLPSYSAEKSHLV 1094
Qy 1216 ---DSQSL--TEKLOJENLEVEYKLOTL-----QEEKNKITTIERNELO 1253
Db 1095 PLMDARINAYIE-----EVQRRLQDHRVISSECGSTADTMKDNKEXLHNGTIOBKLY 1148
Qy 1254 TNFEDLK-----AEHDSLKODLSENI EOSIETODEL-----RAOEELREBK 1295
Db 1149 ELCRDLCLVLMPEPDAAACANHPILQODL---VQSLDMKTEIPDLVLPNGVQVSSKQOT 1205
Qy 1296 QLVDSFRQOOLDGCSGISPNHDAVANOBYSLGEVNSLOSEMLRGERDELQTSCKALVS 1355

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Db      1206 TLVDM1--YFLHGNEVNV-----SLAEVOLLLYTTVKWMDSGHDQCSILV- 1251
Qy      1366 ELELRHVKSVE-----GENLEITTKLNGLEK-----EILKSESESV 1394
Db      1252 ---LANTHALVKEDCVFPRIRSRNIPPPGAQFDIT-KCHALISERCVAVBEKKVSTV 1307
Qy      1395 LKSMLENLKEDNNKLEQAESEYSSKEN--QFSLSEEVSGSKLVDEIEVLKAQLKAEBR 1452
Db      1308 ELVFLQKLPKPSVGSNSRNPHEHQEAPNVQLFTPTPLYLQSSQVAP--EVLWKLTFNSQDA 1365
Qy      1453 L 1453
Db      1366 L 1366

RESULT 15
US-09-914-259-20
; Sequence 20, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 963
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-20

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Query Match 6.0%; Score 890; DB 4; Length 963;

Best Local Similarity 27.5%; Pred. No. 3.8e-36;

Matches 298; Conservative 196; Mismatches 343; Indels 246; Gaps 41;

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Qy      7 VKVCVRVPLQRE--OGDOANLQWKAGNNTISOVDGTSFNFDRVFNSESTQIYOEI 64
Db      9 IKVMCRFRPLNSEVNRGDKYIAKFG-GEDTV--VIASKPYAFDRVFOGSTSQEQVYNDG 65
Qy      65 AVPIIRSAOGNGITFAIGQTSNGKTYTMMG---TPNLSGLIIPQAIQVFKIIEI-PN 120
Db      66 AKKIYKDVLEGNGTIFAYGQTSNGKTHMEKLDHPPEMGIIPIRVODIFNYISMDEN 125
Qy      121 REFLRVSAMEIYNEVTKDLLCDRRKRPLEIREDFNRNVVADLTELVMVBEHYIOWI 180
Db      126 LEFHIKVYFETLYDKIRDL--DVSKTNLSVHEDKNRPVYVKGCTERFVCSPEVMDTI 183
Qy      181 KKGKRNRYGKETKNDHSSRSHITFRMIVESRDRNDPTNSENCDAVMVSHNLVDLAS 240
Db      184 DEGRKNRHYAVATNMNHSRSHIF--LINVQENQTEQK-----LSGLYIVDLAS 235
Qy      241 ERASQTGAEGVRLKGCNINRSLFTIGUYIKLSDGAGCFINRDSKLTILLQNSLGN 300
Db      236 EKVSKTGAAGVALDEAKNINKSLISALAEGST--YVPRDSKMTIRILQDSLGN 293
Qy      301 AKTVICITTPVSFD--ETLSLQFAPSTAKHVRNTPHNEVLDDEALLKRYKEILDLKK 358
Db      294 CRTTIVICSPSSYNESETKSTLLFGQRAKTKIKNTVCUNVELLAQWKKRYEKE----- 347
Qy      359 QLENESSETKAQAKEEHTQLAEIKQLHKEREDRIWHLTNIYVASSQESQODORYK 418
Db      348 -----KEKNKILNNTIOWL--ENELNMRNGETYPRIDEQPDKEKANLE 388
Qy      419 R---KRRVTWAPGKIQNSLHASGVSDFDMLSPGNFSKKAFFSDMPSPFEIDSVCTEF 475
Db      389 AFTVDKDIT-----LTNDKPATAIG-----VIGNFTDAER-----RKCEBEIAKLY 429
Qy      476 SFPDALSMDNSGIDAEWNLASKYTHREKTSLHOSMIDFGQISDSVQFHDSSKENQLOY 535

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Db      430 KQLDDK-----DEEINQSOQLVERKLT-----QMLD-----QEBLLAS 462
Qy      536 LPKDSGDMAECRKASFEKEITSLQOOLQSKKEEKKELVOSFE---LKTALIEEOLSVKAK 592
Db      463 TRRDQNM-----QAEINRLQAEINDASKKEVKEVLQALELAVNYDQSKQEBEDTK 514
Qy      593 NLEMYTNSREH-----SINAEVQ-----TDVER-----EVRKENSVLDSGSYNSNSDL 637
Db      515 EVELLSDELQNSATLASIDAELOKTKENTNNQKRAEMMASLKLDALEIATAGNNDV 574
Qy      638 QDSVVDG-----KRLSS-----SHDECTEHRKML----- 661
Db      575 KQEGCTGMIDEEFTVARLYISKMKSEVKTVMWRCKQLSESTQTESNKKMEENEKEILAACOL 634
Qy      662 -----EQKIVDLEEFTEFNMKSENDKQSSQODMESIQCEALMAEKANLLEELALMR 716
Db      635 RISQHBAKIKSLTEYLQNEQK---KQLESVDALSEELVQLRAQEKVHEME-----K 685
Qy      717 DNFNIILENETLKEIADLERSLKENOETNEFEILEKETQKHEBAQLIHEIGSLKLV 776
Db      686 EHLNKVQTADEVKQ---VEQIQSHRETHQOI-----SSLRDEVAKAKLIT 731
Qy      777 NAEWYNQMLEEDLETKLKLKEQEIQLAELRRADNLQKVRNFDLSVSMGSEKLCDEI 836
Db      732 DLQDQNM-----MLEQERLVEHEKLTQDOEKSRKLTHELTVQDRREQARQDL 782
Qy      837 FOLKQSLDAEAVTDAQKQCSFLRSBNLEKXNE---DTSNNYNQKKAASLFEKOL 892
Db      783 KGLEETVAKELQTLNLRK--LFVODLATRVKKSADISDDTGSGSAQOKK-ISFLENNL 839
Qy      893 ETEKSNYKMM---BADLOKELQSAFNEINLYLGLAGKVPRLDLSRVELEKTV---SEPS 946
Db      840 EQLTVYHQVLVQNDNDLRCELP-----KLEKRLRTAERY 874
Qy      947 KQLEKALEKXALENEVTCLESEYKFLPNEVECLKQKQISKA-----SEEIMLLKQEGEH 999
Db      875 KALESAKKE--AKENASDRKRYQ---QEVDRIKEAIVSKNNARGHSAQKAPIRPGH 929
Qy      1000 SAS 1002
Db      930 PAA 932

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Search completed: October 22, 2003, 21:12:54

Job time : 66 secs

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[illegible]

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Db      964 -----LATERK--VASSIEKSDSPDKVADIMNOIQELRTVCERKTEITDILKQELKIDN 1018
Qy      1201 VK---LLLEMLLKGHLTDQSLSIEKLOLELVETBKQTLQOEKMNKITTIRNELQTNFE 1257
Db      1017 CKYNSALVDRE-----ESRVLIRKOEVDITLDKETLR-----LRLISE 1054
Qy      1258 DLKAEHSDLKODLSENITPO-----SIETODELPAAOEELREOKOLVDSFROQLDSCV 1310
Db      1055 DI--ERDMLCDDLHAHTEQLMMLTBAKKHSGLLQSAOEELTKKHALIQELQHKL----- 1107
Qy      1311 GISSPNHDVANAJOEKVSLGEVNSLQSEWMLRGERDELOTSCALVSEELRAHYKSVGE 1370
Db      1108 -----NOKK-----FEVEQKKNEVNPXKMQL-----EHVDSMAE 1137
Qy      1371 N-----LEITTKLNGLEKELICKSESESVLKSMLNLEKEDNNKKE--QAEYS 1417
Db      1138 DPOSPKPPHPQTHAKLLETQEOEI-----EDGRASKTSLSHLVTKLNEDEVKNAELLR 1193
Qy      1418 SKENQFSLSEVFSQSOKLVEIEVLKQOLKAEBRLIEKIDRYEVLQTN----- 1468
Db      1194 MKEQUREHENVLRLESQOLTEKMWLLQGOGLDITKQKENSDDNHDPNOQLKKEQESIKER 1255
Qy      1469 ---TNIVGKLETPLOADHEEDSIDRSEMEIKVLGKELERNQYLLERLOEKLELSNK 1525
Db      1254 LAKKIVBEMK--MKADLEEVQSAVLNKEKECRLMDEVERTQTLSEKARQOEKQRLSK 1311
Qy      1526 LEILOKEMETSVLLKDLQCKLESULSEN--TIKENIDITLTKHISDTQAOLOKTQOELQ 1583
Db      1312 LEEMVEERERTSOEMEMLRKQVECLAENGKLVGHQNL-----HOKIQYVVRKKENVR 1365
Qy      1584 LAKNLAIALASDNCPILOEKETSA 1606
Db      1366 LAEETEKIRAEVNPFLKEKKRSES 1388

RESULT 2
US-10-171-311-4
; Sequence 4, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171.311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3899
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-4

Query Match      6.9%; Score 1015; DB 15; Length 3899;
Best Local Similarity 19.6%; Pred. No. 1,5e-43;
Matches 700; Conservative 630; Mismatches 1164; Indels 1072; Gaps 148;

181 KKGKRNRRHYGTKNNDHSSRSHTTFKMTIVBSRDRNDPTNSNCGCAVWVSHLNTVDLAGS 240

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Db 34 KQOKKR---KTSSEKHDSAHNDLIDQSQCNEMVINSQCVSESTVIPESITMTLHSG 90
Qy 241 ERASQTGBGVRLK-----EGCN--INRSLFITGVYIKLSDQAGGFIVRDSKULR 291
Db 91 EITSHOQFSVLBESEISTTADCSSEVNGCSFVM-----RTGKPTN 132
Qy 222 ILQNLGNAKTVIICITTPVSFDETLSTLOFASTAKVVRNTPHNVENLDEALLKRYK 351
Db 133 LREBEFG-----VDDSYS-----EQGADSPTHEWMESELAGQH-- 169
Qy 352 EILDKQLENLESSETKA-----QAMAKEH---TOLLAETIKOLHEKEDRIWHLT 401
Db 170 EIEELNRELEBRVYVGTBGLQLOLQEFALIKORGIITQLTANIQARREDEMTREPL 229
Qy 402 NIVASSQSQODQVKKRRVTA PGKIQNSLHAGVSD-----FDMLSR 447
Db 230 EL-----TEOSQLOIQFOOLOQASETLRNSTHSTADLLQAKQOILTHOQOLEQDH 282
Qy 448 LRGNSK-----KAKSDMPSPFEIDSVCTESFDDDLMSMDSNGDAE 493
Db 283 LLEDQKKEDFTWQISFLQEKIKVYEWQDKKVENSKKEIOEKETIIEELNTIKIIEE 342
Qy 494 ---NLASKVTHREKT--SLHOSMIDFGQ-----ISDSVQFHDSSKENOLQYLPRXS 540
Db 343 KKTLELKQTLTADKULGELQEQIYQKQEIKNMKLELTNSQKQROSEELIKOLM---- 398
Qy 541 GDMACRK---ASFKEKITS-LQOQLOSK--EBEKKEIVOSFELKLALEBOL--SVKA 591
Db 399 GTVELQKRNHKSQFETDI VQRMQEQTORKLEQRAELDEWYGOQI VQMKELIRQMA 458
Qy 552 KNLWNTNR---EHSINAEVOTDVEKVVKEMSVLQDSGYANASNDLODSVUGKLS 648
Db 459 QMEKKTTHKEMENALRSYSNITVNEQIK---LNNVAINELNIKQDINSQEKELK 513
Qy 649 SSHDCIHRKMLEQKIVDLSEFIENLNKSENDQKSSODFM-----ESTOLCEATMA 703
Db 514 BELGILBEKCALQOLEDVLELFSRQIQORAQITAEQSKNEAKHSITVEDIKA 573
Qy 704 EKANALE---ELAL-----MRDNFNIILENETLKEIADLER----- 738
Db 574 EIVSASESRKELELGHAEVNTYKIKLEWLEKEKNAVLDRMAESQE--ALELRLTQLLFS 632
Qy 739 ---SLKE-----NOTNEPELL--EKETOKEHE 761
Db 633 HEEBELSKLEDELEIHRINIEKLDKNLGIHYKQOIQDQNEWSQKILETQFQKMLITQO 692
Qy 762 AOLIHEISLKLVAENAEVYQNLNE-----DLETKTKLKE-----OEIOL 803
Db 693 NQILIEISKLQDLOOS--LVNSKSEEMTLQINELQKEIILRQEKKEKTLQEQVQELQ 750
Qy 804 ---AELRKRADNLOKKVRNFDLSV--MGDSEKLCSEIFQLKQSLDAEAV----- 849
Db 751 KTELLEKQMKEMENLOKQFQLEAENSLKDEKTLDEMLKIHNPVSGEBELILDSIK 810
Qy 850 ---TRDA--QKQCSFJRSEN-----LEIKEMERTSWYVNOKEQKQASLFEQOLETEKSN 898
Db 811 SKSKQSVWEKEIIEIENEDLKQOQIQINEIEIKQRYNTPFAEKNFVYQELQOEYAC 870
Qy 899 YKKMADLO---KELQ-----SAFNEINYLN----- 921
Db 871 LLKVKQDLEDSKQOLEYKSKLALNEBELHQRINPTTVKKKSVFDEDKTFLVATLBM 930
Qy 922 GLLAGKVERDIL-----SRVELEKVSFESKQLEKALEKNALENEVTLSSEYK-- 970
Db 921 GEVVEKQDTLEMEKLEVTIKREKLEISQRLSDSEQDKQNGEISFLNEBVKLSKQEKQV 990
Qy 971 -FLNEVECLKQ-----QISKASEIMILKQEG--EHSASITISK----- 1006
Db 991 SLRCELEIITINHNAEVNOQSCDTQVSSLLDGVNMTSGAGSVSKVKKSGEBSKATMV 1050
Qy 1007 ---OEIINOQSEO---ILQDLDEVHTHQS--KVQOTEQOYLE-----MKKHNDLFL 1050

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Db 1051 EDKVSFENMTVGEESKQEQILDLHLPSVTKESSLRATQPSENDKLQKELANVLSKQNDL- 1109
Qy 1051 EKYIRNKSEAE-----DLRE--MENIKT-----MESVEKTAIDTKH 1086
Db 1110 ---RLQNEAORICLSLVYSTHVQVREYMEKQKALCSLKEELIFAQEEKIKELQKIH 1165
Qy 1087 ELE-ETIR-----DKQULLH-----EKKYFQAOQITFPIPLSDSLSPSKLV 1128
Db 1166 QLELOTMTQETGBGKRLHLILGLQKQAVSEBQSYFQITLQSV-----LGEYTPALKC 1220
Qy 1129 EGNQSDPIEINDY-----HNLLALATERNNIMWCLET----- 1160
Db 1221 EYNAEDKENSQDYSISNEDEPELODYREVQFQEMWHTLLKNVVEEYKLVVLQTRLSKI 1280
Qy 1161 ---ENSLKEQV-----IDLNTQLOSLQOQSIKSLQKRPK 1193
Db 1281 WQOQTDGKMLEFGEENLRKEETEFLSHSQMTNEDIDVNHKSKLSDLEKTLQEEQV 1340
Qy 1194 QDLR-----EGEVKLLLEMLKQHL-----TDSQSLI 1221
Db 1341 QELBESLSSLOOQKLETQNTQNAEHLQKRLQAVSESTVPSPSLPVDSVVTESDAQRTM 1400
Qy 1222 ---EKLOLENLEVTEKLOTLQOEMKNITTI-----ERNE 1251
Db 1401 YPGSCVKKNIDGTIEFSGEFGVKEETINIVKLEKQYQOLBEEVAKVIVMSIARAQOTE 1460
Qy 1252 L-----QTNFEDLKAENDSLKQOLSENIESISIEFQDLBRLAQ 1288
Db 1461 LSRISGKENTASSKQAHAVCOOEQHYFNEKLSQDQGFQTFETVD--VYRKEFEKLS 1518
Qy 1289 EELREQ-KQLVDSFRQ-----QLDSCVGIS---SPNHDVANO---EKVSLGEVNS-- 1333
Db 1519 KELGEHGEIILSNSDPHDIPESKDCUTLIEBMSKSKTITVROSIDELISSVMSDMSR 1578
Qy 1334 ---LOSEMLRGEDELQTSKALVSELELR-AHYKSVGENLEITTKLNGLEKEILQKS 1389
Db 1579 QLMNEBQLEDMRQGLVAYQEHQOATELLRQAHMRQNE-----RQ 1619
Qy 1390 ESEVYKSLMLENKEDNNKLEQOAEYVSKENQPSLEVPFGSQKLVIEIYKALQKQA 1449
Db 1620 REDQ-----BOLQBEIRLRLQOLAORSSINENIVS--REBYLLELALQKLSLQ 1670
Qy 1450 EERL--EIKDRDYFELVOTANTNLVEGKLETRPLADHEDSDIDRSEMEIKVLGEXLER 1507
Db 1671 REKLCCETLRNNS---TOTQNGENQGEVE--BOTFEKELDKRPEVVPPEILSNF--- 1720
Qy 1508 NOYLLERLOEBKLELNSKLEILOKEMETSVLLKD-----LQOKLESLSENIILKE 1559
Db 1721 -RYALQKAN-----NRLKITLLEVVKTTAAVEETIGRHVGLIDRSSKQSSASLIVRS 1773
Qy 1560 NIDPTLK--HNSDTQALQK-----TOBELQAKVL--ALIAS 1593
Db 1774 EAEASVSKCVHBEHTRVDESIPSYSGSDMPRNDIMMSKTEBETELSORLVNSGFGAGT 1833
Qy 1594 DNCPIQOE-----KETSADCVHREBKILLTELMOKTNEOKL 1633
Db 1834 EIDPENELMNTISRLQAAVEKLEIAISFSSQLEHNAKVUTQTELMRSPFQKQOEAATSL 1893
Qy 1634 ---LHEKNEL--EQAOVELKCEVENHMKMSITESKSSLESLOHEKHD-----TEOOL 1679
Db 1894 KQOEBLRLRLHBSARQGLAVELS-KAEYIGDQADBKTLFENQIQKTDIIDLREBEL 1952
Qy 1660 LALKQOMQVTOEKKELQOTNEHLTAEVDHLKENIELGLNFKNEAQOKTTTEOCLINENK 1739
Db 1953 LCASNRLOELBAQOQIOEBERELLSROKEMAK--AEAG-----PYEQOOLDETE 1999
Qy 1740 ELESQNRHLOCEIEELIMSKLQDKESALETLESEQKVNLNLOQEMWMLMEBELKNSQRT 1799
Db 2000 KLMKEKLEVQOAEKVRDQKQVAYALF-----IDVEQVSR-FTELQEKNTLELM 2049
Qy 1800 VIAERDQLODLRLRESVENSIEOTDRLKQAOELQOKQKVQELTSQISVL----- 1849
Db 2050 DLROQNALERKOLEMKRKFLEQOALDRNEHNDVQO--EIQKLEQOLKVVRFRPQISHO 2107

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QY 1850 OEKISLLENOMLVNATVETLSEBDLNOQKOHLESEIETLSLSEKEFAL----- 1902
DB 2108 TREVGEOLANHLKEKTKSCSELILSKOELOBDIOERNEIEIKLEFRVRELEQALVDRKH 2167
QY 1903 -----EOAECDKADDAKRTIDITEK-1SNEEOLOQATNLKETLYEREL-1QCKE 1952
DB 2168 FGAVEAKPELSLEVOLOAERDAIDRKEKITNLEEOLEOFREBLEKNSEVOQLHMQLEI 2227
QY 1953 OLALNTEHRETLKSDALGKME-----OERDEAKVIALTEKMSLEB 1998
DB 2228 OKKESSTRLOELEQENKLEFKODMEKGLAIKESDANSTODQVLFKFKAOITIOEKVEID 2287
QY 1999 QINENVTTLKEGGEKETFYLPORPSKOSSQMEELRESIKTDQLE-----E 2047
DB 2288 QINQVTKLQ-----QOLKITTNKVIIEKNELRIDLETOIECLMSDOECVKEN 2336
QY 2048 AEKISEATNEIKNLAKISSLEBEILQNASILNEAVSERENLRHSKQOLVSE--LEQ- 2103
DB 2337 REEBEIQOLNEVIEKLOOEELANIGOKTSMNAHSLSE--EADSLKHQLDVIAIEKALBEQ 2393
QY 2104 -----LSLTKSRDHAFAQ-----SKREDEAVNKIASLAE-----IKLTR 2141
DB 2394 VETANEEMTPMKVNLKETNPKANQLOLTOELFSLKRE-ESVEKIQSTIPENSUNVAIDHLK 2452
QY 2142 ENDEF-----RDSKESLOEQSHLSE-----LCTYKTELQWLKQOKEDINNKLAEKV 2190
DB 2453 DKPELEVLVTEDALKLENQTYFKSPENGKSGIINLETRILQLESTVSAKDELQCYK 2512
QY 2191 EV-----DELIO-----HLSLKEQ-----LDQIMELELN----- 2216
DB 2513 QIKMOEOGOFETEMLOKKIIVNLOKIVEEKAALVSOIOLEAVOYAKFCODNOTISB 2572
QY 2217 -----KLKNVLECEKMDIMEKISVLRMQNEP-----OOEEDVAERMILBS 2260
DB 2573 PERTINQNLNLEBDELSGDISALTRISELSQVAVEMTSLILEQVEIABK-NVLEK 2631
QY 2261 RNO--EIOELMEKISAVSBOHTLLSLSSELOKETEAHNGCMLIKESLSTLSRFS 2318
DB 2632 EKKLELOKLBNENEKKEKKEKSPDVEVLKTTTELPH-----SNBESGFNELBA 2685
QY 2319 LQTEHVKLNTQLOTLINKRVVTRIAVVEDH--SLIKVE--KDLAAEK-----RH 2367
DB 2686 LBAESVATRAELASVYEKAEKLOEBLLVETNMTSLQKLSQVRDHAIEKEXLSLEKE 2745
QY 2368 DELRLQ--LOCL--BOHGRKMSDSASEB--LKPEIEFLNLTFKKANIISVODDS 2419
DB 2746 DETEVESKKAQCFEPLPIKLSKISASQTDGTLKISSNOTFOILVAKAGIQINLOSBS 2805
QY 2420 --EVQVFLNQVSTLOEBLEHKKGMQWLEFGDLHVDAKLSSEGMOENRIAST-- 2473
DB 2806 SEEVTEIISQ-----FTEKIEKQELHA-----AEIDMSRHISSETJLK 2846
QY 2474 -----IOLLTKR--LKAVVO-----SKT-----QRETT-----VY 2496
DB 2847 REHYAVAVOLLKECCGTLKAVIQCLRSKESGSIPELAHSDAYOTREICSSDGSQWQGIY 2906
QY 2497 LNO--FEAKLOEKKEON-----KELMRREHHGPSA-----SW 2528
DB 2907 LTHSGOFDILASBERGESSESATDSFKKIKGLRAVHNGSMOVLSTLESFYSIGEDHSIQ 2966
QY 2529 E-----ENARLLGLIKTVODESKLQSRIKMLENELNLVKDAMH-----KGRVAI 2576
DB 2967 QUSEPFLERKAVYINTISLKDILITMQ-----LQREAEVYDSSQGHESPSDMRGELLLA 3021
QY 2577 LODKLI-----SRNAEELNAMOVLTKKODNIQAMK----- 2609
DB 3022 LOQVFLERSVLLAARTEIYALGTDAVGLNLCBRCIOEQCEVEYOAMECLOKADRS 3081
QY 2610 -----ELENLOKMAKAVPYKEID-----NLKTR-----VVKIMEKIKYSKAT 2650
DB 3082 LLSIEIALHAKONGKRITTLKREOESSEKPSOELLVYNIQOKOSOMLENOVELLSMK--DRAT 3140

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QY 2651 DOIYVLSCEBDEKEGLRLKEEDLRPAODNTTVCPKDYOKASTPVTGCGSGGIYQ 2710
DB 3141 E-----LOEQLSSEKMWVAEELKSELQTKLEBETTLKQKHKL----- 3179
QY 2711 STAMVLQSEKALRELSHYKKKYHHL.SRTWSSSEDR-----KTKAKSDAHSSHT 2762
DB 3180 -----ELEAFLEVKDKTDEVLHNDTLASQOKSRELOMABEKAK-----L 3223
QY 2763 GSHRSGPHKRTYRNG--PVTPERSEMPSLHSGPKSESSYKRVVSPNRSEIYQVWS 2821
DB 3224 GRSERDKREELDLKFSLESQQRNLQNLILLEQOKOLNIESQOKIESQRMUYDAQLSBE 3283
QY 2822 PGKTGMKHILSPSVYGLHKRALSPNSSEMTQVIVISPKTGLKULTESTLFPNLSSP 2881
DB 3284 QGRNLEQVLESEFEVRIREMSSTLDRREHLAOLQSSDGTQSGRPPPLESDLEKLOKO 3343
QY 2882 C--KOQVOENLN--SPKGLFVRSK 2904
DB 3344 LEEKSRIVEELNTEKTKYKLSLOTR 3369

RESULT 3
US-10-171-311-8
; Sequence 8, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3917
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-171-311-8

Query Match 6.9%; Score 1015; DB 15; Length 3917;
Best local Similarity 19.6%; Pred. No. 1.6e-43;
Matches 700; Conservative 630; Mismatches 1164; Indels 1072; Gaps 148;

QY 181 KKGKRNHAGETKMDHSGRSHTIFRMTVESRDRNDPTNSGCGAVMWVSHNLVLAGS 240
DB 34 KKQKKR--KTSSSKHVSAHDLNIDQSCNENYINSQVSESTVPIPESTIMTTHSG 90
QY 241 ERASOTGAEGVRLK-----EGCN--INRSILFLOVYIKLSDQAGGFINYRDSKLTR 291
DB 91 EITSHQGSFVLEBEISITTDADCSVNGCSFV-----RKGKPTN 132
QY 292 ILQNSLGNNAKTVIITTPVSPFDTLSTLOPASTAKHVRNTPHNEVULDEALLKRYK 351
DB 133 LIREEFQ-----VDDSYS-----EOGQDPSPTLLEWSESLAGKH-- 169
QY 352 ETLDLKQJENLESSETKA-----QAMAKEH--TOLAEIKQJHKEDEIRIMHLT 401
DB 170 ETEBLNRELEEMRVYTGIEGLOQLOEFEPALIKORDGIITOLTANLOQARREDETRRELT 229

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QY 402 NIVVASOESODORVYKRRBYTWAPGKILONSLSHAGVSD-----FDMLSR 447
Db 230 EL-----TEBOSQKLOIOPOLQASSETIRNSTHSTAAIDLQAKOQIILTHOOQLSEBQH 282
QY 448 LPGNFSK-----RAKPSDMPSPFEIDSVCTERSFPDALSMDMSNGIDA 493
Db 283 LLEDYOKKEDFTMQISFLQEKIKVYEMBODKKVENSKBEIQEKTEIEBLNTKIIEBE 342
QY 494 ---WNLASVYTRREKT--SLHOSMIDFGO-----ISDSVOFHDSKXENLOLYIPKOS 540
Db 343 KKTLEIKDYLTTADKILGELQEOIVOKNOEIKMKLELTSKOKEROSSEBIRKOLM----- 398
QY 541 GDMABEGR-----ASPEKEITS--LOOQLOSK--BEEKELVQSPFKLIALEROL--SVKA 591
Db 399 GIVEELQKNNKDSOFEDIDVORMEOETORKEQLQALDEMGQOIVOMKQELLIRQHMA 458
QY 592 KNLWAVNISR---EHSINAEVOTDVEKEVYVRKEMSVLGDGYNASNSDLQSSVDGKRLS 648
Db 459 QMEBKTRHKGEMENALRSYSNITVNEDOI-----LNMVAINELNKLQDTNSQEKJL 513
QY 649 SMDCEIEHRKMLEOKIYDLBEPIENLNKXSENDKOKSSEODPM---ESIQLCEALMA 703
Db 514 BELGILIEKCALORQLEDLVEELSPSREQIARQOTIAOESKLNEMAKHSISTVEDLKA 573
QY 704 EKANLE---ELAL-----MRDNFNIILENETLKREIADLER----- 738
Db 574 EIVASASESRKELELKHAEVNTYKIKLEMLEKKAVALDRMAESOE-ALELERFLQOLFS 632
QY 739 ---SLKE-----NOETNEFEIL--EKETOKEHE 761
Db 633 HEEELSKLDEDEIEHRIINIEKLNGLIHVYKQOIGLONEMSOKIETMQEPKDLITQ 692
QY 762 AOLIHEIGSLKLVENAEYNYONLEB---DLETKYLLKE-----QETOL 803
Db 693 NOLIEISLKDLOOS--LVNSKSEBMTLOINELQKEIILROEKEKGTLEBOVQEOQL 750
QY 804 ---AELRKADULQKKVRNFDLSV--MGDESKCEIIFOLKOSLSAEAV----- 849
Db 751 KTELLEKQMKKEENDLOEKFQALEENSLIKDEKKTLEBMLKIHPPVSOEELIFLDSIK 810
QY 850 ---TRDA--OKECSPLSEN-----LELKEKMEPTSNMYNOKERKASLFEKOLETEKSN 898
Db 811 SKSKSVAWEKEIILIEBENEDLKQOCIOINEIEKORNTFPAEKKNFEVYQELOBEVAC 870
QY 899 YKKMEADLO---KELQ---SAFEINLYN----- 921
Db 871 LLKVADLEDSDKNQOLEVYKSKLALNEELHLQRIINPTTVKMKSVFDEKTFVATLELM 930
QY 922 GILLAGVPRDL-----SRVELEKAYSEFSKOLEKALEKMALENEVTLSEYK-- 970
Db 931 GEVVKDQTTLEMEKLEVTREKRELTESORLSDSEQLKQKHGEISPLNEKVSILKQEKQV 990
QY 971 -FLPREVECLKY-----OISKASEEIMLLKQEG--EHSASITSK----- 1006
Db 991 SLRCELEIILINHAENAVQCDTOVSSLLDGVVMTSRGAGSVSKVXKSGESKIMV 1050
QY 1007 ---OELIMOEOEO---ILQITDEVHTOS--KVQOTEEQYLE---MKKMHDLIF 1050
Db 1051 EDKVSFEMMTVGEESKQEBOLLIDHLPSTVKESSLRATQPSENDIKQKELNVLKXSQNDL- 1109
QY 1051 EKYINKSEAE-----DLIRE--MENLKGK-----MESVEVKIADTKH 1086
Db 1110 ---FLQWAEORICLSLVSTHVDQVREYEMENKDKALCSLKEEILFAOEKIKELOKIH 1165
QY 1087 ELE-ETIR-----DKEOULH-----EKKYFQAMQTIPIPIPLSPSKUV 1128
Db 1166 QELQETMTQOETGDEGKPLHLILIGLQKAVSEECSYFQTLCSV---LGSYYTPALKC 1220
QY 1129 EGNSDPIEINDY-----HNLIALATERNNIMVLEF----- 1160
Db 1221 EYNADDEKMSGDYISENDEPELODYRYVEVQDFQEMHHTLNLKVTEBYNNKLVLQTRISKI 1280

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QY 1161 -----ERNSLKEQV-----IDLNTQLOSLQAQSIKESDLQKPK 1193
Db 1281 WGOQTDGKMLFEGEBNLPRKEETPELSTHSQMTNLIEDIDVNHKSKSLSDLEKTLREBV 1340
QY 1194 QDL-----EGEVKLLLEMLLKHGL-----TDSQLSI 1221
Db 1341 QELFESLISLQOQLKETEQNVAEILHQLQKRLQAVSESTVPSPSLPVDSVVTESDAQRTM 1400
QY 1222 -----EKLQLENLEVTREKLTQLOEMKNITI-----ERNE 1251
Db 1401 YPGCVKKNIDGTIEFSGEFGVKEETNTVKKLEKYOQOLEEVAKVIVSMIAQAQOE 1460
QY 1252 L-----OTNFEDELKAEHDSLKODLSENIQESIEFODELRMAO 1288
Db 1461 LSRISGKENTASSKQAHAVCQOEQHYRENMKLSODQIGQTFEYVD--VKKEEFPKLS 1518
QY 1289 BELREO-QOLVDSFRQ-----QLLDCSVGIS---SPNHDAVANO---EKVSLGEVNS-- 1333
Db 1519 KELGEHGEKILLNSDPHDPIPSKDCVLTISEMFSKDKTFIVRSIHDEISVSSMDASR 1578
QY 1334 ---LOSEMLRGRBDLQTSKALVSELELR-AHYKSVGEVLEITTKLNGLEKEITLGS 1389
Db 1579 QLMINEBQLEDKROELVBOYQEHQATELLROAHMRQME-----RO 1619
QY 1390 ESEVYLKSMLEVLKEDNNKLEKQAEVYSSKENQPSLEEYFSGSOKLVDBEIVLKAQLKMA 1449
Db 1620 REDQ-----BOLOEIKRLNQLAQRSSIDENLVSE---REVLLEBELKQLSLNG 1670
QY 1450 BERTL-EIKDRDYFELVOTANTNLVEGKLETPLQADHEDSIDRSSEMEIKVLEKLER 1507
Db 1671 REKLCCELRNSG---TQONGENQGEVE---EQTFPEKELDRKEDVPPEILNE--- 1720
QY 1508 NOYLLEIROEKELELSNKLLEILOKEMETSVLLKQD-----LOOKLESLSSENIILKE 1559
Db 1721 -RYALQKAN---NRLKLTILEVYKTTAAVEETIGRHVGLIDRSSKSSQSSASLIRMS 1773
QY 1560 NIDTTLK---HNSDTQALQK-----TOOELQAKUL---AIVAS 1593
Db 1774 EAEASVKSQVHEHTRVYDESIPTSYSGDMRPANDIMMSKYTEBETELSQRLVNSGFAGT 1833
QY 1594 DNCPIETO-----KETSADCVHPLKEKILLLTLELQKTNEOKL 1633
Db 1834 EIDPENEBMLNMISSRLQAAVBKLLAISPTSSQLEHAKVYQTELMRSPFQKQATESL 1893
QY 1634 ---LHEKNEL--EQAOVELKCEVHEHLMKMSIESKSSLESLOHEKHD---TEQOL 1679
Db 1894 KCOEELRELRLEHESFARQLAVELS-KAEGVIDGADDEKTLFERQIOEKTDIIDRLQOEL 1952
QY 1680 LALKQOMVAVQEKKELOOTHEHLTAEBVDHLKENIELGLNFKNEAQKTTTEQCCLINEOK 1739
Db 1953 LCASNRLQELABEQOQIOEBRELLSROKEANK--AEAG-----PVEQOLOETE 1999
QY 1740 ELEQSOHRLQEIIEMLKSLDKDESALFETLKESQKVNLNLOQEMEMWALEMELKNSORT 1799
Db 2000 KLMKEKLEVOQAOAEKVRDLOQYKALE-----IDVEQOYVR-FIELEQENKTELM 2049
QY 1800 VIAERDQLODDLRESVENSIEFTODDLRYAQALQOQKQVQELTSQSVL----- 1849
Db 2050 DLRCQNALQOLEKEMKRFLEQALDRHERHDFVQO--EIQKLEQOLKVVPFRQFISEHQ 2107
QY 1850 QEKISLENQMLYNAVATYKETLSEBDDLNOQKQHLFSEITFLSLSLKEKEPAL----- 1902
Db 2108 TREVEQLANHHKEKTDKCEILLSEQLOQORDIOERNBEIEKLEFFRVELQALVLVEDRKH 2167
QY 1903 ---EOAEKDADARKTIIDITEK-ISENIEBLOQATNLKETLYERESL-IQCKE 1952
Db 2168 FGAVKAPKELSLVQOLOKBRALDRKEKEITNLEBQLOFQREBELKNKEVQOQLHMOLEI 2227
QY 1953 QALANTEHLRETLKSKDLALQME-----QERDEANKVIALTEKMSLSE 1998
Db 2228 QKKESTRLOLEQENKLFQDMEXLGLAIKESDAMSTODQHVLFGRFAQIIOEKEVEID 2287
QY 1999 QINENVTTLKEGEGEKEFFYQRPSSKOSSQSMELRESLTKLOLE-----E 2047

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Db 2288 QINEVOTKLO-----QOLKITTDNKYTEEKELLIRDLFOTJELCLMSDQECVKN 2336
Qy 2048 AEKEISEATNEIKNITAKISSLEBEIILQNASIINEAVSERENLHNSQOVLSE---LEO- 2103
Db 2337 REEBIEQUNEVIKLOQLANIGQKTSNNHSLSE---EADSLGHQDLVDVIAEKLALEOQ 2393
Qy 2104 -----LSLTKSRDHAFAQ-----SKREKDEAVNKIASLAEE-----IKILTK 2141
Db 2394 VETANEEMTFMKNVKJKEITNFKNNOLOTOELFSLKRER-ESVEKISQIPENSUNVAILDLSK 2452
Qy 2142 EMOEF-----RDSKESIOESSHISE-----LCTYKTELQMKOQKEDIINNKLAEKVK 2190
Db 2453 DKPELEVVLTDALSKLENQTFKSPENGKSIINETRLLOLESITVSAKDILETQCYK 2512
Qy 2191 EV-----DELLQ-----HLSLKEQ-----LDPOIOMELANE----- 2216
Db 2513 QIKMOEQGFETEMLOKKIIVNLOKIVEKVAALVQIOLEAVQETAKCQONOTISSE 2572
Qy 2217 -----KLRYVELCEKMDIMEKEISVLRMONEP-----QOEEDVAERMILLES 2260
Db 2573 PERTNIONLQREDELGSDISALTREISELESQVVMHTSLILEKQVEIAEK-NVLEK 2631
Qy 2261 RNQ--EIOELMEKISAVYSEOHLLSSLSSELOKETEBAHGMCHMLIKESISLTSFSG 2318
Db 2632 EKLLLEQKLEEGNEKQREKEKRSQDVEVLKTTTELPH-----SNEESGFVNELEA 2685
Qy 2319 LOPEHVKLNTQLOTLINKFVVVYRTAAVKEDH--SLIKDYE--KDLAEOK-----RH 2367
Db 2686 LRRESVATKABLASYSKEKAEKLOEELLVKEITNMTSLOKXDSVRDHLAEKELSTLEKE 2745
Qy 2368 DELRLQ---LOCL-EQGRKMSDSASE---LKFCIEFELNELFRKANITIOSVODDPS 2419
Db 2746 DEFEVDSKKAQCFEPPIKLSKSIASOTDGTKLSSNOTPQILVKNIGIQINLOSECS 2805
Qy 2420 --EVOVFLNQGSTLOELEHKKGFOMLEBFGDLHVDAKULSEGOENRRLAST----- 2473
Db 2806 SEEVTEIISQ-----FTEKIEKQELHA-----AEILDMSRHISETEITLK 2846
Qy 2474 -----IQLTKR--LKAVVO-----SKI-----OREIT-----VY 2496
Db 2847 REHYVAVOLKKECGTLKAVITQCLRSKEGSIPELAHSDAYOTREICSDSGDMWQGIY 2906
Qy 2497 LNO---FEAKLOEKEEON-----KELMRMEHHPGA-----SYM 2528
Db 2907 LTHSGQFDLASBEGSEBSATDPSFKTKIGLIRAVHNEGMOVLSTLSPYDGEDHSIQ 2966
Qy 2529 E-----EENARLLGLIKTVODESKKLOSRIKMLLENELNVYDDAMH-----KGEKVAI 2576
Db 2967 QVSEPWLEERKAVINTISSLKDLITKQO---LOREAEVYDSQSHESFSDMRGELLILA 3021
Qy 2577 LQDKL-----SNNAEAEINAMVUKLTQKODMLQAMK----- 2609
Db 3022 LQOVFLSEBSVLLAARTTELALGTTDVAGLLNCLFORLQEOGVEYOAMECLOKADRRS 3081
Qy 2610 ---ELENLOKNNVAKGAVPYKEID-----NLKTR-----VVKIEMEKIKYSKAT 2650
Db 3082 LLSFIOALHAQNMGRKITLKREQSEKPSQELLEENIQOKOSOMLEMOVELSSMK-DYAT 3140
Qy 2651 DOIIVNYSCLDEKBEGLRLKEELRPAQADNDTIVCVPKDYOKASTPVTTCGGSGGIYQ 2710
Db 3141 E-----LOFOLSSEKVVVAELKSELAQTLLETLTLKAQHKLK----- 3179
Qy 2711 STAMVLQSEKAAALRELSHYKKKYHHLSTRVSEDR-----KKTAKKSDAHSHT 2762
Db 3180 -----ELEAFPLEVVKOTDEVHNLNDITLASQOKSREIOWALEKEKK-----L 3223
Qy 2763 GSSHGSPHKITETVPHG--PVTPERSEMPSLHSGPKSESTKRVVSPNREIYSQVLMS 2821
Db 3324 GRSEERDKBELEDLKFLESQKQRMQLNLLLEQOKOLNSESQKITESQRMVLYAQULSEE 3283
Qy 2822 PGKTMHNGHLLSPSGVUGLHKKKALSPNNSMPYTOGVNIVPGKTGLHKLITESTLFDNUSSP 2881

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Db 3284 QGRNLEQVLLSEKVRIREMSSITLDRERELHAQLOASSDGTQSRPPLPSEDLLEKLOQ 3343
Qy 2882 C--KQKQVQDNLN-SPKGLFPVSK 2904
Db 3344 LEEKSRIVELLNETEKYKLDLSQTR 3369

RESULT 4
US-10-171-311-2
/ Sequence 2, Application US/10171311
/ Publication No. US20030087270A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Chen, Yan
/ APPLICANT: Zhao, Xumei
/ APPLICANT: Monahan, John
/ APPLICANT: Kamatkar, Shubhangi
/ APPLICANT: Glatz, Karen
/ APPLICANT: Gannavarapu, Manjula
/ APPLICANT: Hoersch, Sebastian
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
/ FILE REFERENCE: MRI-035
/ CURRENT APPLICATION NUMBER: US/10/171,311
/ PRIOR FILING DATE: 2002-06-12
/ PRIOR APPLICATION NUMBER: US 60/298,159
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/298,155
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/335,936
/ PRIOR FILING DATE: 2001-11-14
/ NUMBER OF SEQ ID NOS: 238
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 3907
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-171-311-2

Query Match 6.9%; Score 1013; DB 15; Length 3907;
Best Local Similarity 19.1%; Pred. No. 2e-43;
Matches 691; Conservative 637; Mismatches 1115; Indels 1182; Gaps 148;

Qy 181 KXGKKNHYGETKANDHSSRSHTIFRMIVESRDRNDPTNSENCDAVMVSHMLVLDLAGS 240
Db 34 KKQKKR---KTSSEKHDVSAHHDNLNDQSCNEMYINSGQRESVIYIPESTIMRILHSG 90
Qy 241 ERASQTAEGVRUK-----EGCN--INRSLFILGOVYIKKLSDGAQGFINYRDSKLT 291
Db 91 EITSHGQGFVELESEISTADDCSSRVNGCSFVM-----RTGKPTV 132
Qy 292 ILQNSLGNKAVIYICITIVSPFETLSTLQFASTAKHVNTPHVNEVLDEALLRYRK 351
Db 133 LREBERG-----VDSYS-----EQGADSTTHLEMMSESLAGKH-- 169
Qy 352 EILDLLKQLENLSSSETKA-----QAMAKEH---TOLAEIKOLHKEREDRIWHLT 401
Db 170 EIEELNLELEMEVVTGTGLQLOLQEFPAIKORDGIITQLTANLQARREKQETREPL 229
Qy 402 NIVVASSQESQDQQRVKKRRTVMARQKIONSLHAGVVD-----FMLSR 447
Db 230 EL-----TESQKQLOIQFOLOQASSETLRNTHSTADLLOAKOOLLTHQOOLEEODH 282
Qy 448 LPQNFSK-----KAKFSQDPSFEIDSVCTEFSDFPDALSMDNSGIDAE 493
Db 283 LLEDYQKKEDFTMQISPLQEKIKYVEMQDKVENSNEELQEKETIIEELINTKIIEE 342
Qy 494 ---WNLSKVTREKT--SLHOSMIDFGQ-----ISDSVQFHDSSKENOLOVLPKDS 540
Db 343 KTLLELKDKLITADKLGLBLOQIOVOKNOEIKMKLELTNSKQKROSSEELIKQML--- 398
Qy 541 GDMAECRK-----ASPEKEITS--LQOQLOSK--EEEKKELVQSFELKIMLEBQL--SVYA 591

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Db 399 GIVEBELQKNNHKSQFETDI VQMBEQETQRKLEQALBELDENYGCQI VQMKQELLRQNH 458
 Qy 592 KYLEWNTNR---EHSINAEVOTDVEKEVVRKEMSVLGDSCYNASNDLODDSVDGKRLS 648
 Db 459 QMEKERTKRGKEMENALRSYSNITVNEQIK-----LNMVAINELNIKLODINSQKEXK 513
 Qy 649 SSHDCIEHRKMLEOKI VDLPEEIEHLNKKSENDDKQSEODFM-----ESTOLCEAIMA 703
 Db 514 BELGILBELKCALQROLEDVBEISFRQIQPARPTIAEQSKLEAHKSLSTVEDLKA 573
 Qy 704 EKXANLE---ELAL-----MRDNFDNIILENTLKEBIADLER----- 738
 Db 574 EIVSASESKLELKHAEVNTYKIKLEMLEKKNQAVLDRAHMSQD-ALBELRLQRLFS 632
 Qy 739 -----SLKE-----NOETNEFEIL--EKETQKEHE 761
 Db 633 HEEELSKLEDELEIHRINIEKLNGLIHYKQOIDGLQNMESOKIETQOFEKDMLITQ 692
 Qy 762 AOLHEIGSLKLVENAMYNQNLB-----DLKTKLKE-----QEIOL 803
 Db 693 NOLILIEISKLQLOOS--LVNKSSEMTLOINELQKEILEIROEKEKGTLEQOEVOELQ 750
 Qy 804 -----AELRKRADLQKKVRNFDLSV--MGDSEKLCBEI POLKOSLDAEAV----- 849
 Db 751 KTELLEKQMKKEKENDLOEKFAQLEAENSLKDEKLTLEMLKIHTPVSGEERLIFLDSIK 810
 Qy 850 --TRDA--QKESCFI RSEN-----LELEKMEEDTSNMVYNOKEKAASLFEKOLETKSN 898
 Db 811 SKSKSVMEKEIEILIEENEDLKQOOCI QLENEIEKQRPNTFPAEKNFVAYQOLOEYAC 870
 Qy 899 YKQMEADQO---KELO-----SAPNEINVLN----- 921
 Db 871 LKLVQDLEDSKNKOLEYKSKLKALNEBELHQRINPTTVKXKSVFDEKTFVATLELM 930
 Qy 922 GILACKVRPDLI-----SRVELEKVSFEFSKOLEKALEKKNALENEVTCLSEYK--- 970
 Db 931 GEVAVKOTTELMKLEVTREKLEBLSQRSLDSEQKQKHGELSFLENEVKSLEKQEKY 990
 Qy 971 -FLPNEVECLKN-----QISKASEBIMTLKQEG--EHSASITSK----- 1006
 Db 991 SLRCELEIILHNRAENVQSCDQVSSLLDGVVMTMTSGAGSVSKVXKSGEBSKIMV 1050
 Qy 1007 -----QEIIMQGEQO---ILQITDEVYHTOS--KVQOTEBOYLE-----MKXHHDLF 1050
 Db 1051 EDKVSFEMMTVQEBESKOBOLILDHLPSYKSESLRATQPSENDKQKELANLVKSSONDI- 1109
 Qy 1051 EKVIRNKSEAB-----DLRE--MENLKGT-----MESVEVKIADTGH 1086
 Db 1110 ----RLQMEBAQRICLSLVSTHVADQVREYMEKDKALCSLKEELI PAOEEKIKELQKIH 1165
 Qy 1087 ELE-ETIR---DKQOLH-----EKYFFQAMQOTIFPITPLSDLPSPSKLV 1128
 Db 1166 QLEIOTMTQOETGDSGKPLHLLIGLKQKAVSECSYFLOTCSV-----LGSYVYPAKJC 1220
 Qy 1129 EGNSDPPILEINDY-----HNLIATERNINMVCLET----- 1160
 Db 1221 EVNAMEDKENSQDIYISENEDPELODYRYEVODFQENMHHTLANKVTEBYNVLALQTRLRSKI 1280
 Qy 1161 -----EENSILKEQV-----IDLNTQLOSLQOSLEKSLQKPK 1193
 Db 1281 WGOQDQMKLEFGEENLPKEETEPILSIHSQMTNLBDDIVNHRKSLSSLODEKTYKLEHGV 1340
 Qy 1194 QDLF-----EGEVKLLLEMLLKGLH-----TDSQLSI 1221
 Db 1341 QELBESLISLOQQLKETEONFAELHCLQKRLQAVSESTVPSPSLVDVSVITRESAQKTM 1400
 Qy 1222 -----EKLOLENLEVTREKLOTLQOEMKNITL-----ERNE 1251
 Db 1401 YPGSCVKKNIDGTIEFSGEFVGVKLEKQYOELBEEVAKVIVSMSIAFAQOTE 1460
 Qy 1252 L-----QTNFEDLKAHEDSLKQDISENIEQSIETQODELRAAQ 1288

Db 1461 ISRISGKENTASSKQAHAVCOQEOHYFNEMKLSQDQIGCFQFTFTVD--VKFEKFEKPLS 1518
 Qy 1289 BELRQO-QOLVDSFRQ-----QLODQVQIS-----SPNHDAVANO---EKVSLGEVNS-- 1333
 Db 1519 KELGHEGKEILLNSDPDHPIDIPESKDCVLTISEMPSKKTFTVROSIDELISVSSMDAR 1578
 Qy 1334 ---LOSEMIRGERDLOTQSCALVSELELLR-AHYSVGEENVLETIKLNGLEKIELGKS 1389
 Db 1579 QALMBEQEDMRQOLVQYOQHQAOTELLROAHNRQHE-----RO 1619
 Qy 1390 ESEVVLKAMLENLKEDNNKLEQAEYSSKENQSLFEVFSQOKLVDEIVLKAQOLYAA 1449
 Db 1620 REDQ-----EQLOEIKRLNQLAQRSSIDNENLVSE---REVILBELALQKQSLAG 1670
 Qy 1450 EERL--EIKDRPYFELVQANTNLVSGKLETPLOADHEDSDIDRSSEMEIYVQEBKLER 1507
 Db 1671 REKLCCCELRNNS---TOTONGENQGEVE---EOTFKEKELDRKREDVPEILSNE--- 1720
 Qy 1508 NOYLLERLOEBKLELNSKLEILOKEMETSVLLKOD-----LOQKESLSSENIILKE 1559
 Db 1721 -RYALQKAN-----NRLKILLEVAVKTTAAVEETIGRAVLGILDRSSKQSSASLIMRS 1773
 Qy 1560 NIDTTLK---HNSDTQAOLOK-----TOEQLQAKNL---AIAAS 1593
 Db 1774 EABASVKSQVHEHRTVTDSEI PSYSGSDMPRNDIMNMSKYTEBGTELSQRVRSQFAGT 1833
 Qy 1594 DNCPI TOE-----KETSADCVHPEEKIILLITBELHOKTNEOKYL 1633
 Db 1834 EIDPNEEIMLNITSSRLQAAVEKLELAISETSSQLEHNAKVOTELMRESFRQKQEATSL 1893
 Qy 1634 -----LHEKNEL--BOAOVELKCEVHLMKMSIESKSSLSLESQHEKHD---TEOOL 1679
 Db 1894 KQEBELRERLHEESARQOLAVELS-KAEGVLDGVADEKTLFERIOIEKTDIIDLBEQL 1952
 Qy 1680 LALQOMQOVVTOEKKELQOTHEHTLAEVYDHLKENITELGNFKNBAQOKTTEQOCLYNENK 1739
 Db 1953 LCASNRLOLELEAQOQIOEBRELISROKQKANK--AEAG-----PVEQOLOETE 1999
 Qy 1740 ELEQSOHRLQCEIEIEBMSKLDKESALETLSEBQKVINLNOEMMYLMBELKNSORT 1799
 Db 2000 KLMKEKTEVQCAEYVRDLOKQVLALE-----IDVEQVSR-FIELEQKXNTIELM 2049
 Qy 1800 VIAERDQLODDRESVEKSIETQODLRKAQOELQOQKQVQELTQIS-----VIOE 1851
 Db 2050 -----DLROONALEQOLREKMRFLDEQAI DREHERDVQO 2085
 Qy 1852 KISLEENQLVYVATVKEITLESRDLDNQSKOHLFSEIETLSLSEKE-----FALEQ 1904
 Db 2086 EIQKLEQOL--KVVRFPQPISE-----HQTRVEVQOLANHLKEKTDKSGELLSQEO 2134
 Qy 1905 AEKDKADARKTIDITEKISINEBQLLOQATNLKETLYERE-SLIQCKEQLALNT--BHL 1961
 Db 2135 LQRODIOERNEIEKLEFVRELEQALLVASDTPQVDEBRKHFGVAEAKPELSLEVOLOAE 2194
 Qy 1962 RETLSKRLALQKQEO---RDEANKVIALTEKMSLSLEQOINENVTTLKGESEKETF 2017
 Db 2195 RDAIDRKKEKITNEBQEOQFREBELNKNNEVQOOLMOLEIQKKESTTRLOLEBENKLF 2254
 Qy 2018 YLQRPSSQOSSOMELRESLTKDLOLEBAE-----KEISATNIEIKNLTKAKISSL 2069
 Db 2255 -----KDNMEKLGALIKESDAMSTQOQHVLFQFPAQILOKEVEIIDLQNCQVTKL 2304
 Qy 2070 EBEILQNASITINEAVSERENLRHSQOVLSELOSLTLKSRDHAFAQSKREKDEAVNKI 2129
 Db 2305 QOOL--KITTONKVIEE-----KNELIRDLQETIDECLMDOECVKANREBEIQLMEV 2355
 Qy 2130 A-----SLAEIKILTLEMEDFBRSKXSLSQOSSHLSBELCTYKT- 2169
 Db 2356 IETLQOELANTIGOKTSMNAHSLSEBADSLLKQOLDVIAEKLALQOQVETANEEVTFMKXV 2415
 Qy 2170 -----ELQMLKQOQKEDINNKLAKEVEVD-----LLOHLSLSEKQOLDQIQM 2211
 Db 2416 LKETNFKNOLTOBELFSLKREBSV-----EKIQSIPENSUNVAIDHLSKQKPELEVULT 2470

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QY 2212 E-----LRNEK-LRNYELCEKMDIMEKEISVLR-----WONEQO 2245
DB 2471 EDALKLENQYTFKSEENGKSGIINLETRLLQLESTVASKDELTOCYKQIMDEQOQ 2530
QY 2246 QEDDDVAEMDILESNOEIOELM-EKISAVSEORTLLSSLSSELQKET--EAKHCHWL 2302
DB 2531 FE-----TEMLOKKIVNLQKIVEEKVAA-----ALVSQIOLEAVOEYAFECOD 2573
QY 2303 N-----IKES-----SLSSTLSRSPSLOTENHAKNTQLOTLINKPKVYV 2341
DB 2574 NQITSEPERTNIQNLQREBELSDIGALTIRISELSQVEMHTSL--ILEKQVBI 2631
QY 2342 RTAAVKEDSLIKDYEKDLAEQKRDHRLQIOCLEQHGKRWSDASSELK----- 2393
DB 2632 AEKNVLEKEKLELOKLEEGNEKKQREKE-----KKRSPQDVHVLKTTTELPHS 2681
QY 2394 -----FCIEFL-----NELFKRNIQSVQDPSEYQVFL 2425
DB 2682 NEESGFNELEALRASVATKELASYEKAEKLOEBLLVKEFN-MTSLQKDLQVYRDL 2740
QY 2426 NOVGSFLQ-----EELEHKKG----- 2441
DB 2741 AAKAEKLSLEKEDFEVQESKACPFEPPIKLSKISASQTDGTLKISSNOTPOLVAK 2800
QY 2442 -----FMQMLEPFGDLHVDANKLSEMOENRRIAST----- 2473
DB 2801 NAGIOINLOSECSESEVTEIISOFTERIEKMOELHA-----AELMESRHISEETLKR 2855
QY 2474 -----IQLITKR---LKAVVO-----SKI-----QREIT-----VYL 2497
DB 2856 EHYVAQVLKEBEGTILKAVIOCLRSKESGISPELAHSDAYQTRIELSSDSDMGQIGYL 2915
QY 2498 NO--FEAKLOEKKQON-----KELMRMEHSPSA-----SWME 2529
DB 2916 THSOGFDIASEGGESESATSPFKKIKGLRAVINEGMOVLSLTSEYSDGEHDSIQ 2975
QY 2530 -----EENARLLGLIKTVODESKLQSRICKMLENELNVKDDAMH-----KGEKVAIL 2577
DB 2976 VSEPMLEERKAYINTISSKDLITTKQ-----LQREABVYDSSQSHESPSDMRGELLAL 3030
QY 2578 QDKL-----SRNAEALNAMQVILTKKQNLQANAK----- 2609
DB 3031 QOVFLERSVLLAAPTETLALGTTDAVGLNCLQRIOEGVEYQAAMECLQKADRSLL 3090
QY 2610 --EIEMLQWVAKGAVPYKEID-----NLTKT-----VYKIMEKIKYKATD 2651
DB 3091 LBEIOALHQMNGRKITTLKREGESEKPSQBLEYNIQOKQSOQLMEQVELSMK--DRATE 3149
QY 2652 QEIAVLKSGCLEDEKGLRRLKEELRRAQADNDTTVCVPRKYOKASTFPVTCGGGSGIYOS 2711
DB 3150 -----LOEQOLSEKRMVVAELKSELAQTKLEETTLKAQHNLK----- 3187
QY 2712 TMLVLQSEKALERLSHYKKYHHLSTRMSSSEDR-----KTKYAKSAHSHHG 2763
DB 3188 -----ELEAFRLVKKOXTDEVHLLNLTJLASEQKSRLOMALEKEKAK-----LG 3232
QY 2764 SSHRGSPTHETRYRHG--PVTPERSEMPSLHLSGPKSESSTKRVSPNRSEIYSQLVMP 2822
DB 3233 REBERDEKLEBDLKFSLESOQRNLDJNLLEBOQULNESQOKISQOMLDAQSEBO 3292
QY 2823 GKTGMHKLILSPSKVGLAKKRALSPNRSEMPTOHVISPGKTGLAKHNLTESTLFDNLSPC 2882
DB 3293 GNLLEQVLESEKVAIIRMSSTLDRERELHAQLOSDGSGSRPPLPSEDLLKELQKOL 3352
QY 2883 --KQKVQENLN--SPKSGLPDVYSK 2904
DB 3353 BEKHSRIVELNTEKYLKDLQTR 3377

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RESULT 5
US-10-171-311-6
; Sequence 6, Application US/10171311

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; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
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; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OR CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
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; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3925
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-171-311-6

Query Match 6.9%; Score 1013; DB 15; Length 3925;
Best Local Similarity 19.1%; Pred. No. 2e-43; Indels 1182; Gaps 148;
Matches 691; Conservative 637; Mismatches 1115;

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DB 34 KKQKKR---KTSKSHDVSAHNDLNIDQSCNENYINSSQVESTVPESTIMRTLSG 90
QY 241 ERASOTGAEVRLK-----EGCN--INRSLFILGOVIKULSDQAGFINYRDSKLT 291
DB 91 EITSHQGSFVLESEISTTADDCSEVNGCSFVM-----RTGKPTN 132
QY 292 ILQNSLGNNAKTVITCTTPVSFDETLSTLOPASTAKHVRNPRHNEVLDDEALLKRYK 351
DB 133 LRREBEFG-----VDDSYS-----EQGAQSPFTHLEMMESLAKQH-- 169
QY 352 EILDKQOLENLESSSETKA-----QMAKEEH---TOLAEIKQLHKEREDRIMHLT 401
DB 170 EIEELNRELEERKRVYGTBGLQOLOEFPALIKORGIITQLTANQOARREKDEIMRETL 229
QY 402 NIVVASQESQODQVKRRRYTMAPKIQNSLHAGVSD-----FDMLSR 447
DB 230 EL-----TEOSQKLOIQOOLQASETLRNSTHSTAADLLQAKQOILTHQOLEBDH 282
QY 448 LQGNFSK-----KAKFSMPSPFELIDSVCTESPDDDLASMDMSGIDAE 493
DB 283 LLEDYQKKEDFTWQISFLOEKIKYVEMEODKKVENSKKEIOEKTIIIEELNTKIIIEE 342
QY 494 ---WNLASVTRHEKT--SLHQSMDIFQO-----ISDSVQFSDSKENOLQVLPKDS 540
DB 343 KTTLELKDCLTTADKLGLGELQEIYQKQOELKNMTELNSQOKROSSEELKOLM----- 398
QY 541 GDMAECRK-----ASFKEKITS--LOQLOQSK--EERKEKLVQSEFKLAELEEQ--SVKA 591
DB 399 GTVEELQKRNHNDQSFETDVIQRMEOGTQKLEQRAELDEMYGQOIVQMKELIROHMA 458
QY 592 KULEWYNTSR---EHSINAEVQTDVEKEVVRKEMSVLGDGYNASNSLODSSVQKRLS 648
DB 459 QMEEMKTRHKGEMENALRSYSNITVNEDOIK-----LNNVALNELNLIKLODTSQKEKIK 513
QY 649 SSHDECIEHRKMLEQKIVDLDEEFLENLKKSENDKQKSSQDFM-----ESTQLCEAJMA 703
DB 514 BELGILIEBKALQROLEDVLELSFSREQIORARQITAEQESKLENAHKSISTYEDLKA 573

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QY 704 EKANLE---EIAL-----MRONFNUIIENETLKREIADLER-----738
Db 574 EIVSASERKLELHKAEBVTNYKIKLEMLEKEKNAVLDRAESOE--HELELRLTQOLLFS 632
QY 739 -----SLKE-----NORTNFEIL--EKETOKEHE 761
Db 633 HEEELSKLEDELEIHRINIEKLNGLHYKQOIGDLONEMSKOITFMQFEXDLITKQ 692
QY 762 AQLIHIGLSKLVENAMYNONLE-----DIETKTILKE-----OETOL 803
Db 693 NOLIHIEISKLQLOOS--LVNSKSEEMTLQAINELQKEIILHQBEEKGTLEQVQELQOL 750
QY 804 -----ALRKRADULQKVRNFDLSVS--MGSEKULCEEIPLQKOSLSDAEAV-----849
Db 751 KTELLEKQMKKEKENDLOEKFAQLAEENSLKDEKKTLEBMLKIHPPVSOEELIFLDSIK 810
QY 850 --TRDA--QKECSFLRSEN-----LELKEKEDTSMNMYNOKEKAASLFEKOLETEKSN 898
Db 811 SKSKDSVWEKEIETIIEENEDLKQOCIOINBEIEKORNTFPAEKNFENVQELQEBYAC 870
QY 899 YKKMEADLO-----KELQ-----SAFNEINYLN-----921
Db 871 LLKYVDLEDGSKNKQELVYKSKLALNEBHLQRIINPTVKMKSSVPEDKTFVAETLEM 930
QY 922 GLLAKGVPRDL-----SRVELEKVSFEFSKOLEKALEKNALENYTCLSEYK--970
Db 931 GEVVEKDTTELMEKLEVTREKLELRSQRLSDLSBOLKONGEISFLNEBVKSLKQEKQOV 990
QY 971 -FLPNEVECLKN-----QISKASEIMLQKEG--EHSASITSK-----1006
Db 991 SLRCELEIITINHNAENVQSCDIOVSSILDSGVVMTSRGABGSVSKVNSKSGESKIMV 1050
QY 1007 -----OELINOOSEQ--ILQLTBEVHTOS--KVOQTEBOYLE-----MKKMHDLF 1050
Db 1091 EDKVSFEMMTVGESKQOLILDHLPVTKESLSLATQPSBNDKQKELANLVKSEOND--1109
QY 1051 EKYIRNKSAAE-----DLIRE--MENUKGT-----MESVEVKIADTKH 1086
Db 1110 -----RLQMEAORICLSLVSTHVDOVREYEMENEKDALCSLKEBILFAOEBEKIKLOKH 1165
QY 1087 ELE--ETIR-----DKEOULH-----EKYFQAMQTIPIPIPLBSLSPSKV 1128
Db 1166 QLEIQTMTQETGDEGKPLHLILGKLOKAVSEECSYFQTLQSV-----LGGYVTPALKC 1220
QY 1129 EGNSSODPIEINDY-----HNLIALATERNNIMVCLT-----1160
Db 1221 EVNADKENSQDIYSENEDPELODYRYEVODFOENMHTILNKVTEYVKLVLQTRLKSI 1280
QY 1161 -----ERNSLKEQV-----IDLNTQLOSLQASIEKSDLOKPK 1193
Db 1281 WGOQDTGAKLEFGEENLPKEETEPFLSIHSQMTNLBDIDVNHKSLSLQDLEKTKLEBOV 1340
QY 1194 QDLF-----EGEVKLLIMELKGLH-----TQSQSLI 1221
Db 1341 QELBSLISLOOQLKETEQNEAEIHCLOKRLQAVSESTVPSPSLPVDVSVITESDAQRTM 1400
QY 1222 -----EKLOLENLEVTETKLOTOJEBEMKNTI-----ERNE 1251
Db 1401 YPBGCVKKNIGTIFPSGEPFGVKEETNIVKLEKQYQOEBLEEVAKVIVMSIAAQOTE 1460
QY 1252 L-----QTNFEDLKAHDSLKQDLSENIEOSIETQDELRAAQ 1288
Db 1461 LSRISGKENTASSKQAHAVNQOEQHUFENEMKLSQDQIGOFTEFTVD--VKFEKFPKLS 1518
QY 1289 EBLRQO--KQLYDSFRQ-----QLDQSVGIS-----SPNHDAVANQ--EKVSLGEVNS--1333
Db 1519 KELGHEKEIILSNSDPHDIPESKDCVLTISEMFSKCTFIVROSIDHELISVSSMDASR 1578
QY 1334 ---LOSEMVLGRBDELQTSCKALVSELELLR--AHKVSVEGENULBITTKLNGLEKEILGKS 1389
Db 1579 QLMNEBOULEMROELVROYQOEHOQATEILRQAHNRQME-----RQ 1619

QY 1390 ESEVYLKSMLENTKEENKKNLEKQAEVSSKENOFSLSEEFSSGQKLVDEIVLKAQLKAA 1449
Db 1620 REDQ-----EQLOEIRKILRQOLAORSSIDENIVSE---RETVLEBELHLOKSLAG 1670
QY 1450 EERL--EIKDRDYELVOTANTNVEGKLETPLOQADHEEDSIDRSSEMEIKVIGSEKLER 1507
Db 1671 REKLCEELRNS--TQONGENENOGEVE---EQTFKEKELDRKPEDVPEILSNE---1720
QY 1508 NOYLLERQOEKLETSNKLEILOKEMETSVLLKD-----LOOKLESLSSENIILKE 1559
Db 1721 -RYALQKAN-----NRLKILLEVVKTTAAVEITIGHVIGLIDRSSKQSSASLIMWS 1773
QY 1560 NIDTTLK---HNSDPOAQLQK-----TOELOTAKNL---AIAAS 1593
Db 1774 EBAASVSCVHEHTRVYDSEIPISSGSDMPRNDINMMSKYTEEGTELSQRLVRSGFAC 1833
QY 1594 DNCPIQOE-----KETSADCVHPLEEKILLITTELHOKTNEOEKL 1633
Db 1834 EIDPENEBELMNTISSRLQAAVEKLELAISETSOLEHAKVTQTELMRESFRQOEATEEL 1893
QY 1634 -----LHEKHEL--EQAOVELKCEVDBHLMKSMIESKSSLSLELOHEKND---TEOOL 1679
Db 1894 KQOEBELRELIHESFARQOLAVELS--KABGVIDGYADEKTULFERQIOEKTDIIDRLBOEL 1952
QY 1660 LALQOMQVVOQEKKELOQTEHNLTAEVNDHKENIELGINFNGEAQOKTTKEOCLNEMK 1739
Db 1953 LCASNRLOEBENBOQOIOBERELSRQEKANK--AEAG-----PVEQOLOETE 1999
QY 1740 ELEQSOHRLQCEIEBELMSLKDRESALTELKSEOKVINLNOEMEMVLMELNKSORT 1799
Db 2000 KLMKEKLEVOQAEKVRDLOKQVAKLE-----IDVEQOVR--FILEQEKNTLEM 2049
QY 1800 VIAERDQLODDLRESVEMSIETODDLKRAQELAQOQKQKVOELTQIS-----VLOE 1851
Db 2050 -----DLROONQALKEQLTEKMRKFLDEQAIIDREHERDVFOQ 2085
QY 1852 KISLEENQMLNVATVKETLSERDDLNOSKQLPFEITLSLSTKEKE-----FALEO 1904
Db 2086 EIQKEQOL--KVPRFQPISE-----HOTREVQOLANHLKEKTDKCSSELLSKQ 2134
QY 1905 AEKDQADARKTIDITEKISNIEBOLLQOATYLTKEITYERE--SLIOCKEQLALNT--EHL 1961
Db 2135 LQROIGERNNEIEKLEFRVRELEQALVLSADTQFQVBERKHNCAVEAKPELSLEVQLOAE 2194
QY 1962 RETLSKDALQAKMEQOE---RDEAKVIALTEKSSLSLEQINENVTTLKEGESEKETF 2017
Db 2195 RDAIDRKEKEITNIEQOEQFPELEKNKEEVQOLHMOLEIOKKESTRLOLEQENKLF 2254
QY 2018 YLQRPSSKQOSSQMELELSLTKDLOLEBAE-----KEISATNEIKVLTAKISL 2069
Db 2255 -----KDMEKLOLAIKESDAMSTODOHVLFGFAQIIOEKEVEIIDQINBOVTKL 2304
QY 2070 BEEILQNASILNEAVSERENLRHSKQOLVSELEQSLTKSRDHAFQASKREKDEAVNKI 2129
Db 2305 QOOL--KITTDKVIIE-----KNEILRIDLETOIECLMSQOECVKNRREIEIOLNEV 2355
QY 2130 A-----SLAEBIKILTREMDFRDSKSLQOSHSLSSELCTYKT--2169
Db 2356 IEKLOQELANIQOKTSMANHSISEBADSILKQDLVIALEKALLEQOVERTANEMTFMKV 2415
QY 2170 -----ELQMLKQOKEEDINNKLAEVKAVDE-----LIQHSLSLEQOLDQOM 2211
Db 2416 LKETNFKMNQULQOELFSLKREBEAV---EKIQSIIPENSUNVALDHSKDPRELEVLVT 2470
QY 2212 E-----LANEK--LBNVELCEKMDIMEKEISVLRU-----MONERO 2245
Db 2471 EDALKSLENQYTFKSPENGKGSITNLBTRLQLOESTVSAKDLBETOCYKOIKMOBOQO 2530
QY 2246 QOEDDVAERMDILSRNOEIOELM--EKISAVYSEQHTLSSLSSELQKET--EAKHQCML 2302
Db 2531 FE-----TEMLQOKKIVNLOKIVEKVA-----ALVSOIQLEBAVOEYAKFCOD 2573
QY 2303 N-----IKE-----SLSSITLSRSGSLQTEHVKANTQLOTLNKFVVY 2341

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Db      2574  NQTISSEPTNINOMINQREBELGSDISALTLRISSESOVEMHTS--TLEKEQVBI 2631
Qy      2342  RTAAVKEDSHLKDYEKDLAABOKRDELRLOQCLEHGKRWSDASELK----- 2393
Db      2632  AEKVLKKEKKLELOKLEGEKKEKREK-----KRSPODVVLKTTTELPHS 2681
Qy      2394  -----FCBIEFL-----NELLFKKANIIOVODFESEVQFL 2425
Db      2682  NEESGFENELALRAESVATKAELASYKEKAEKLOCELLVKEFN-MTSLQKDLSCVRDL 2740
Qy      2426  NOVGSSTLO-----ELEHKKG----- 2441
Db      2741  AAEKELSTLEKEDETEVEQSKACMFEDLPKLSKSIASQTDGTLKISSNOTPOILVK 2800
Qy      2442  -----FMWLEBFGDLVDADAKKSEGMQENRIAST----- 2473
Db      2801  NAGIQINLOESSESSEVTETIISOFTKIKMOELHA-----AELDMESRHISTETTLK 2855
Qy      2474  -----IOLLTKR--LKAVVO-----SKI-----OREIT-----VYL 2497
Db      2856  EHYVAVQLLKEEGOTLKAVIQCIRSKESGSIPELAHSDAYQTRREICSDSDGDMQGIYL 2915
Qy      2498  NO--FEAKLOEKEON-----KELMRHEHGPSA-----SWNE 2529
Db      2916  THSOGFDIASBESGESATDSFPKKIKGLRAVNEGVOVLSTESFSDGDEHSIQ 2975
Qy      2530  -----EENARLLGLTKVODESKLQSRIMLENLNVKDDAMH-----KGEKVALL 2577
Db      2976  VSEPMLEEKAVINTISLKLDTTMO-----LQRAEVDYDSSQSSESDMRGELLALL 3030
Qy      2578  QDKLL-----SRNAEALNAMOYKLTAKODNIQAANK----- 2609
Db      3031  QQVFLBEERSVLLAAPTETLTALGTTDVGHLNCLBQRIQEGVEYQAAECLQKADRSL 3090
Qy      2610  -----FIENLOCMVAKGAVPYKEID-----NFKTK-----VKIMEMKIKSKAD 2651
Db      3091  LSEIALHAKQMMGRKLTTLRKEQSEKPSQELLEYNIOQKOSOMLEWVLSMK-DRATE 3149
Qy      2652  QGIAVLKSGCLEDEBEELRLKEELRAQADNDPTVCVPDYOKASTFPVTCGGSGSIVQS 2711
Db      3150  -----LQEBLSEKMWVAALKSELAOTKLELTTLAQKHMLK----- 3187
Qy      2712  TAMLVLOSEKALERELSHYKKYVHLSRTMSSSEDR-----KKTAKSDAHSSHTG 2763
Db      3188  -----ELBAFRLVKDKTDEVHLNDTLASEQKSKRELQWALEKEKAK-----LG 3232
Qy      2764  SSHRGSFKTEYTRHG-PVTPERSEMPSLHLSPKKSSESTKRVSPNSETYSQIVMSP 2822
Db      3233  RSEERDKELLEDLKFSLESQKQRNLQNLNLLLEQKQNLNESQOKIESQMLYDAQLEBQ 3292
Qy      2823  GKTGMHKLHLSPSKVGLHKKRALSPNRSMPPTQHVISPQGTGLHKULTESTLFDNLSSPC 2882
Db      3293  GNNLEIQLVLESEKAVIREMSSTLDBRELIHAQLOQSSDGTGSRPPLPSBDLLKELQKL 3352
Qy      2883  --KQOKVQDENLN-SPKSKLFDVKS 2904
Db      3353  EKHRSRIVELLNETEKYKLDLSQTR 3377

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; CURRENT APPLICATION NUMBER: US/10/082,830
;
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,802
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; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 260
; LENGTH: 2383
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-082-830-260

Query Match      6.7%; Score 993; DB 15; Length 2383;
Best Local Similarity 21.2%; Pred. NO. 1,1e-42;
Matches 562; Conservative 472; Mismatches 929; Indels 690; Gaps 101;

Qy      370  KAAQAAKEEH--TOLLAIRK--QJHK-EREDRIWHLNIIVVASSQESQODQVRKRRV 423
Db      227  KTOELEKEAHERSGLIQKSGDLKAELELDRTVELSNALLOSQONEDYKMTKALRE 286
Qy      424  TWAPGKIONSLHAGVSDFDMLSRLLPKNFSKKAKESDMPSEIDSDVCTEFSFDAL 483
Db      287  T-----VEILETNHTELMHEASL- 305
Qy      484  MMDSGIDAENMLASKVTHREKTSIHQSMIDFGQI-----SDSVQFHDSSK 529
Db      306  -----SRNAOEKLSIQOVIKDTTQVWEAGDNIAGSGHENSLEL-DSGI 350
Qy      530  ENQLOYLPRKDSG-----DMAECKRASFKEITSHQOOLQSKKEEK 569
Db      351  FSQFYQADAKALTLVRSVLTTRRQAVODLRQOLAGCGEA-----VNLLOQHDMQWEEBG 405
Qy      570  KELVOSFEL-----KIALEBQLSVYAKNLEMTNSREHSINAEVQTVKEVVR 619
Db      406  KALRQRLQKLTGERDPTLAGQTVDLQGEVDSLSKERELLQKARE-----LR 451
Qy      620  KEMSVLGSQGYVASSD-----LQDSSVQKRLSSHD--ECIEHKKMLEKQTVDLBEFTE 673
Db      452  QOLEVLEQEAURLRRVNELOLQGSAGQKEEQEELHLAVRERERLOEMLMGEA--- 508
Qy      674  NUNKSENDKOKSSQODFMESIQL-CEAIIHMAKANALBEALMRNFDNIILENETLKE 732
Db      509  ---KQSELSLEITTRREALFESHGLBELLROQTEVTALARAOSINAELESSENTIKTE 565
Qy      733  IADERSIKENQETNEFEILEKETQKEHAQIINHEIGSLKVLVNAEMYNQNLLEDLLETK 792
Db      566  VADLRAAAVKLSALNEALALDKVGLNQQLQLEENOSVCSHMAEAOQRNALQVD--- 621
Qy      793  TKLKEQELQLAELKRRADNLQKVRNFDLSVSMQDSSEKLCBEIQLQKQSLSDAEAVTRD 852
Db      622  -----LAAEAKR-----REALWKNTHLEQOLQKAEAGAE 652
Qy      853  AQEGCSPLRSENLLEKEKMDTSMNWNQKEKAASLFEKQLETENKSNYKMEADLOKELOS 912
Db      653  LQADLRDIOEKEKEIQLKLSER---HQDEAATTQLE-QLHQBARKQEBVLARAQEKKA 708
Qy      913  AFNEINYNGLLAGVPRDLSRVELLEKVKVSEFSQLEKALEE-----KNALEN 961
Db      709  LVREKAALVEVRLQA-VERDRQDLAQLOGLSSAKELLESSLFEAQOQNSVIEVTRQGLEV 767
Qy      962  EVTCISEYK-FLPNVECKKNOISKAASEIMLLKQEGESASIIISQETIMQESQILQ 1020
Db      768  QIQVTOAEVIOGEVRCIKLELDTE-----RSQAQBERDAARQ-LAAQDEGKTA 818
Qy      1021  LTDEVTHTQSKVQOTEQOYLEMKKMHDDLFEKYIRNKSAAEDLLREMENTLQTMESVEYK 1080
Db      819  LEQQAHAHEKVENQUREKWEKRSNHQ-----QBLAKALBSELEKXKMLELR 865
Qy      1081  IADTHHELEETIRDKQOLHHEKKYFFQAMQITPITPLSDSLPFSKLVGNSQDPIEIND 1140
Db      866  LKEQOTEMALQAGEEBERTQAESALCQWQ----- 895
Qy      1141  YNLIATLATERNNINVCLETENSLKEQOVIDNTQLOSQASISKSDLOKPKOLEBE 1200

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Db      896 -----LETE-----KERVSLLETTLLQTOKELABASQOERLRQDM---K 931
Qy      1201 VKLLEME---LLKGLTDSQSISTEKLQLENLEVEITEKLOTOEMKNITIEENELQTNF 1257
Db      932 VOKLEQOETTTGLOTOLOAEQRELKEMARQH---RDDLAALOESSLLQDKMDLOKQVE 988
Qy      1258 DLKAEHDSLKODLSENIEOSIFENODELRAAOEELRQXQLVDSFRQQLDCSGVSSPMH 1317
Db      989 DLKSO--LVAODDSQRLVEQ-EVQEKLTRETQENRLOKEL-----ERKASTLTSLEMK 1039
Qy      1338 DAVANOEKVSLGEVNSLOE---MLRGERDELQTSCKALVSELELRAHVKSVEGENLEI 1374
Db      1040 E-----QRLVLQEAOSIRQOELSAIRQDMQOEAQOEBEKELSAQOMELLRQEVKEKEDFL-- 1093
Qy      1375 TKLLNGLEKEIIGKSESESVLKSMLENKEDNNKKEQAEVYSKKNQPSLEEVPSGQK 1434
Db      1094 -----AOEAOELLEASHITEQOL-----RASLMAQEAKAQOLRLRSTES---- 1136
Qy      1435 LVDEIEVLKAOLKABE-RLEIKDRYFELVQTNANNLVEGKLEPRLQADH-----BE 1486
Db      1137 ---QLEALAAEQQPGNOAQOALASLYSALOALGSVCESRPELSSGGDSAPSVWLEP 1193
Qy      1487 DSIDRSEMEIKVLGEKLERNOYLLERLOEKELETS-NKL-EILOKEMETSVLLKLDLO 1544
Db      1194 DONGARS-----LFRGRLTLTASAANVASALHKLHODLMKTOQTRDVLRDQV- 1241
Qy      1545 OKLESLSBENITLKENIDITLKHNSDTQAOLOKTOQLOLAKNLAIASDNCPTQOKEK 1604
Db      1242 OKLEERLTDTBEAKSQVHTELQ---DLQRLSONOEKSK-----WEGKON 1284
Qy      1605 SADC-VHRLPEKILLTTELHOKTNBOEKLHKELEBOAYELKCEVHLMKSMIESK 1663
Db      1285 SLESLEMEIHEWTASLOSLRRAELQRMWAQGERELLQAKENLTAQVHENLOAAVAEANA 1344
Qy      1664 SLESLOHEKNDTEQOLLALKOOMOVVTOEKE---LOOTHEMLTAEVDLKENIELGLNF 1720
Db      1345 QASAGIIEEDRTARSALKLKNBEVYESRERAOALOEGELKVAQKALQENLAL---- 1400
Qy      1721 KNEAOQTTKEOCLLNENKELEBSQHLQCEIIEELMKSLKESALLETLKESQKVINLN 1780
Db      1401 -----LQTLAREEVEVETLRGQIOELKQREMQKALBELLSLKK---RN 1444
Qy      1781 QMEMVMIEMELKNSQRTVIAERDQLODLRESVEMSIETODDLRKAQOALQOQKQV 1840
Db      1445 QEVDLQOBOIOELEKC-RSVL-----EHLMAVO-----ERQOKLTVOREQR 1486
Qy      1841 EL-----TSOISVLOEKISLE--NQMLYNVATVKETLSERDDLNSKOHLPSEIETLSIS 1894
Db      1487 ELEKRETOGVNLEHOLELEKKQVIE-----SQRGOVODIKQOLV-LTECLALE 1536
Qy      1895 LKEKEFALE-----QAEKDKADARKTIDITEKISNIEEO-----LLOQATNL 1937
Db      1537 LEENHNKMECCQOKLKELEGQRETOQVALLTHLTDLBERSQGLQOQSIHDLSEHSVL 1596
Qy      1938 KETLYERSLLOCK---EQALANTHELRRTKSDALGKNQOER---DEANKVIA 1988
Db      1597 ARELOEROEVAQSKQREOIEELOROKENHLODERRDOEL-MQOKRIGVLEQRQRTQKI 1655
Qy      1989 LTEKMSLSEQOINE---NVT-----LKEGEGKEFFVYQRSKQOSSQOMELRES 2037
Db      1656 LEEDLEQIKLTSRREGRELTQOROLOMORBAEKGK-----PSKQORS-LEHMKIT 1705
Qy      2038 LKTKDLOLEAEKEISEATNEIKNTAKISSLEEBILOQASILNABVSE---RENLRHS 2093
Db      1706 LRDKKEVEGCOQENHLELOELKDQOQOGLHRKVGEISLLSGRQEIVVLQOQLOQA 1765
Qy      2094 KOQVSEIPEQUSLTLSKRDHAFQSKREKDEAVNKIASIEIKILTKEWDEFDSKESL 2153
Db      1766 REQ--GELKEQSL-----QSQIDEAQRLAQRDQDELEALQOEOQOQOQCEERV 1811
Qy      2154 QEOSHLSBEL---CTYKT---ELQMLKQCKEDINNKLAEVKVDLQHLSSLKQEL 2206

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Db      1812 KEKADALQALBQAMTLKERNHEGIELDNKEQARBLEEBLAVEGRV-----QALEEVL 1864
Qy      2207 DOIQMELREKERNLECEKMDIMEKEISVULMQN---EPOE-----EDDAERMD 2256
Db      1865 GDLRAESR-----EOBKALLQOQCAQOAEHEVEVTRALDQSLQAOA 1908
Qy      2257 ILESNOEIOELMEKISAVVSEQHTLLSSLSSELOKETEAHGMCLINIKESLSTLSRSF 2316
Db      1909 VKKERDQELALRAE-----SQSRHBEAARAR-----AEALOELGKXH 1949
Qy      2317 GSLQTEHVYKNTQLOTLNKFVYVRYTAAVKEDSHLIKQYEKDLAEOKRDE-----LR 2371
Db      1950 AALQ-----KEOHLLEQ-----AELSRSLASASTATLO 1977
Qy      2372 LOLQLOEHGRKWSASABELKFCETIEPLNELFPKANIGQVODFSEVQVFLQVQST 2431
Db      1978 ASLDAQHRSRQ---LEBALRIGOEGLQDQD---RYQBDVQOLOQALAO--- 2021
Qy      2432 LOEELKHKGFQWLEEFQDLHVDAKLSSEGQOENRRIASTIOLTLKRLKAVQSKIOR 2491
Db      2022 RDEELRHQOERQOLLEK-----SLAQVOENMIOEKUNIQOERE---EEIRGLHQS--VR 2072
Qy      2492 EITVYLANFEAKLOEKQONKELMRMEHNGPSASVMEENARLGLKTVODESKIQS 2551
Db      2073 ELQTLAQOQOETLLELRETQOQNNLEALPHSHKTSPMEOQSLKDSLEBRLORELEBQA 2132
Qy      2552 RIKMLENE-----LNLVQDAMHK--EKVALQDKLSRNAEALMNOVL 2597
Db      2133 ALRQTEAREIEWEKAODLALSLAQTKASVSSLOEAMFLQASVLERDSEQO----- 2184
Qy      2598 TKQODNLOAMKEINLOKMAKGAVPYKE-----EINLKTKVYKIMEKIK 2645
Db      2185 RLQDELELTRALK-BKLSHPGAITSALCSRSQOQVQLOEVEGVLEBPSPDGMEKOS 2242
Qy      2646 YSKATDOEIALYKSLCEDEKEBGLRLEKELRYAQAANDTVCVPXQYQKASTFTPTCGG 2705
Db      2243 W-----RQLEHLQQAVARLEIDRSLLQHN-----VOLRSTLE---QDG 2279
Qy      2706 SGIVOSTAMLV--LOSEKALEBLS-HYKKYVHNLSTWSSSEDRKKTAKADASHST 2762
Db      2280 RGQKNSDAKCAVLELOKEVULLQAOQLTLERKQKQDYITSAQTSRE-----L 2325
Qy      2763 GSHRSGPHKTTYNHGVTPERSSEMPSLHLGSPKSSSTKRVVSPNRSEIYQSLQVMSR 2822
Db      2326 AGLHNSHSLSLAAVQAP-----BATVL-----DESLTQSLTSP 2366
Qy      2823 GKTGMKHILSPS 2835
Db      2367 GPVLDHP---SPS 2376

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RESULT 7
US-10-116-712-670
; Sequence 670, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-712-670

```

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Query Match      6.4%  Score 946;  DB 12;  Length 1232;
Beet Local Similarity 24.9%  Pred. No. 1.3e-40;

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Matches 351; Conservative 249; Mismatches 453; Indels 356; Gaps 53;

OY		3	EGBADVAVVRRIQOE--OGDOANLOMKAGNNTISQVDT-KSPNDRFVNHSNSQ	59
Db		6	KGIPRVALRKPRPKPKEISEGCWMSFVGEBPV-VGTDXSFYDFVPDSTEOE	63
OY		60	IYOEIAVPIIASALOGVNGTIFAYGOTSIGKTYTMG-----TENSIGIIPAQIEVF	112
OY		64	VENFAVADBLIKGVFNATVLAIVAGOTSGKTYSMGCAVTAEONEPTFGVIPVIOQLF	123
OY		113	KIIOEIPIREPLARKSVMEINETYKDLCDRRKKPELETFEDFRNNRYVADLNEELMV	172
Db		124	KEIDKPSFEETLKSYLEYNEBELIDLCSREAQAINIEDDEKXIKITGLTEKTVLV	183
OY		173	PEHVLOWIKEKNHYGETKMDHSSRSHTIFEMIVSRBRNDPTNSEDCGAWMVSHL	232
Db		184	ALDPYSCLEGONNSTVASTAMNSSSHAFITLSLEGRKKSDSNS-----FSKL	236
OY		233	NLVDIASERASQTGAEGVRLKEGNINSRLFILGOVTKULSDOAGGFITYRDSKLTRI	292
Db		237	HLVDLAGSEBOKTKAEBDRLEKGINIRGLICGNVISALGDCKGGFFVEYRDSKLTRL	296
OY		293	LONSLSGAKTYIICTTPV--SPEPTSLTIOPSTAGHAVNTPVNVLDDEALLKYR	350
Db		297	LODSLGSHTMTMCVSPADSNEETINTLRADRAKIKNPVLN-IDPOT-----	348
OY		351	KEIIDIKOLENLESSESETKAOMAKEHTOLLAIEIKOLHKREDRIMHLTINIIVASSOE	410
Db		349	AELNLTKOOVOOL-----QVLL-----	365
OY		411	SQODORVKRRKVTAAPKIQNSLHASVSPDMSTR.PGNPFSAKARSDMSPFEIDS	470
Db		366	-----LOAHG-----GLPGSIUYE-----PS-----	382
OY		471	VCFESFDDDALSMDSNGIDAEMWLASKVTHREKTS-LHOSMIDFQISDSVOFHDS	528
Db		383	-----ENLOSIMEKN-----QSLVENEKLSGLSPAAGTQMILERIILTBOA	426
OY		529	KENOLOYLPKOSGDMAECK-ASFKEITSLOOQSCKE-BEKKELVOSFELKIAELEEQ	586
Db		427	NE-----KNNAKEELROHAACKLDLOKIVETEDELKENBEIIONLOULTOLDE	479
OY		587	LSVAKNLEMVYNSEHSINAEVORDVEKEVVRKEMSVLGSGVYANSDDLQSDSDGKR	646
Db		480	-----TYACMAAADTVADEDAUQETSPE-----TSSSDAPTQQALR	518
OY		647	LSSHDECIEHRKMLOEKIVDEEPFIENLNKK-SENDKO-KSSEODFMESIQLCEAIAB	704
Db		519	QAOMSKEIYELNKALK-----FALARMTONDQSLOPFOYODNIKELE----	565
OY		705	KANALEELAMKDNNDNIILENETUKRELADLERLKENQETNEFEILLEKETOKHEAQ	764
Db		566	-----LEVINLOKEK-BELVLELOTKKANNOAKLSERRRRIQBLEGGIADIKKK-	615
OY		765	THEIGSLKLVENAMYNQNLEBEDLETIKTLKEOEIOELAIRKPADNLOKKVNRFDLSV	824
Db		616	INEGSKLTKXTERTYSTKUNQEI-----RMKNQRVOL-MRQKEDAB-KFRQM----	664
OY		825	SMGDESEKICEEIFOLKOSLSBAAVTRDAQECSFLRSLENLEKMKMEDTSNMWYOKXA	884
Db		665	-----KOKDKEXIOLKE-----RORKRO-----YELLKLENNFOKOSVLRKTEE	706
OY		885	ASLFKOLETERSNYKWEADLOKELOSAFNFINVNLGL-LAGVUPDILSRVLETKV	942
Db		707	AAANKRLDALOKOREV-ADRKRRTQS-----RGHEGTAAYKVMWLGNEIWMYST	757
OY		943	SEFSKOLEKALEEKNALENEVTCSEYKFLPNEVECLKNQISKASEEIMLKQOSEHAS	1002
Db		758	BEAKRHINDLDRKIADQVAOLKE-----KXSEGENPP	793
OY		1003	IISKOEIMOBOSEQILOLTDVENTHQVKVOOTEEOYLEMKMHDDLEPKYRNKSEED	1066
Db		794	KLRRTFSLTEVRGOV-----SSEBD	814

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OY      1063 LAREMNKGTMSVSEVKIADTHGL---ETIRDEQO-----LHHEK---KYFF-OA 1108
Db      815 SITQOISLETEMFEPSAQIDLOOKLDBASEDRPKORMENTITIEAKALKYLLGEL 874
OY      1109 MOTIFPTPLSDSLPPSKIVEGNSQDEIEINDYHLALATERNNIVCLETERNSLKEQ 1168
Db      875 VSKTIQVSKLESSLKQKSTSCADQKYL-FERRNHFAIEIETDLAELVPMQCH---QEK 930
OY      1169 VIDNTLOQSIQASIEK-----SDLOKPKODLEEGLVLLLE 1207
Db      931 VLVLISQOQ-QSGMAEKQLESVSEKQOULLSTLKCODELEFKRMREVCEQNO-QLTREN 987
OY      1208 ELKGLHLLDSLOLSTIEKIQLEN---LAVTEKIQTIQEMKNITIRN--ELDTNEDLK- 1260
Db      988 EIIQOKLTLIQVARSQKHLPKDTLLSPDSPEFYVPPKPKESVXKEKLEQSGMDIEDLYC 1047
OY      1261 -----AEHDSIKQPLSENIEGSIETQELRAAOEELR-----EGKOLVDSFROULL 1307
Db      1048 SEHSVNEHEDDGDGDDDEGDEEMFKTLKVQSRNIGQYSCKMGCMGNKQC--GCRKQKSD 1105
OY      1308 CSVG-ISEPNHDAVANOEVSLIEGVNSHQ 1335
Db      1106 CGVDDCCDPYTCRRNRQOGKDSLGTIVERTQ 1134

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RESULT 8
US-10-116-712-664
Sequence 664, Application US/10116712
Publication No. US20030194764A1
GENERAL INFORMATION:
APPLICANT: Bangtur, Chaitanya S.
APPLICANT: Switzer, Ann
TITLE OF INVENTION: COMPOSITIONS AND METH
TITLE OF INVENTION: AND DIAGNOSIS OF LUN
FILE REFERENCE: 210121.568
CURRENT APPLICATION NUMBER: US/10/116,712
CURRENT FILING DATE: 2002-04-07
NUMBER OF SEQ ID NOS: 670
SOFTWARE: FastSeq for Windows Version 4.0.
SEQ ID NO 664
LENGTH: 1232
TYPE: PRT
ORGANISM: Homo sapiens
US-10-116-712-664

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Query Match 6.4% Score 941.5: DB 12; Length 1232;
Best Local Similarity 24.5% Pred. No. 2.2e-40;
Matches 375; Conservative 262; Mismatches 492; Indels 403; Gaps 60.

QY      3  EGDAAKVCVVRPILQRE--QGDQANLQMKAGNNTISCVDDGT-KSFNEDRVFNHSHTSQ 59
DB      6  KGIPRVALRCRPLVPKREISGCGQCCISFVGEQPV--VVGIDKSFYDFVDFPESTQEE 63

QY      60  TYQETAVPITISALQINGTIFAYGQTSISGKTYTMG-----TPNSLGIIPQALQEVF 112
DB      64  VFNTAAVPLIKGVFQGNATVALAYQOTISGKTYSGKGYTAQENEPVGVIPRIQTLLF 123

QY      113  KIIQIEIPREFILRRSYMEIYNETKDLCDRRKKPLEIREDFERNRYVADLTIELVMV 172
DB      124  KEIDKSPFEFLKAKSYLEIYNEELDLDCSRERQAQINIEDPREGIKIYGLTEKTVLV 183

QY      173  PEHVQMKKEGKKNRYGETKMDHSSRSHTIFRMIVESRDRNDFPNSENCDAVMVSHL 232
DB      164  ALDITYSCLEQGNNSRTVASTAMNQSRSASHAIFTLSEQKKSDKNSS-----FRSKL 236

QY      233  NLVLDAGERSQTAEGVRLKEGNINRSLFILGOYIKKLSDGAGGFIVYRDSKLRRI 292
DB      237  HLVLDAGEROKTKTAEDRLKEGINIRGLLCAGNVISALGDGDKGGFAPRDSKLRRL 296

QY      293  IONSILGNAKTYITITPV--SPDETSLTQFASTAGHVNTPHVNSVLDEALLKRYR 350
DB      297  IODSISGNSHTMLTICVSPADSNLEETLNTLRVADRAKIRNKPVLN--IDPQT----- 348

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QY 351 KEILDKQOLENLESSSETKAQAMAKEHTOLLAETIKOLHKEREDRIWHLTNIVASSOE 410
Db 349 AELNLKQOVQOL-----QVLL----- 365
QY 411 SOQDORVKRRRVTAAPKIONSLSHAGVSDPDMLSRLPGNFSKAKAFSDMSPFEIDDS 470
Db 366 -----LQAHG-----CTLPGSITIVE-----PS----- 382
QY 471 VCTERSDFPDALSMWDSNGIDAEMNLASKYTHREKTS--LHOSMIDFGOISDSVOFHDSS 528
Db 383 -----ENLOSIMEKN-----QSLVEENKLSRSLSEACQTAQMLERITWEOA 426
QY 529 KENOLOYLPKDSGDMAECCR--ASFEKEITSLOOQLOSKE--EKKELVOSFELKIALEBO 586
Db 427 NE-----KONAKLELRQHAACKLDLOKLVETLEDOELKENVETICNLQOLITQLSDE 479
QY 587 LSVKAKNLEMYNREHSINAEVQTDVEKEVVRKEMSVLGDGYNASNDLDDSSVDGR 646
Db 480 -----TYACMAAIDTAVEGEAQVTSPE-----TSRSSDAFTQOHALR 518
QY 647 LSSSDECEHRRKMLEOKTVLDEEFTENLKK--SENDKO--KSESDFMESIQLCEAIAAE 704
Db 519 QAOMSKEVELINKALALK-----EALARKWQNDSQLQPIQYQYQDNI----- 561
QY 705 KANALEELALMRDNFDNITLENETLKREIADBERSIKENOETNEPEILEKEKOEKEHQAOL 764
Db 562 KEPELEVINLOKEK--EELVLELOTAKKDQNAQKLSERRRRKLOELGQIADLKK----- 615
QY 765 IHEIGSLKVLVNAEMYNONLEEDLETTKLKEOEIOQLAEPLRKARDNLQKKVRNEDLSV 824
Db 616 LNEQSKLKLKSTERTYSKLNQET-----RMKKNQVQOL--MROMEDAE--KFRQW----- 664
QY 825 SMGDESEKCEEIFOLKQOSISDAEAVTRDAQEKCSFLRSNLELKEKEMEDTSWYNQEKKA 884
Db 665 ----KOKRDEKVIQJKE-----RDRKQO-----YELLKERNFQOSVNLRRKTBE 706
QY 885 ASLFEKOJETESKNKKMEADLOKELQSAFNEINYLNGU--LAGKVPRLLSRVELEKVV 942
Db 707 AAANKRKLKDALQOKREV--ADRRKKTQS-----RGMGTAPARKMNLGIEIEMVST 757
QY 943 SEFSQOLEKALEBEKNALENEVTCLSEYKFLPNEVECKLNQISKASBEIMLLKOEGBHSAS 1002
Db 758 BEAKHNLMDLEDRKILADQVAKKE-----KKEGSENP 793
QY 1003 IISKOELIMOESQOILQUTDEVTHTQSKVOQTEBOYLEMKQMDLDFEKYLRNKSBAED 1062
Db 794 KLRRRTFSLTEVRGQV-----SESED 814
QY 1063 -LLREMNULKGTMEVEVKIADTKHEL--EETINDKEO-----LHEK--KYFF--QA 1108
Db 815 SITKOIESLETMEPRSAQIADLOOKLDAESEDPRKORMENIAVILKEKALKYILGEL 874
QY 1109 MOTIPIPIPLSDSLPPSKLVEGNSODPIEINDYHMLALATERNNIMVCLTERNSLKEO 1168
Db 875 VSSKIQVSKLESLSQOSKITSQCADMQKML--FEERNHFAEJETELOALVAMEQOH--QOK 930
QY 1169 VIDLNTQLOSLQAOISIEK-----SDLOKPROLDEBEVLLLEEM 1207
Db 931 VLYLISQOQ--QSQMAEKQLESSEKQOQLSTLKCOBELEKKNREVEQNOQ--QLLRN 987
QY 1208 ELKHLHLDQSLSIKLOLEN--LEVTKELOTLQOEMKNITIERN--ELQTNFEDLK-- 1260
Db 988 EIIKOKLTLLOVASQOKHLPKDTLLSPDSFEYVQPKPKPSRVKKEFLQOSMDIEDLKVC 1047
QY 1261 -----AEHDSLKQDSENIEOSIETODELARAQOEIR-----EOKLOVSPFOQLLD 1307
Db 1048 SEHSVNEHEDGDGDDDEGDDEEWKPTKLVNYSRKNIQGSCKMGKNKQC--GCKKQASD 1105
QY 1308 CSVG--ISSPNHDAVANOEKVSLGEVNSLOSEMRLGERDELQTSICALVSELELRAHVS 1366
Db 1106 CGVDCCPPTKCRNRNQOGKDSLGTVERNQ-----DSSESPK-----LE----- 1143

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QY 1367 VEGNLEITRKINGLEKEILKSESEVLSKM--LENLEKE-----DNKKLEQAE 1414
Db 1144 ---DEPLEVTPGSLFNP--VCATPNSKILKEKCDVQVLSKTPAPSPFDLPBLKHVAT 1198
QY 1415 EY-----SSKENOFSLEEVFGSQOKLVDE 1438
Db 1199 EYQENWAPGKKKKRALASNTSPFSGCSPIEE 1230

RESULT 9
US-10-116-712-669
; Sequence 669, Application US/10116712
; Publication No. US20030194764A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FaalSEQ for Windows Version 4.0
; SEQ ID NO 669
; LENGTH: 1232
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-116-712-669

Query Match      6.4%; Score 941.5; DB 12; Length 1232;
Best Local Similarity 24.5%; Pred. No.2,2e+40;
Matches 375; Conservative 262; Mismatches 492; Indels 403; Gaps 60;

QY 3 EGDAAVAVCVVRPLIQRE--QGDQANLQWKAGNNTISOVDGT-KSFNFDVFNHSTISQ 59
Db 6 KQIPVRVALRCRPLVPKEISEGCQWCLSFVGPBPQV--VVGTDKGFYDVPFDPSTEQBE 63
QY 60 IYQELAVPLISALQGNVGTIFAYQOTSSGKTYTMG-----TPNSLGITPOLAOEYF 112
Db 64 VENTAVAPLIKGVFGYNATVLAAYQOTSGKTYSGMGAVTAEQENEPVGVIPVYQLLF 123
QY 113 KIOEIPRREFLLRYSMEIYNETVKKDLLCDDRKRPLEIRDPFRNVVADLTLELVWV 172
Db 124 KEIDKSPPEFLTKSYEINIEINBEILDLCRSREAOQININREDPREGKIYVLETKYVAV 183
QY 173 PEHVIOWKKEGKNRHYGETKNDHSSRSHTIFRMIVBSRBRNDPTNSENCDAVWVSHL 232
Db 184 ALDVTSCLEQGNNSRTVASTMANSQSSRSHAFITSLQKKSKDNSS-----FRSKL 236
QY 223 NLVLDAGSEBRASQTAEGVRLKEGCNINRSFLICQVTKKLSGQAGGFINYRDSKLTTRI 292
Db 237 HLVDLAGSEROKTKYAEEDRLKEGININRGLLCLGNVISAIGDDDKGGFAPYRDSKLTRL 296
QY 223 LQNSLQAGKATVYICTIPV--SPDETSLTIQAPASTAGHVNTPHVNEVLDQEAALKRYR 350
Db 237 LQDSLQSGSHTLMLACVSPADSNLEETLNTLRVAPARAKIKKPLVN--IDQOT----- 348
QY 351 KEILDKQOLENLESSSETKAQAMAKEHTOLLAETIKOLHKEREDRIWHLTNIVASSOE 410
Db 349 AELNLKQOVQOL-----QVLL----- 365
QY 411 SOQDORVKRRRVTAAPKIONSLSHAGVSDPDMLSRLPGNFSKAKAFSDMSPFEIDDS 470
Db 366 -----LQAHG-----CTLPGSITIVE-----PS----- 382
QY 471 VCTERSDFPDALSMWDSNGIDAEMNLASKYTHREKTS--LHOSMIDFGOISDSVOFHDSS 528
Db 383 -----ENLOSIMEKN-----QSLVEENKLSGSLSEACQTAQMLERITWEOA 426
QY 529 KENOLOYLPKDSGDMAECCR--ASFEKEITSLOOQLOSKE--EKKELVOSFELKIALEBO 586
Db 427 NE-----KONAKLELRQHAACKLDLOKLVETLEDOELKENVETICNLQOLITQLSDE 479

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QY 587 LSVKAKNLEMYNNSRHSINAEVOTDVEKEVYRKENSVLGDSGYNASNDLODSSVDGKR 646
DB 480 -----TVACMAAIDTAVEOEAOVTSPE-----TSRSSDAFTTOHMR 518
QY 647 LSSSHDECIEHRKMLEOKIVDLFEFLENLNRK-SENDKO-KSSBODFMSIOLCEAIMAE 704
DB 519 OQOMSKEVELKALALK-----EALARKTQNDSQLOPYOYODNI-----561
QY 705 KANALEELAMRDNFNPIILENETLKRBIADLERSKENEOTNEFILLEKTOKEHEAOL 764
DB 562 KPELEVINLOKKEK-BELVLEIOTAKKANOAKLSRRKROJOLEGOLADLKK-----615
QY 765 IHEIGSLKLVNAEMNYNOLLEDEETKYLKKEOEIOALBKRAINILOKKVNRNFDLSV 824
DB 616 LNEOSKYLKKESTERTVSKLNOEI-----RMKNQOVRQV--WROMEDAE-KFRQW----664
QY 825 SNGDSKLCCEBIFOLKQSLSDAEAVTRDAOKESFARSINLELKEMEDTSMMWYNOKEXA 884
DB 665 ----KQKRDEVIQLE-----RDRKRO-----YELLKERNFOQSUNLRKKTBE 706
QY 885 ASLFEKOLETEKSNYKMEADLOKELQSAFNEINYNGE--LAGKVPBDLSRVELEKKV 942
DB 707 AAANKRLDALOKQREV-ADKRKETO-----RGMETARVYKMLGNIEIVMWST 757
QY 943 SEFSKOLEKALEKNALENEVTCLSEYKFLPNEVECLKNQISKASEIMLLKOEHSAS 1002
DB 758 BEAKRHLNLDLEDRKITADVAQLE-----KKEGGENPPP 793
QY 1003 IISKEIIMQOSEOQLOLTDEVTHTOSKVQOOTEBOYLEMKKHMDLFEKYIRNKSEAD 1062
DB 794 KLRRTFSLEVRGOV-----SESED 814
QY 1063 -LLREMENTKGTWESVVKIADTKHEL---EERTIRDEQ-----LLHEK--KYFF-QA 1108
DB 815 SITKOLESJETEMEPFSAQIADLOQLDAESDRKQEMENATILKCKALKYILGEL 874
QY 1109 KOTIFITPLSDLSPPSKLVEGNSODPIEINDYHNILALATERNNIMVCLETERNSLKQ 1168
DB 875 VESKIOVSKLESLSKOSTKSCADMQML-FEERNHFAELETTELQAEVLMEQOH---QEK 930
QY 1169 VIDLNTQLOSLQASIEK-----SDLOKPRQODEEGEVKLLLM 1207
DB 931 VYLLSLOLQ--OSQMAKOLESVSEKQOOLSTLKCQOBELEKMRVEBOQO--QLRREN 987
QY 1208 ELLKGLHLDQSLSIEKLOLEN--LEVTETLOLQOEMKNITLERN--ELQTNFEDLK--1260
DB 988 EIIKQULTILOVASRQKHLPKXTLLSPDSFEYVQKPKRSRYKEKFLQSMOIEDLKXC 1047
QY 1261 ----AEHDSLKODLSENIEQSIETODELRAQOEIR-----EOKOLVDSFRQOILLD 1307
DB 1048 SEHSVHEHEDGDGDEGDEBEMKPTKLNVVNSRKNIOGSCCKGMCNKCQ--GCRQOKSD 1105
QY 1308 CSYG-SSSNHDAVANQEKVSLGEVNSLOEMLRGERDELQTSCKALVSELELRAHVNS 1366
DB 1106 CGVDDCCCDPTKCRNRQOGKQDLSGTVERTQ-----DSSESFK-----LE-----1143
QY 1367 VEGENLEITRKLNGLEKEILGKSESEVLKSM--LENLKE-----DNMKLEQAE 1414
DB 1144 ----DPEVTPGLSFNRP--VCATPNKXILKEMCDVQVLSKTPRAPSPDLDELGHVAT 1198
QY 1415 EY-----SSKENOFSLEEVSSGOKLVE 1438
DB 1199 EYOENKAPGKKKKRALASNTSPFSGSGPIEE 1230

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RESULT 10
US-10-203-823-419
; Sequence 419, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.

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; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatchar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 419
; LENGTH: 1979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-823-419

Query Match 5.9%; Score 872; DB 15; Length 1979;
Best Local Similarity 21.5%; Pred. No. 1.6e-36;
Matches 500; Conservative 404; Mismatches 788; Indels 634; Gaps 92;

QY 266 LGOVKKLSDQAGGFIVRPSKLRILLQNSLGNKAVIITCTIPVSPDELSTLQFAS 325
DB 12 LGO-----SLQGVGSLASTLGOISNFTKDMV-----38
QY 326 TAKHVRNTPHNVLEVD-----EALLKRYKEILDLKKOLENLESSSETKAQAMAKEEH 379
DB 39 ----MEGEBEVAELPDRKTEIEAIIHILSENERLKLCTDLEKHA-SEIQIKQOS 93
QY 380 TOLLAEIKQLHKEERDIRIWLHTNIVASSQSOQORVYKRRVTWAQKIONSILHASV 439
DB 94 TSYRNLOQO---KEVEISHL-----KARQIALQDQLKLQSAQSVPS-----GAGV 137
QY 440 SDFDLNLRPGNFSAKAFSDMPSPFEIDDSVCTEFSDFPDALSNMDSNGIDAEWNLASK 499
DB 138 -----PATYASSSF-----AYG 149
QY 500 VTHREKTSIHQSMIDFGQISDVQPHDSKENOLOYLPRDSG---DMAECRA-----SF 551
DB 150 IGH-HPSAFHDDMDPGDISSQO-EINRLSVEVGRLEGEVGHMWHIAQTSKAQGTDND 207
QY 552 KEKITSLOQLOSKKEBEKELVQFELKIALEBOLSV--KAKNLEMYNNSRHSINAEV 609
DB 208 OSEIKLQNI-----KELKONRSQEIJDQHEMSVLONHQOKLEISRHH---RBE 257
QY 610 QDVKEVYRKEMSVLSDSGYNASNDLODSSVDGKRSSSHDECIEHRKMLEOKIVDE 669
DB 258 LSYDERIEHEE-NLLQOGGSGVITLDSKIYEMOXTIOVLQEVESIKRQEO---LE 312
QY 670 FEIENLNKK--SENDKOKSEBODFMSIOLCEAIMAEKANALEELAMRDNFNPIILEN 726
DB 313 DKIKOINKLSSAENDR-----DILRRQO--EQUNVEKROQIMERC-----350
QY 727 ETLKBIADLERSLKENOTNEFILLEKTOKEHEAOLIHETIGSLKLVNAEMNYNOL 786
DB 351 ENLKLECSKLQPSAV-----365
QY 787 EDLEFTRKYLKKEOEIOALBKRAINILOKKVNRNFDLSVSGDSSEKLCBEIFOLKOSLSDA 846

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Db 366 -----KQSDMTTEKERILAQASASV-----EEVFRLOQALSDPA 397
Qy 847 ---EAVTRDAQKCSFLRSENLELKEMEDTSMWYNQKKAASLFEKQLETEKSNKYKMA 904
Db 398 ENEIRLSSLDNDSNLAEDNLKWKRIE-----VLEKEKSLISOEKE 439
Qy 905 DLQKLOSAFNFNYNLGLAGKVPDDLRSVLELEKKVSEFSKOLEKALEEKNALENEVT 964
Db 440 ELQMSLLKLNNEYE---VIXSTATRD---ISLSEHLDLNLNFAKQGLN-----Q 485
Qy 965 CLSEVKFLPNEVECLKNQISKASEEIMLKQEGESHASIISKOEIIMQOSEQIQLTDE 1024
Db 486 SISEKETILAEIEELDRQOQEA TKHMIILKQO-----LSKQO---NEGDSIISLQKD 535
Qy 1025 VTHTSKYOQEBEQYLEMKKHNDLPEKTI RNKSEADLLREMEMLKGMESV----- 1077
Db 536 LNDKKRVHQLDEDDDKITKELDVOKEKLIQSEVALNDLHLTKQKLEDEVNVLVDQUNKS 595
Qy 1078 ---EYKIDTKHELETIRDKQQLHKKYFQAMQTIPTIPLSDSLSPSKLVESGNSQD 1134
Db 596 QESNVSTQKEMLEKHEITQNEE----- 618
Qy 1135 PIEINDYHNLJALATERNNINWCLETERNS-----LKEQVIDLNTQLOSLQASIEKSD 1188
Db 619 -----ELSRIRNELMQSLNDSNSNFKDTLKEREADEVNRLKQNLSELEQLVBN 667
Qy 1189 LQKPKQDLBEGEVKLLLEMLLKHJLTD---SOLSTEK-----LOLENELEVTLEK-- 1235
Db 668 LKKVAFDYKMEKELVLACEDVRHQLSECLAGNNOISLEKNTIVETLTKMEKEIEIAELCWM 727
Qy 1236 ---QLOREBK-NITIER--NELQTNFEDLKAHNSL-----KOD---LSENI EQ--- 1276
Db 728 AKKRLLEBANKYEKTEBELSNARNINTSALQLEHEHLIKLQKQKMEIAELKKNIBQMDT 787
Qy 1277 -SIETQDELRAAQEELREQKQVDSFRQOLDCSVGISGPNHDAVANOKEVSLGCVNSIQ 1335
Db 788 DHKFKDVLSS--LEEQKQLT-----QLI-----NKEIFIEKLKERS 824
Qy 1336 SEMLGERDELOTSKALVSELELIRAHKVSVEGENLEITKKNLEKLEICKSEBSVYL 1395
Db 825 SKL-----OEBLDKYSQAL-RKNEILRQTE-----EKDRSLGSMK-----EENMHL 865
Qy 1396 KSMLEMLKEDNN-----KLKEQAEBSKENSQES-----LEEVFSSQQLVDEIEVL 1442
Db 866 QEEERLEBESRTAPVADPKTLDVTEVLASSVSQNTIKHEHLBEIKHNOKITIEDQONS 925
Qy 1443 KAOUL--KAAERLEIKDRDY-FELVQTANTNLVEGKLETPLOADHEEDSIDRSEMEIK 1499
Db 926 KMQLLOSLQOEKKEKDEPRYQHEQNNANTHOLF-----LKDEBISLQKTIQOIKQ 978
Qy 1500 VLGEKLE--RNQVLLERLOEBKLELSNKLEILQ-KEMETSVLLDLQOQKLE-SLSE- 1553
Db 979 LHEERQDQTDNSDIFQETKVQSLNIBNGSEKHDLSKATERLVAIGIKERELEIKLNEK 1038
Qy 1554 NIILKENIDTTLKHSSTQAO-LQKTOQLQAKLALIASDNCPTQEKETSACQVNL 1612
Db 1039 NISLTKQIDQSLKDEVGKLTQIIOQKDEIQ-ALHARISSTSH---TOD----- 1083
Qy 1613 EKKILTEELHOKTNEOEKLEHKNLEBOAQVELKCEVENHMKMSISKSLSELOHE- 1671
Db 1084 ---VVYLOOQLOAYAMERKFAVLNEKRENSHLKTEYHKMDIYAAKAELIKLODEN 1140
Qy 1672 -----KHDTL-----QQLLALKQOMQVVTQEKEL 1696
Db 1141 KKLSTRESSGQDMFRETIONLSRIIREKDIEIDALSQCQYLLAVLQTSSTGNBAGVN 1200
Qy 1697 QOOTHHLAUVHLKENIELGNFKNQEAQKTKKQCLINENKELDEQSHRLQCEI----- 1752
Db 1201 SHQFELLQERDKLQOQVKMEWK---QQVMTVQNMHESAOLOEBLHOQAOVLVDS 1257
Qy 1753 EELMSLKDKEGALFETKESEQVINLQEMEMMLMELEKNSQRTVIAEBDOQDDLR 1812

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Db 1258 DNNSKLOVDYTGILQSYEQNETKLNFGQELAQVQHSIGOLCNTRKDLLGKLDIISPOL 1317
Qy 1813 ESEVMSIETODDLRKA-----QEAQOQKQDVQELTQISVLOEKISLLENOM 1860
Db 1318 SASLTPQSAECLRSKSEVSESESLQOELEIRKSLQEDATITRTIQENNHLSDBI 1377
Qy 1861 LVNAVATKETSERDDLQNSKQHLFSEIETLSLSKEKEFALQAEKQADARTIDIT 1920
Db 1378 ---AATSELERKEHQDTSEIKQLEKQDVLOKLLKEKD-LIKAKSDQLASSNE--NFT 1431
Qy 1921 EKISNIEBQLOQA-TNLKETLY-----ERESIQCKEQLALNTEHLRET---- 1964
Db 1432 NKVN--ENELRQATNTLKERILLIEMDIGLKGNEKIVEYRQKETEYQALOETNMKF 1489
Qy 1965 -----LKSQDLALGKMEORDEA-----ANKVIALTEKMSLSLEQOINEN 2003
Db 1490 SMLBREKEPECHSMKELAEFQULKEKQGTGGLNOLNANVSKMOETTVFQOERDQV 1549
Qy 2004 VTLTKEGEKEKTFLO---RPSKQSSQWELRESLTKTDLOLEEA-EKEISEATNE 2058
Db 1550 MIALQKQMENTALQNEVQRLDKREFRQNOELERLNLH---LESDSYTREALAAEDR 1605
Qy 2059 IKULTAKISLEBELQNASILNEAVSERENLRHSKQVSEEL-EQLSITLKSQHPAFAQ 2117
Db 1606 EAKLRKKVTVLEEKLVSSNM-----ENASHQASVQVESLOQLNANVSKORDET--- 1655
Qy 2118 SKREKDEAVNKIASLAEIKILTKEMDDEFROSKESLOQSSHL-SEELCTYTELOMKQ 2176
Db 1656 -----ALQUSVQEQVKQYALSLAQLVLEFQOEBKAMYSAELEKQKQ 1700
Qy 2177 QKEDINNKLAEKVEDEHLQHLSLKEQLDQIOMELNREKRLNVELCEKMDIMEKEISV 2236
Db 1701 -----LIAEWKKAENLEKGVISLQECLEBANALDAS----RLTQDLVKEQOIE 1749
Qy 2237 LRLMONEPOQEE-DDVAER-NDILESQNOEIQELMEK-----ISAVYSEQHTLLSSLS 2288
Db 1750 LK-RONELRQEWLDDOVKKMLANSSEKGVKXLMRLFIHFHPKQORHEVLRMGS 1808
Qy 2289 ELQKETEAKHGMNLIKESLSSTLS--RSFGSLQTEHYKLNQLOTLN-KKVVYRTPA 2345
Db 1809 ILGVRREMEBOLFHDDQSVTRKMTGWLGGGKSVNTPPLRPNQOSVANSFSELFVXFL 1868
Qy 2346 VKEDSLIKDYEKDLAEOKRHDELRLQQLCEHGRKMSDSASEE 2391
Db 1869 ETEHSPSIPPEKLSV-----HD-----MKPLDSGKRKRDPINAE 1903

RESULT 11
US-09-820-843A-113
; Sequence 113, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: 063915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 113
; LENGTH: 2354
; TYPE: PRT
; ORGANISM: L. major
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: AC005802_5 L6202.3
; NAME/KEY: misc feature
; OTHER INFORMATION: gi|6899670
US-09-820-843A-113

Query Match 5.6%; Score 821; DB 11; Length 2354;
Best Local Similarity 19.4%; Pred. No. 8.5e-34;

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Matches 514; Conservative 474; Mismatches 1013; Indels 646; Gaps 91;

333 TPVNEVLDDALLKRYKEIILDK-----KOLENSESSETKQAQMAKEEHTOLIA--- 384
 123 SPOPSVSTATLVHVEEDAVSTKPSVEADHLNRSTIIFTLQOLNDEQHNAALAA 182
 385 EIKQLHKEEDRIWHLTNIVASSQ-----ESQODQVKRKRVTAPGKIQNSLAAS 437
 183 AAEQLRTAKEE-----NTALKSTAHLLQORLDTATQORAELEAVARLAADRDEARQOL 236
 438 GUSDPMLSRLPGNFESKKAFSGMPSFPEIDSVCTEFSDPDALSMDSNGIDAMNIA 497
 237 AANAEELQORLDTATQORA-----ELEAVARLAADRDEARQOLAA-----A 279
 498 SKYTHREKTSLHQSMIDFGQISDVQFHDSSKENOLOYLPKDSGMAEGRKSAFEKEITS 557
 280 EELQORLDTATQOR-----AELEAVARLAAD-GDSARQOLAAAE----- 320
 558 LQOQLOSKEEKEKEVOSFELKIA-----ELEBOLSVKAKNLEWNTSREHSINAEVQ 610
 321 LQORLDTATQORAEI-----EAVARLAADRDEARQOLAAAEELQORLDTA-----TQOR 371
 611 TOVEKEVVKEMSVLGDSGMASNSD--LQDSSVDGKRLLSSHDECIERKMLECKIVL 668
 372 AELEAQLARL-----AADRDEARQOLAAAEELQORLDTATQORAELEAVARL 420
 669 BEEFIEIANKSENDKQSEODFMESIQCEAIMAKANAELEALMRNFNIIENET 728
 421 AANAEELQORLDTATQORAELEAVARLAADRDEARQOLAAAEELQORLDT 472
 729 LKREIADLE---RSJKEOETNEFEILEKETQKEHEAOLIHGSLKLVENAEWNYON 784
 473 ATQORAELEAVARLAADGDDEARQ-----OLAAAE-----E 504
 785 LEBEDLETKKLKEQIOIALBELKRADNLQKVRNPDLSVMSGDSKLEBEIIFOLKQOS 844
 505 LQORLDTATQORAELEAVARLAANAELO-----QRD 538
 845 DAEAVTRDAQKECSFIRSENELEKEKEDTSMNWNOKERASLFEKQLETEKSNYKMEA 904
 539 TATQORAELEAVARLAADRDEARQOLAAAEELQORLDTATQORAELEAVARLAANAE 598
 905 DLQKELQSAFNEINYLINGLAG-KVPRDLISRVLEKKVSEFSKQLEKALBEKNALENY 963
 599 ELQORLDTATQORAELEAVARLAADVRD-EARQOLAAAEELQORLDTATQORAELEAV 657
 964 TGLS-----EYKFLPNEVECLKNQJISKASEBEIMLLQOEGHSAIISKQEIIMQESQEI 1018
 658 ARLAADRDEARQOLAAAEELQORLDTATQORAELEAVARLAADRDEARQOLAAAEEL 717
 1019 LQLTDEVTHTQOSKVQOOTEQOYLEMKQMDLFEKYIRNKSSEADLLREMENTLKGTMESVE 1078
 718 QORLDTAT-----QORAELEAVARLAADRDEARQOLAAAEELQORLDTATQORAELE 771
 1079 VKIADTKHELEETTRDKQOLHEKKYFPQAMOTIFPTPLSDSLPPSKLVEGNSQDPIEI 1138
 772 AQLARLAADRDEA---RQOLAAAEELQORLDTA-----TQORAEI 809
 1139 NDYHNILATATERNNIMWCLETERNSLKEGVIDLNTQLOSLQOSIEKSDLOKPKQDLE 1198
 810 E---AQVARLAADRDEARQOLAAAEELQORLDTATQORAELEAV-----VAALAADRE 861
 1199 GEVKLLLEMBELKGHITDSQLSIEKQLENLVEYTEKQLOTLOEBMKITIERNELQTNFED 1258
 862 AAOQOLAAAEELQORLDTATQORAELEAVARLAANAEELQORLDTATQORAELEAVAR 921
 1259 LKAHDSLKQDUSENIEQSTIEQDELRPAQOEELREKQVLDSFRQOLLDCSVIGISSPNHD 1318
 922 LAADRDEARQOLAAAE-----LQORLDT----- 945
 1319 AYAANGKVLGEVNSIQSEMTLGEDELOTSCALYSELELLRAHVKSVEGNETLITTKKL 1378
 946 -TATQORAEI---EAQOLARLAADRDEARQOLAAAELO-----QRLDTA--- 986

1379 NGLKEKELIKGSBESVULKSMLENTKEDNNKLEQ-----AEBYSKENQFSLBEVPSGSOK 1434
 987 -----TQORAELEAVARLAADRDEARQOLAAAEEL-----QQ 1020
 1435 LVDEIEVLKQOLKAAEBELEIKDRPYFELVGTANTNIVGKLEPFLQADHEDSDIDRSE 1494
 1021 RLDTATQORAELEAVARL-AADRDEARQOLAAAEELQORLDTATQ-----QRA 1069
 1495 EMEIKVLEKELERNQYLERLOEBEKLLENKLEILOKEMETSVLKKDLOOKLESLSLEN 1554
 1070 ELEAVARLAADR-----EARQOLAAAEELQORLDTATQORAELEAVARLAADG 1121
 1555 IILKENIDTT-LKHSDDTAQLOKTOEQEOLAKNLAIAASDNCPTIOKETSADCVHP 1611
 1122 DEARQOLAAAEELQORLDT-----ATQORAELEAVARLAADRDEARQOLAAAE-----E 1173
 1612 LEEKILLTEELHQCTNEQEKLLHEKNLEBOAQUELKEVEHIMKSMIESKSLS----- 1667
 1174 LQORLDTATQORAELEAVARLAADRDEARQOLAAAEELQORLDTATQORAELEAVAR 1233
 1668 LOHEKHDTEQOLLA-----LKQOMQVVTQEKKELOQTHHEHLTAEDVHLKENIELGPNFE 1723
 1234 LAADGDDEARQOLAAAEELQORLDTATQORAELEAVARLAADRDEARQ-----QLAAAEEL 1291
 1724 AQOQTTKEQCLINENKELEBOSQHLQCEIIEBLMSL-----KDXESA 1765
 1232 QORLDTATQ-----QRAELEAVARLAANAEELQORLDTATQORAELEAVARLAADRDEA 1347
 1766 LETKESQKVININQOEWMLMEELKNSQRTVIAERDOLQDDLRSEVMSIEFTODL 1825
 1348 RQOLAAAE---LQORLDTATQORAELEAVARLAADRDEARQOLAAAE---ELQORL 1401
 1826 RKAQELAQOQKDVQELTSQISVLQEKISLLENQMLYVNAVYKETLSERDDLQSGOHLF 1885
 1402 DTATQORAELEAVARLAANAEELQORLDTATQORAELEAVARLAADR---EARQOLA 1458
 1886 SEIETLSLKEKEPALQOEKDKADAARKTIDITEK---ISNIEE---QLIQQTNLKE 1939
 1459 ANAEELQORL---DTATQORAELEAVARLAADRDEARQOLAAAEELQORLDTATQORA 1515
 1940 TLVERESLI-----OCKQOLNTEHLRETLKSK-----DLAQKMOERDEANAKYI 1987
 1516 ELEAVARLAADGDDEARQOLAAAEELQORLDTATQORAELEAVARLAADRDEA----- 1570
 1988 ALTERMSLBEQINENVTTLKEGEKETFYLO-----RPSKQSSQSMEEELRESLTKXD 2042
 1571 ---RQOLAAAEELQORLDTATQORAELEAVARLAADGDDEARQOLAAAEELQORLDT-- 1626
 2043 LQLEBAKEISEATNEIKNLTAKISSLEBEILQNASLINEAVSERENLRHSQOLVSELE 2102
 1627 -----ATQORAELEAVARL-----AADRDEAR---QOLAAAE 1657
 2103 QLSLTKSRDHAFAQSKREKEBAVNIASLAEIKILTREMDEFPSKESLQEOSSHSE 2162
 1658 ELQORL-----DTATQORAELEAVARLAADRDEAR-----QOLAAAE 1696
 2163 ELCTYKTELQMLKQOKEDINNKLAEKYVEVDLLOHLSLKEQDLOIQWELNEKLRNVE 2222
 1697 EL---QORLDTATQORAELEAVARLAADGDDEARQOLAAAEEL---QORLDTATQORAE 1750
 2223 LCKEKDIMEKETSVLR-----LMONEQOQEDDYAEMMDLIESNOSTIOELMEKI 2272
 1751 LEVENAVQVLLREBEREARGETAAGVOVQYREVEEBEICKERMWCLIESVQAQLE---A 1806
 2273 SAVYSEQHTLSSLSSELQKETE-HKHCMLNIKESLSSTLSRSGSLQTEHVKNLQTO 2331
 1807 SAAVQOQROEVAKANEVOERLDSWARRCTIAHEGAPQPADRCDALROLANLREBVKIS 1866
 2332 TLINKFKVYVRT-AAVKEDHSLIKDYEKDLAAEQKRHDELRLQLOCLBQHGKMSDQASE 2390
 1867 ---EKQKMERVIIPQVRERQMLE-----AAEBGRAD---LEARLVDBAGDGLRSRPAAS 1914

CURRENT APPLICATION NUMBER: US/09/820, 843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0.
SEQ ID NO: 114
LENGTH: 2310
TYPE: PR1
ORGANISM: L. major
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: AC005893_12 L6202.3
NAME/KEY: misc feature
OTHER INFORMATION: g1|6899664
US-09-820-843A-114

Query Match 5.5%; Score 811; DB 11; Length 2310;
Best Local Similarity 19.4%; Pred. No. 2,76-33;
Matches 475; Conservative 450; Mismatches 926; Indels 596; Gaps 84;

QY 558 LQQQLQSKKEEKEKELVOSFEIKIA-----ELEBQUSVAKNLEWVNSRHSINAAYQ 610
DB 204 LQORLDTATQORAELE-----EAQVARIADADRDEARQOLAAVAEELQORLDTA-----TQOR 254
QY 611 TDVEKEVVRKEMVLDGSGYNASND--LQDSSVDGKRLSSSHDECIEHRKMLEQKIVDL 668
DB 255 AELEAVARL-----AADRDEARQOLAAVAEELQORLDTATQORAELEAVARL 303
QY 669 EEFTEINLKSSENDKOKSSQODPWESIOLCEAIMAEKANAELAL-----MRDNFDNILL 724
DB 304 AANAEELOQRDLDTATQORAELE-----AQALAR-LAADRDEARQOLAAVAEELQORLDTATQ 358
QY 725 ENTLKREIADLERSLKENQETNEFELEKEKTOKEHEAQLIHEIGSL-----KKLVE 776
DB 359 QRAELEAVARLANAAVEELQO-----RLDTATQORAELEAVARLANAADRDEARQOLAA 411
QY 777 NAEMYNQNLSEDELETYKTLKEOEIOLELRKADNLOKKVRFDLSSVSGSEKICEBI 836
DB 412 NAE-----ELQORLDTATQORAELEAVARLANAADR-----QOLANA 452
QY 837 FOLKQSLSDAEAVTRDAQKSCFLRSBENLEKEMEDTSNWNQKKAASLEKQLETERK 896
DB 453 EELQORLDTATQORAELEAVARLANAADRDEARQOLAAVAEELQORLDTATQORAELEAV 512
QY 897 SNVKKMEADLOKELQSAFNEINVLNGLLAKGVRLDSVLEFKKIS-----EPKQOL 949
DB 513 ARLAADRDEARQOLAAVAE-----LQORLDTATQORAELEAVARLANAAVEELQORL 565
QY 950 EKALBEKNALENEVTCLSEYKFLPNEVECLKNQISKASEEIMLLKQEGHSASITSKQEI 1009
DB 566 DTATQORAELEAVARLANA-----NAEELQORLDTATQORAELEAVARLANAADRDEARQ 619
QY 1010 IMQOSEQILQULTDEYVHTQSKYQOTEBQYLEKMKKHNDLFEKYIRNKSEADLLREMEN 1069
DB 620 QLAANAEELOQRDLDTAT-----QORAELEAQLARLANAADRDEARQOLAAVAEELQORLDT 673
QY 1070 LKGTMSVEVKAJADTGHLEBETIRDBKQOLLHKKKYFQAMQOTIFPTLSDBLPSKULVE 1129
DB 674 ATQORAELEAVARLANAADR-----RQOLAAVAEELQORLDTA----- 713
QY 1130 GNSQDPFIEINDYHNTJATATERNNNIMVCLTERNSLKEQVIDLNTQLOSLQASIE-KSD 1188
DB 714 --TQORAELE--AQARLANAADRDEARQOLAAVAEELQORLDTATQORAELEAVARLANAAD 769
QY 1189 LQKPRQDLEBGEVKKLLEWELLKGHITDSQSLSEKQLQLENLEVTETK-----QTOEEMKN 1244
DB 770 GDEARQOLAAVAEELQORLDTATQORAELEAVARLANAADRDEARQOLAAVAEELQORLDT 829
QY 1245 ITIEHNEIQTNPEDLKAHDSLKQD-----SENIQESIETQDLETRA-----QOE 1290
DB 830 ATQORAELEAVARLANAADRDEARQOLAAVAEELQORLDTATQORAELEAVARLANAADDE 889
QY 1291 LREQQLVDSFRQQLLDCSGVIGISSPNHDAVANQEKVSLGEVNSLQSEMLRGERDELQTSQ 1350
DB 1291 LREQQLVDSFRQQLLDCSGVIGISSPNHDAVANQEKVSLGEVNSLQSEMLRGERDELQTSQ 1350

DB 890 AROQLAANAEELOQRDL-----TATQORAELE-----EAQARLANAADRDEARQOL 933
QY 1351 KALVSELEL-----LAAHYKSVGEMLEITTKL-----NGLEKEITLKSESEVYL 1395
DB 934 AANAEELOQRDLDTATQORAELEAVARLANAADRDEARQOLAAVAEELQORLDTATQORAELE 993
QY 1396 KSMLENLKEDNNKLEKQ-----AEYSSKRNQPSLSEVFGSQKLVDEIVLEAOLKAABE 1451
DB 994 EAQARLANAADRDEARQOLAAVAE-----QORLDTATQORAELEAVOYA 1037
QY 1452 RLEIQRDQYFELVQANTNLVVGKLETPLOADHEBDSIDRSEEMEIKVLGEKLERRNOYL 1511
DB 1038 RL-----AANAEELOQRDLDTATQ-----QRAELEAVARLANAADR----- 1072
QY 1512 LERLOEKLELSNKLLEILOKEMETSVLKDDLOQKLESLSENITLKENIDITLKHSDT 1571
DB 1073 -----BARQOLAAVAEELQORLDTATQORAELEAVARLANAAVEELQORLDTATQORAELE 1127
QY 1572 QOQLOK-----TQOELQAKNLIAIASDNCPITQEKETSADCVHPLEEKI 1616
DB 1128 EAQVARIADADRDEARQOLAAVAEELQORLDTATQORAELEAVARLANAADRDEARQOLAAVA 1177
QY 1617 LLLTEELHOKTNEOEKLLHEKNELEQAVLEKCEVEHLKSM-----IESKSSLESLO 1669
DB 1178 -----ELOQR-----DTATQORAELEAVARLANAAVEELQORLDTATQORAELEAQLARLA 1230
QY 1670 HEKHDTBOQLLA-----LKQOMQVVTQOEKKEILOQHNEHLTAEVHDHUKENILEGLNFKNAQ 1725
DB 1231 ADRDEARQOLAAVAEELQORLDTATQORAELEAVARLANAAVEELQORLDTATQORAELEAVAR 1284
QY 1726 QKTTKEQCLLNENKLEQSOHRLQCEIELEMLKSLKXKESALETTKESEOKVININOEWEM 1785
DB 1285 QRAELEAVARLANAADRDEARQOLAAVAEELQORL-----DTATQORAELEAVARL----- 1335
QY 1786 VMLMEHELKNSQRTYIARQDLODDLRBSVMSLETQDDLRKQABALQOQKQXOELTSQ 1845
DB 1336 -----AADGDEARQOLAAVAE-----ELQORLDTATQORAELEAVARLANAAN 1377
QY 1846 ISVLQEKISLENNOMLVAVATVKETLSERDDLNASKOHLFEIEITLSLSEKKEFALQEA 1905
DB 1378 ABELOQRDLDTATQORAELEAVARLANAADR-----BARQOLAAVAEELQORL-----DTATQOR 1431
QY 1906 EKDQADAAKRTIIDTERK-----ISNIEE--QLLQATNLKETTLYERESLI-----QCKEOL 1954
DB 1432 AELEAVARLANAADRDEARQOLAAVAEELQORLDTATQORAELEAVARLANAADRDEARQOL 1491
QY 1955 ALNTEHLRETLKSK-----DLALGKMEQERDGAANKVIALTEKMSLSLEQINENVTYL 2007
DB 1492 AANAEELOQRDLDTATQORAELEAQLARLANAADR-----RQOLAAVAEELQORLDTA 1544
QY 2008 KEQGEKETFYLO-----RPSKQOSSQOMELRESLTKDLOLEAEKEISEATNEIKNL 2062
DB 1545 TQORAELEAVARLANAADRDEARQOLAAVAEELQORLDT-----ATQORAELE 1590
QY 2063 TAKTSSLEBELONASILINEAVSERENLRHSKQOLUSELQSLTLKSRDHAPASQKREK 2122
DB 1591 EAVARL-----AADRDEAR-----QOLAAVAEELQORL----- 1619
QY 2123 DEAVNKIASLAEIEKILTKEMDEFPRDSKESLOESSHLSSELECYTKELQMLKQOKEDIN 2182
DB 1620 DTATQORAELEAQLARLANAADR-----QOLAAVAEEL-----QORLDTATQORAELE 1669
QY 2183 NKLAEKVEYDELLQHLSSLSKEQLODOIQWELRNEKLNVELECKMDIMEKEISVLK----- 2238
DB 1670 AQLARLANAADRDEARQOLAAVAEEL-----QORLDTATQORAELEAVEMAVILREREARGETA 1726
QY 2239 -----LMQNEPOQEEEDVVAERMDILESROQEOLEMEKISAYVSEQHTLSSLSSELOK 2292
DB 1727 VAGBOVOLYRETVVEEELCKEERWCLSESVQOLRE-----ASAAKQOOREVAAKANAEVQ 1782
QY 2293 ETEA-HKGCMLNTKESLSTLSRSPGSLQTEHNYKLTQLOTLNKKFRVVYRT-AAVKEBH 2350
DB 1783 RUDSMARCTAHGSDAPQRADGRDADLRQLANIREEVKLS-----EKQKAMERVLPGVREKQ 1839


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OY 1824 ULRKQOELQOQKDVQVQETQSIQVLOKQISLLEQOMQYVAVQETVETSEDDQNDQSKOH 1883
Db 1470 ALTKSSKQULQVQGNQSKSELQSDQSKQVSKELKQFQEK--YN-----QETISLQDQEIQEKK- 1522
OY 1884 LFSQEIETLSLSKEQEFALQEQAKQKADAKRTIDITIKISQINQEQOLQOQATNLKETLYE 1943
Db 1523 ---EIVTLQOTELKQD---ISEQEKRAMQSENQETVQIKQSDQIKSLQESKINSIKEN--- 1573
OY 1944 RESLIQCEQOLALNQHRLQETLSKQDLQIGKQEQERDA---AKQVQALQEKQSSQEQ 1999
Db 1574 ---HSKQ---ITTHNQKQTSKQODIA--KQSQQHBQAQOTQLEKQENQULQELKQSLQKH 1623
OY 2000 INENVTTLKEGHEQKQETFYLOQPSKQOQSSQOMQELRESLIQTQDQLEAQEKQISEQATNEI 2059
Db 1624 NTQESQTSIQE-----KQNQQLKQELQETIKSLQETKLTQSGALQKQSQQEQY 1666
OY 2060 KQLTKAQISSLEBEILQONQNSILNEAVQSEBQNLHQSKQOQVSELEQSLTLQKSDHQAFQSK 2119
Db 1667 KTLKTKQNSDTE-----SKLEQOQLEBEQKQ-----SDLOQDQEKQLQITQEREQALK 1712
OY 2120 REKQDQVQKQIASLQAEIKILTQEMQEFQDSQKSLQEQSSHSLEQACTQKTELQOMQKQOE 2179
Db 1713 SELETVQKQSGSTQSELTQELQALITQVQSLQEKQELQDQPSQKQSKQELQEDYIQHQSDISEQLK 1772
OY 2180 DINNKLAQKQVQEDQLQHLQSLQKQDQLOQIQLQELNNEKQLQVYQLCEKQDIMEKEI---S 2235
Db 1773 ALTDQLKQKQTKQFQDQSKKQLQTELENDQLSTQKQELQETQKQTSKQFQNLQEQKQDQETQVLNK 1832
OY 2226 VQLRQMQNEPQOQEDQVQARMQDLQERQDQIQELQEMQISQVQS--EQH 2280
Db 1833 EQLQLKQNSQAKKQELQEKQVQSLQES---EQLTSLKQLDQKQSVQMKQH 1876

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Job time : 177 secs